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	MAMMA1001161	4.3	5.27	19.53	18.34	10.8	14.8	
	MAMMA1001162	1.98	1.77	3.16	5.25	5.13	2.25	
	MAMMA1001181	2.44	2.28	4.87	5.06	4.74	3.62	
5	MAMMA1001186	2	2.66	4.66	5.38	5.48	3.9	
	MAMMA1001189	2.23	3.68	7.17	11	11.17	9.9	*
	MAMMA1001191	2.54	2.07	5.49	4.37	3.89	2.97	+
	MAMMA1001198	368.47	416.05	784.82	647.17	738.61	605.52	
10	MAMMA1001202	11.78	11.85	30.06	34.39	28.74	25.16	
	MAMMA1001203	2.57	3.01	7.15	8.72	6.26	5.56	
	MAMMA1001206	1.91	3.28	4.5	3.69	6.66	2.65	
	MAMMA1001208	2.66	2.93	3.31	3.82	4.95	3.19	
	MAMMA1001215	2.9	3.08	6.55	3.49	8.09	4.74	
15	MAMMA1001220	2.63	3.03	7.25	7.16	7.17	6.03	
	MAMMA1001222	1.25	1.18	4.18	2.18	5.85	0.53	
	MAMMA1001223	2.48	3.32	6.53	4.95	6.51	4.1	
	MAMMA1001232	2.82	4.27	8.08	12.22	8.82	9.57	
20	MAMMA1001234	1.25	3.27	3.17	5.05	3.91	3.26	
	MAMMA1001237	1.22	1.56	4.21	1.94	3.66	2.09	
	MAMMA1001243	2.18	2.28	4.06	4.05	4.89	1.99	
	MAMMA1001244	1.22	1.16	2.86	2.96	4.79	2.22	
	MAMMA1001249	2.3	1.89	5.93	5.19	5.8	3.75	
25	MAMMA1001256	3	3.09	8.29	5.89	7.83	8.01	
	MAMMA1001259	4.38	3.25	7.15	7.94	9.24	6.63	
	MAMMA1001260	1.76	2.71	5.42	6.51	5.33	7.33	
	MAMMA1001262	2.1	4.11	5.28	7.86	8.04	6.25	*
	MAMMA1001268	2	2.16	4.59	2.56	4.23	2.48	+
30	MAMMA1001271	4.84	5.78	17.37	18.29	14.24	15.67	
	MAMMA1001274	2.88	3.06	6.17	6.22	8.55	7.93	
	MAMMA1001280	2.09	1.48	4.36	1.84	3.78	1.73	
	MAMMA1001283	1.63	1.71	6.34	6.88	5.63	4.83	
	MAMMA1001284	2.27	2	8.67	5.08	9.09	9.51	
35	MAMMA1001286	13.83	9.72	17.39	12.15	11.83	14.63	
	MAMMA1001289	17.63	13.49	23.32	21.02	26.39	36.8	
	MAMMA1001292	3	3.01	5.94	7.26	6.31	6.85	*
	MAMMA1001296	3.55	3.76	12.61	14.11	12.37	12.8	+
	MAMMA1001298	1.26	1.7	6.26	4.25	6.78	4.07	
40	MAMMA1001305	0.86	1.59	4.43	2.49	4.07	2.63	
	MAMMA1001309	0.61	0.9	2.7	1.84	3	1.49	
	MAMMA1001310	1.72	2.17	3.64	4.81	7.38	4.42	
	MAMMA1001322	0.99	1.54	1.83	2.83	1.77	2.13	
	MAMMA1001324	1.3	1.12	3.16	2.03	2.83	1.94	
45	MAMMA1001330	3.35	2.65	9.53	7.93	9.75	5.36	
	MAMMA1001333	3.1	3.74	10.23	9.88	11.4	9.07	
	MAMMA1001334	5.53	4.17	4.83	10.97	8.23	10.16	**
	MAMMA1001337	2.49	3.54	6.6	6.99	9.16	8.05	*
50	MAMMA1001341	1.21	1.14	3.48	1.54	5.66	1.41	+
	MAMMA1001343	2.37	1.89	8.07	8.17	9.75	10.95	
	MAMMA1001344	9.59	9.07	11.75	13.63	11.67	15.98	
	MAMMA1001346	1.34	1.25	3.9	2.05	3.9	2.94	
	MAMMA1001383	3.07	3.61	8.52	8.3	9.02	9.38	
55	MAMMA1001388	1.62	1.93	5.34	3.38	6.11	4.58	
	MAMMA1001396	4.2	2.12	8.12	11.39	10.42	8.68	

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	MAMMA1001397	2.59	2.27	5.79	8.33	8.96	7.78	*	+
	MAMMA1001401	26.87	16.48	32.72	43.47	57.55	45.66	*	+
5	MAMMA1001408	1.06	1.06	2.57	0.65	4.22	1.19		
	MAMMA1001411	1.65	1.26	3.84	4.38	3.33	3.51		
	MAMMA1001414	3.12	3.85	5.74	12.58	10.67	15.28	**	+
	MAMMA1001415	2.45	3.16	11.93	14.57	20.15	13.69	*	+
	MAMMA1001418	0.66	2.2	5.36	3.57	6.04	4.46		
10	MAMMA1001419	0.8	2.43	4.93	6.03	7.01	3.92		
	MAMMA1001420	0.96	3.09	4.5	3.23	4.11	3.41		
	MAMMA1001426	20.24	32.21	42.42	44.31	39.63	38.75		
	MAMMA1001428	1.94	2.83	6.35	3.8	6.93	4.33		
15	MAMMA1001432	1.19	2.33	8.19	5.62	6.19	6.68		
	MAMMA1001435	1.43	0.78	3.32	3.48	3.67	2.64		
	MAMMA1001442	1.96	3.94	7.41	8.18	8.6	6.63		
	MAMMA1001446	2.17	2.57	6.71	6.9	7.34	7.97		
	MAMMA1001450	1.22	2.05	3.58	2.81	4.18	2.39		
20	MAMMA1001452	1.99	1.78	5.92	8.38	6.19	4.83		
	MAMMA1001465	3.93	3.25	13.61	16.65	14.6	13.82		
	MAMMA1001476	1.63	1.09	4.25	5.87	5.95	4.64	*	+
	MAMMA1001478	2.28	2.12	5.98	3.55	6.27	4.19		
	MAMMA1001479	3.11	4.71	8.32	5.58	6.74	6.21		
25	MAMMA1001487	1.1	1.14	3.84	4.73	3.26	2.08		
	MAMMA1001498	1.93	3.41	7.78	6.17	7.45	5.64		
	MAMMA1001501	0.88	1.97	4.49	2.8	4.77	2.36		
	MAMMA1001502	1.82	1.91	6.48	3.29	6.29	6.26		
	MAMMA1001510	0.48	0.78	2.92	0.54	3.04	1.19		
30	MAMMA1001522	1.03	1.29	3.94	5.05	4.9	3.39		
	MAMMA1001529	0.72	2.06	3.22	3.74	4.07	2.57		
	MAMMA1001532	1.74	1.86	4.27	3.79	5.71	3.12		
	MAMMA1001533	0.61	1.31	2.9	1.52	3.06	1.64		
	MAMMA1001534	0.44	2.59	2.4	1.48	3.64	1.14		
35	MAMMA1001535	1.38	1.91	3.99	2.12	3.98	2.38		
	MAMMA1001547	2.8	2.89	7.77	9.23	8.22	6.22		
	MAMMA1001551	1.1	1.48	4.46	2.23	2.88	2.99		
	MAMMA1001569	1.27	1.68	3.41	2.03	3.41	1.94		
	MAMMA1001575	1.48	2.41	3.42	4.01	4.43	2.81		
40	MAMMA1001576	4.79	8.23	9.65	14.75	9.39	17.03		
	MAMMA1001584	0.89	2.48	3.33	3.11	4	3.09		
	MAMMA1001586	1.43	2.41	3.34	3.78	3.31	1.84		
	MAMMA1001590	2.96	2.53	5.55	5.44	6.47	6.04		
45	MAMMA1001599	4.64	7.15	16.79	15.8	15.18	15.06		
	MAMMA1001600	1.45	2.22	4.73	2.98	4.68	2.11		
	MAMMA1001604	1.03	1.76	3.62	2.35	4.01	1.64		
	MAMMA1001606	1.64	2.04	5.15	3.58	5.45	4.27		
	MAMMA1001609	1.31	2.37	4.36	3.05	5.43	1.59		
50	MAMMA1001614	2.91	3.57	6.15	5.94	6.11	4.14		
	MAMMA1001615	3.98	2.61	10.12	8.87	8.29	8.41		
	MAMMA1001619	7.73	7.8	14.29	16.33	12.93	14.61		
	MAMMA1001620	2.53	2.41	7.98	5.77	7.13	4.54		
	MAMMA1001623	4.11	4.58	9.3	7.34	9.28	6.75		
55	MAMMA1001626	0.83	1.98	2.52	3.24	3.93	1.93		
	MAMMA1001627	1.11	1.98	3.57	2.63	3.68	1.63		



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	MAMMA1001630	2.02	3.08	7.83	7.49	7.53	4.29		
	MAMMA1001633	2.64	3.12	8.8	12.09	9.59	6.16		
	MAMMA1001634	2.83	2.7	6.11	8.69	8.27	6.9	*	+
5	MAMMA1001635	5.65	2.39	9.52	7.92	8.3	8.37		
	MAMMA1001649	1.61	1.63	4.71	2.95	4.62	2.53		
	MAMMA1001654	8.14	9.45	39	43.4	55	46.79		
	MAMMA1001660	19.61	17.92	37.43	40.94	27.03	34		
	MAMMA1001663	1.9	4.73	9.42	9.59	9.56	6.58		
10	MAMMA1001670	1.12	2.66	3.97	3.65	4.09	2.62		
	MAMMA1001671	1.08	1.42	3.56	1.37	4.64	1.77		
	MAMMA1001679	6.85	6.37	13.89	11.48	17.04	13.91		
	MAMMA1001683	2.15	3.29	9.6	6.58	6.53	6.96		
	MAMMA1001686	1.25	1.34	3.77	1.39	2.97	3.06		
15	MAMMA1001688	113.39	113.61	245.56	392.2	458.41	413	**	+
	MAMMA1001689	1.01	3.76	4.1	5.04	3.79	4.44		
	MAMMA1001692	1.97	2.59	5.37	3.66	5.3	3.88		
	MAMMA1001711	1.99	3.64	8.65	4.35	5.51	6.1		
	MAMMA1001715	1.31	1.64	3.95	4.64	4.87	4.13		
20	MAMMA1001730	2.01	2.15	2.5	2.8	4.42	2.83		
	MAMMA1001735	44.73	48.32	102.35	94.99	156.23	119.88		
	MAMMA1001740	0.64	1.6	4.59	2.06	3.91	1.95		
	MAMMA1001743	9.84	11.15	33.16	41.97	51.62	49.6	*	+
25	MAMMA1001744	0.63	0.72	0.86	1.1	1.72	1.71	*	+
	MAMMA1001745	1.41	2.15	6.15	3.27	4.46	3.93		
	MAMMA1001751	1.38	2.41	3.24	2.85	4.51	4.32		
	MAMMA1001752	4.7	4.78	9.75	6.12	9.61	8.4		
	MAMMA1001754	7.25	7.89	7.34	11.04	9.63	9.39	*	+
30	MAMMA1001757	1.21	1.1	2.32	2.21	3.25	2.43		
	MAMMA1001760	3.87	4.52	20.01	22.91	24.2	27.59	*	+
	MAMMA1001764	2.62	2.36	5.97	7.13	10.17	6.51		
	MAMMA1001767	1.22	1.55	2.13	1.61	2.96	1.55		
	MAMMA1001768	0.57	1.18	4.25	4.74	4.72	4.37		
35	MAMMA1001769	2.48	2.83	9.22	9.3	9.81	8.94		
	MAMMA1001771	2.66	1.58	3.74	2.86	5.85	6.77		
	MAMMA1001773	2.7	3.53	3.87	4	6.29	7.61		
	MAMMA1001778	0.88	1.92	3.14	3.13	4.21	3.61		
	MAMMA1001783	2.01	2.1	11.25	11.63	18.46	13.04		
40	MAMMA1001785	3	3.52	8.85	10.56	13.38	11	*	+
	MAMMA1001788	0.49	0.86	1.21	0.72	1.72	1.11		
	MAMMA1001790	1.68	1.67	5.1	2.37	3.73	3.93		
	MAMMA1001800	0.83	0.99	1.47	1.5	2.24	3.25		
	MAMMA1001804	1.02	1.41	3.18	2.37	4.16	2.4		
45	MAMMA1001806	2.13	2.78	6.4	3.15	5.5	4.72		
	MAMMA1001812	1.46	1.33	5.52	4.21	5.86	5.05		
	MAMMA1001815	0.33	1.76	3.07	1.22	3.67	1.24		
	MAMMA1001817	3.19	3.38	9.5	6.78	10.89	13.3		
	MAMMA1001818	1.68	2.08	3.41	3.94	8.52	3.41		
50	MAMMA1001819	2.57	4.12	5.82	8.7	10.29	7.87	*	+
	MAMMA1001820	2.68	4.51	8.27	7.51	10.98	6.07		
	MAMMA1001824	1.66	2.83	8.36	7.55	9.8	7.11		
	MAMMA1001832	6.72	7.99	11.85	20.17	21.28	17.21	**	+
55	MAMMA1001836	1.74	1.66	5.08	4.79	8.19	4.88		

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	MAMMA1001837	2.61	2	5.84	7.1	9.19	5.37		
	MAMMA1001848	1.02	1.61	3.3	2.81	5.33	3.18		
5	MAMMA1001850	3.79	4.51	9.31	9.98	9.93	14.19		
	MAMMA1001851	1.49	2.33	4.98	4.97	4.12	4.02		
	MAMMA1001852	2.98	4	9.68	6.4	7.56	6.8		
	MAMMA1001854	2.56	3.11	9.16	10.59	10.64	9.98		
	MAMMA1001858	3.11	2.22	5.28	9.93	7.91	8.87	**	+
10	MAMMA1001864	1.69	1.91	4.09	8.91	6.18	4.37		
	MAMMA1001868	0.71	0.92	2.64	1.68	2.58	0.91		
	MAMMA1001874	1.2	0.87	2.52	1.06	3.48	1.17		
	MAMMA1001878	3.1	3.46	10.86	7.7	13.37	6.77		
	MAMMA1001880	2.67	2.99	7.24	5.58	7.17	8.12		
15	MAMMA1001885	1.14	1.93	6.19	4.7	5.54	4.58		
	MAMMA1001890	3.54	3.95	12.93	13.59	13.29	12.2		
	MAMMA1001893	3.74	3.42	6.25	6.59	5.49	5.58		
	MAMMA1001901	1.13	1.5	5.4	4.53	5.72	2.67		
	MAMMA1001907	2.57	1.62	6.43	4.15	7.36	6.34		
20	MAMMA1001908	3.2	3.36	8.35	11.83	12.96	12.46	*	+
	MAMMA1001919	0.23	0.97	3.3	2.24	3.9	2.07		
	MAMMA1001931	0.76	1.65	4.04	3.36	5.89	3.25		
	MAMMA1001937	2.27	3.15	5.5	6.44	5.06	3.78		
25	MAMMA1001951	1.74	2.57	6.47	6.48	6.15	4.83		
	MAMMA1001956	3.02	3.48	9.72	8.52	7.66	6.76		
	MAMMA1001957	3.39	3.51	9.15	7.88	9.47	7.66		
	MAMMA1001960	3.1	3.34	7.24	12.06	9.14	6.1		
	MAMMA1001963	0.57	0.78	2.14	1.3	2.36	1.06		
30	MAMMA1001969	1.7	3.43	10.86	8.54	11.14	8.74		
	MAMMA1001970	2.86	3.04	8.48	13.11	6.59	6.64		
	MAMMA1001978	0.57	1.85	1.76	2.42	3.87	1.53		
	MAMMA1001992	2.07	2.04	5.65	6.79	6.75	5.09		
	MAMMA1001994	7.97	3.65	11	18.83	13.23	17.17	*	+
35	MAMMA1002008	3.28	3.77	6.42	3.43	4.06	1.24		
	MAMMA1002009	1.46	2.94	5.17	5.73	7.57	4.06		
	MAMMA1002011	1.77	1.71	4.26	6.5	6.45	3.37		
	MAMMA1002022	1.51	2.1	5.92	6.64	7.42	5.2		
	MAMMA1002024	9.79	9.67	19.03	17.61	16.96	22.43		
40	MAMMA1002032	2.78	2.41	7.25	5.29	6.16	8.07		
	MAMMA1002033	3.23	3.95	7.73	11.24	7.23	6.62		
	MAMMA1002041	2.87	2.25	3.18	4.74	5.39	1.71		
	MAMMA1002042	2.54	2.34	5.66	5.65	5.78	3.76		
	MAMMA1002045	2.33	3.51	7.28	8.39	5.05	4.44		
45	MAMMA1002047	2.58	2.98	8.83	8.7	8.9	6.89		
	MAMMA1002056	2.01	5.78	11.14	11.35	10.64	9.14		
	MAMMA1002058	1.67	2.61	8.19	4.84	4.66	4.27		
	MAMMA1002060	1.08	2.08	1.41	2.5	4.09	1.2		
	MAMMA1002065	1.81	2.75	6.04	7.19	5.19	3.26		
50	MAMMA1002068	2.43	1.84	5.29	4.98	5.6	4.47		
	MAMMA1002070	4.5	2.92	4.15	2.58	5.23	2.81		
	MAMMA1002078	1.32	1.43	2.94	1.12	4.4	1.07		
	MAMMA1002080	7.98	9.71	13.38	14.92	20.84	14.26		
	MAMMA1002082	2.54	4.96	13.04	9.67	8.15	7.78		
55	MAMMA1002084	1.78	3.47	3.38	4.68	4.48	3.6		

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	MAMMA1002087	1.12	2.15	5.37	3.6	4.67	2.36		
	MAMMA1002091	3.79	3.22	4.32	7.18	6.76	6.41	**	+
	MAMMA1002093	0.72	1.4	4.31	2.74	4.39	2.33		
5	MAMMA1002095	2.4	3.22	7.5	4.73	7.52	4.54		
	MAMMA1002108	1.84	1.02	2.63	1.87	3.24	1.31		
	MAMMA1002112	2.94	3.4	7.03	12.79	16.02	11.28	**	+
	MAMMA1002118	1.02	1.61	2.24	1.41	3.18	2.01		
10	MAMMA1002119	0.76	2.15	3.61	1.51	3.12	2.54		
	MAMMA1002125	1.79	2.61	6.95	4.52	4.19	4.11		
	MAMMA1002126	3.72	4.25	9.79	10.08	9.02	11.03		
	MAMMA1002128	0.9	2.36	3.07	2.7	3.49	2.88		
	MAMMA1002132	3.78	3.24	11.42	6.18	9.05	6.81		
15	MAMMA1002140	1.46	1.87	3.68	2.18	3.24	2.33		
	MAMMA1002142	3.13	3.43	7.06	5.18	7.62	5.46		
	MAMMA1002143	5.42	2.27	7.96	7.98	9.87	13.23		
	MAMMA1002145	1.47	1.34	3.3	2.9	4.02	2.64		
	MAMMA1002147	0.81	1.59	2.9	2.71	4.4	3		
20	MAMMA1002153	0.99	1.92	5.55	3.52	6.41	4.75		
	MAMMA1002155	2.11	1.93	6.76	4.4	6.46	4.46		
	MAMMA1002156	0.81	0.8	1.94	0.67	2.63	0.78		
	MAMMA1002158	1.38	1.83	5.12	4.09	7.73	5.2		
	MAMMA1002164	2.01	2.09	5.86	3.17	3.18	4.04		
25	MAMMA1002165	4.04	4.29	7.25	8.65	8.1	6.81		
	MAMMA1002170	1.01	1.48	154.53	2.65	3.24	4.11		
	MAMMA1002174	1.66	2.9	5.88	4.55	7.78	8.58		
	MAMMA1002175	3.27	3.3	7.02	6.95	6.64	7.22		
	MAMMA1002180	8.59	6.53	35.97	55.49	48.49	51.08	*	+
30	MAMMA1002198	3.11	2.3	9.33	7.6	11.22	7.13		
	MAMMA1002205	2.93	1.66	6.15	6.3	8.04	7.54		
	MAMMA1002206	4.6	3.59	8.14	12.4	13.97	11.74	**	+
	MAMMA1002209	1.7	1.93	4.03	4.43	4.23	4.57		
	MAMMA1002215	4.17	2.72	15.2	11.05	12.43	17.14		
35	MAMMA1002219	1.57	1.96	4.99	4.84	6.34	5.96		
	MAMMA1002224	3.18	2.9	8.13	5.49	7.25	5.86		
	MAMMA1002229	3.74	2.21	8.83	8.48	9.26	6.82		
	MAMMA1002230	2.02	2.21	6.63	5.31	8.91	6.58		
	MAMMA1002233	3.01	1.6	6.03	4.21	7.91	6.14		
40	MAMMA1002234	3.05	3.06	6.7	8.6	10.45	10.76	*	+
	MAMMA1002236	4.13	3.68	14.08	26.56	20.38	24.71	*	+
	MAMMA1002243	0.97	2.48	3.48	3.28	3.43	2.96		
	MAMMA1002250	1.06	2.09	5.2	3.95	6.82	6.01		
	MAMMA1002253	2.77	2.39	3.45	4.84	6.18	3.37		
45	MAMMA1002267	17.17	19.95	51.7	130.02	108.53	115.75	**	+
	MAMMA1002268	1.72	2.28	5.82	6.92	11.3	6.52		
	MAMMA1002269	0.89	0.73	2.25	2.32	2.58	1.67		
	MAMMA1002282	0.86	1.09	4.95	5.87	5.31	6.81		
	MAMMA1002292	2.71	2.25	7.77	10.57	10.52	11.53	*	+
50	MAMMA1002293	3.71	3.31	12.31	8.54	10.47	12.05		
	MAMMA1002294	0.9	1.71	4.61	3.68	6.03	4.2		
	MAMMA1002297	1.53	3.25	7.45	5.77	7.8	6.91		
	MAMMA1002298	1.48	1.4	3.98	3.85	3.11	2.46		
55	MAMMA1002299	1.5	1.69	3.16	3.91	2.97	2.2		

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	MAMMA1002308	1.39	1.35	6.55	4.5	3.11	2.54		
	MAMMA1002310	3.56	3.84	12.73	9.92	12.66	11.48		
5	MAMMA1002311	2.52	2.13	6.82	9.61	9.66	6.9	*	+
	MAMMA1002312	1.63	2.22	5.19	3.51	8.45	2.55		
	MAMMA1002317	2.08	2.55	4.89	4.08	3.85	4.09		
	MAMMA1002319	0.8	2.78	3.51	2.68	3.97	2.85		
	MAMMA1002322	2.48	3.23	7.84	12.21	10.02	8.55	*	+
10	MAMMA1002329	1.64	1.67	2.93	2.9	3.3	2.76		
	MAMMA1002332	2.17	2.38	4.58	5.98	4.14	3.05		
	MAMMA1002333	1.7	1.74	4.19	5.35	5.07	3.54		
	MAMMA1002335	1.75	2.72	8.53	6.93	11.32	4.23		
	MAMMA1002339	2.09	2.42	7.34	5.21	7.5	5.14		
15	MAMMA1002347	1.7	2.3	6.39	5.5	5.32	4.64		
	MAMMA1002351	2.08	2.68	5.74	3.03	4.48	4.84		
	MAMMA1002352	1.27	2.28	3.66	3.53	4.63	2.8		
	MAMMA1002353	4.46	2.5	5.84	5.95	4.19	4		
	MAMMA1002355	3.97	3.38	8.37	7.98	7.31	8.57		
20	MAMMA1002356	2.18	1.49	4.36	5.43	4.13	3.75		
	MAMMA1002359	3.95	3.35	16.09	23.81	24.53	19	*	+
	MAMMA1002360	0.93	1.73	3.77	2.48	3.2	1.67		
	MAMMA1002361	2.01	2.64	4.53	4.17	4.95	4.03		
	MAMMA1002362	2.33	2.33	3.36	5.31	5.51	3.99	*	+
25	MAMMA1002367	2.97	3.64	14.63	18.34	21.06	21.56	*	+
	MAMMA1002371	2.28	3.75	8.3	6.15	6.74	5.88		
	MAMMA1002380	1.81	2.26	4.9	4.71	5.76	3.55		
	MAMMA1002384	2.14	1.53	4.73	4.48	5.36	4.05		
	MAMMA1002385	1.19	2.05	5.63	3.34	4.8	2.47		
30	MAMMA1002390	1.41	2.04	3.75	5.48	5.4	3.43		
	MAMMA1002392	1.94	3.1	6.1	4.06	5.95	3.32		
	MAMMA1002396	4.87	3.49	12.87	10.79	12.9	8.08		
	MAMMA1002399	4.42	5.13	10.69	10.95	8.66	4.57		
	MAMMA1002400	3	2.22	4.69	3.11	4.36	3.53		
35	MAMMA1002409	51.57	55.16	63.3	77.54	80.62	77.88	**	+
	MAMMA1002411	1.08	1.88	4.13	3.43	5.49	1.92		
	MAMMA1002413	2.02	3.01	9.19	5.93	7.17	6.75		
	MAMMA1002417	1.83	2.24	4.87	3.45	4.25	2.63		
40	MAMMA1002427	1.5	2.38	4.54	4.78	5.56	3.41		
	MAMMA1002428	2.47	2.26	5.38	4.46	5.11	4.28		
	MAMMA1002433	1.74	2.18	6.84	6.72	6.96	6.22		
	MAMMA1002434	2.94	2.4	7.38	5.34	4.65	5.03		
	MAMMA1002446	1.39	2.34	5.62	3.98	5.84	5.96		
45	MAMMA1002447	2.51	1.38	6.4	5.11	6.26	5.45		
	MAMMA1002454	7.77	9.16	18.07	21.71	17.12	18.35		
	MAMMA1002461	2.06	4.11	7.7	4.92	5.41	6.47		
	MAMMA1002463	3.28	3.32	8.09	6.98	7.82	5.39		
	MAMMA1002464	16.58	16.77	20.05	19.41	20.41	18.09		
50	MAMMA1002466	9.48	9.89	14.22	14.58	15.75	13.93		
	MAMMA1002470	1.39	1.51	5.13	3.54	5.01	3.73		
	MAMMA1002475	0.72	1.85	5.03	3.86	5.17	4.65		
	MAMMA1002480	0.66	1.21	2.31	1.68	2.84	2.03		
	MAMMA1002485	29.98	27.24	46.09	64.83	74.9	80.68	**	+
55	MAMMA1002494	2	2	4.11	4.48	5.12	5.13	*	+

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	MAMMA1002498	0.97	2.57	3.16	2.07	3.18	1.55		
	MAMMA1002524	3.04	2.96	6.43	5.18	7.34	6.1		
	MAMMA1002530	2.5	3.24	4.88	3.17	4.41	2.55		
5	MAMMA1002538	2.34	2.38	5.62	5.46	5.13	4.91		
	MAMMA1002545	2.37	2.64	6.26	4.56	6.49	4.56		
	MAMMA1002554	1.96	1.42	5.43	5.3	6.01	7.81		
	MAMMA1002556	1.3	1.9	3.6	3.73	5.75	3.89		
10	MAMMA1002561	2.3	2.99	7.19	8.13	10.46	7.98		
	MAMMA1002565	1.22	2.15	3.52	2.57	4.51	2.55		
	MAMMA1002566	0.98	1.87	6.21	1.65	4.7	3.9		
	MAMMA1002571	0.53	1.8	3.06	1.43	3.1	4.3		
	MAMMA1002573	2.14	1.86	7.06	4.54	5.66	5.97		
15	MAMMA1002576	118.77	131.84	363.97	348.62	471.73	358.66		
	MAMMA1002584	3.52	2.27	11.91	12.86	17.82	13.46		
	MAMMA1002585	0.76	1.86	4.38	1.85	3.6	5.26		
	MAMMA1002586	1.98	2.55	3.85	4.12	5.02	3.3		
	MAMMA1002589	1.08	1.26	2.44	2.36	5.06	3.19		
20	MAMMA1002590	1.01	1.57	5.87	2.58	6.75	4.57		
	MAMMA1002593	2.48	2.48	4.89	4.18	4.07	3.04		
	MAMMA1002597	2.47	2.52	7.25	8.06	9.48	8.78	*	+
	MAMMA1002598	12.12	13.52	30.83	37.28	48.14	38.91	*	+
	MAMMA1002603	1.2	1.39	3.69	3.25	6.24	4.35		
25	MAMMA1002612	3.51	3.39	12.6	7.66	7.78	9.76		
	MAMMA1002617	4.3	3.41	10.15	6.3	7.29	10.05		
	MAMMA1002618	1.68	2.27	4.02	2.76	3.59	3.91		
	MAMMA1002619	2.96	2.8	5.24	3.22	5.88	3.49		
30	MAMMA1002622	2.51	2.12	8.02	7.1	7.18	7.15		
	MAMMA1002623	2.31	2.21	6.27	5.89	6.17	6.19		
	MAMMA1002625	1.32	1.3	3.23	2.3	6.42	2.6		
	MAMMA1002627	0.98	0.82	2.93	0.6	1.29	0.21		
	MAMMA1002629	1.8	2.23	6.09	5.03	6.74	7.02		
35	MAMMA1002631	1	1.86	3.61	3.07	4.55	2.97		
	MAMMA1002633	6.61	7.44	21.47	19.33	24.55	21.53		
	MAMMA1002636	1.02	2.46	6.97	6.79	8.77	9.25		
	MAMMA1002637	1.05	1.4	4.66	3.39	4.85	4.28		
	MAMMA1002646	1.69	0.8	3.32	2.33	2.86	1.53		
40	MAMMA1002648	10.51	14.07	21.18	42.29	31.45	39.76	**	+
	MAMMA1002650	1.33	0.56	1.62	1.76	2.08	0.57		
	MAMMA1002652	1.76	2.82	7.31	7.5	7.41	9.79		
	MAMMA1002655	1.7	2.11	3.65	2.54	4.23	3.78		
	MAMMA1002662	0.84	2.24	4.33	3.57	5.68	4.13		
45	MAMMA1002665	3.61	3.57	10.05	13.42	17.97	19.59	*	+
	MAMMA1002671	2.84	3.63	10.17	17.04	16.47	19.3	**	+
	MAMMA1002673	1.32	2.14	4.93	4.07	5.03	2.82		
	MAMMA1002684	2.95	3.11	3.84	6.61	8.19	7.54	**	+
	MAMMA1002685	0.68	1.49	2.57	2.05	3.74	2.97		
50	MAMMA1002692	1.28	1.96	5.45	2.46	4.14	3.62		
	MAMMA1002693	1.84	4.18	8	4.63	7.68	6.61		
	MAMMA1002698	0.99	1.91	4.05	2.92	4.42	3.3		
	MAMMA1002699	2	2.35	4.43	4.05	5.22	3.64		
55	MAMMA1002701	2.41	2.56	8.46	6.72	8.94	8.93		
	MAMMA1002708	1.51	1.55	5.38	4.08	6.16	6.18		

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	MAMMA1002711	1.58	2.08	7.04	4.37	7.35	5.81		
	MAMMA1002712	3.05	3.13	6.98	4.88	7.12	7.39		
5	MAMMA1002716	0.56	1.75	3.39	2.38	6.29	2.9		
	MAMMA1002721	2.11	2.01	5.57	3.72	6.34	4.59		
	MAMMA1002723	2.43	2.46	4.91	3.85	5.98	4.88		
	MAMMA1002727	3.85	5.55	5.78	5.29	4.45	6.22		
	MAMMA1002728	21.35	22.03	57.81	49.09	54.73	65.13		
10	MAMMA1002742	4.12	4.39	10.35	7.92	8.63	7.61		
	MAMMA1002743	4.12	3.89	6.17	13.81	14.09	13.46	**	+
	MAMMA1002744	2.07	3.15	9.18	9.33	12.98	13.16		
	MAMMA1002746	0.93	1.28	3.09	2.29	4.31	1.68		
	MAMMA1002748	2.71	2.65	4.52	7.15	5.86	4.72	*	+
15	MAMMA1002754	1.12	2.41	5.56	5.05	5.65	6.26		
	MAMMA1002758	0.71	1.66	2.55	1.57	4.41	1.69		
	MAMMA1002762	11.3	11.14	36.64	38.42	34.23	48.71		
	MAMMA1002764	1.83	3.2	5.95	5.11	6.06	4.26		
	MAMMA1002765	1.19	1.63	4.29	4.63	5.26	2.67		
20	MAMMA1002769	7.4	6.44	13.04	13.78	8.03	12.41		
	MAMMA1002771	1.41	2.41	3.31	3.54	5.39	4.39		
	MAMMA1002775	4.56	4.48	19.79	22.54	29.77	24.29	*	+
	MAMMA1002780	2.59	1.83	3.03	2.11	4.89	3.78		
	MAMMA1002782	1.43	2.49	3.85	2.51	4.79	4.11		
25	MAMMA1002795	1.89	2.03	3.46	6.45	7.68	5.35	**	+
	MAMMA1002796	4.35	3.97	7.51	7.2	8.09	8.17		
	MAMMA1002805	6.61	11.12	16.52	15.95	24.7	16.5		
	MAMMA1002806	1.47	2.02	3.51	2.28	4.62	2.17		
	MAMMA1002807	1.63	2.4	6.77	6.78	9.66	6.4		
30	MAMMA1002814	3.43	3.52	7.92	9.58	12.39	10.66	*	+
	MAMMA1002817	1.28	1.56	2.87	2.89	5.43	2.91		
	MAMMA1002820	1.66	1.93	2.61	2.52	4.77	2.21		
	MAMMA1002830	67.67	70.46	130.59	165.92	139.33	187.18	*	+
35	MAMMA1002833	4.16	2.88	9.4	8.22	10.68	10.58		
	MAMMA1002835	0.77	1.87	4.03	1.73	3.97	2.79		
	MAMMA1002838	1.85	2.66	5.31	2.91	4.44	3.93		
	MAMMA1002842	1	3.83	3.84	3.32	4.63	5.15		
	MAMMA1002843	1.72	2.92	2.33	4.09	4.81	3		
40	MAMMA1002844	3.05	3.64	6.52	5.26	7.3	4.09		
	MAMMA1002845	1.25	1.57	2.45	3.59	3.55	4.67	*	+
	MAMMA1002857	92.1	106.97	208.17	209.17	202.29	249.13		
	MAMMA1002858	317.94	188.78	378.89	560.7	620.76	724.33	**	+
	MAMMA1002863	2.17	2.83	6.91	3.51	5.12	3.96		
45	MAMMA1002868	2.73	3.7	6.26	6.35	9.53	10.25	*	+
	MAMMA1002869	5.43	6.83	26.64	22.68	30.03	29.85		
	MAMMA1002871	0.61	1.7	1.78	1.9	3.8	1.97		
	MAMMA1002875	1.9	2.59	3.99	4.48	6.35	4.06		
	MAMMA1002879	8.42	9.2	14.19	22.55	23.63	27.96	**	+
50	MAMMA1002880	1.23	2.02	2.12	1.48	5.42	2.03		
	MAMMA1002881	1.21	1.43	1.84	3.01	5.43	2.46		
	MAMMA1002885	0.96	1.59	2.71	2.6	3.26	1.59		
	MAMMA1002886	2.63	2.52	3.9	6.01	5.37	7.05	**	+
	MAMMA1002887	1.28	1.83	2.78	2.98	5.14	4.32	*	+
55	MAMMA1002890	0.79	1.7	4.05	4.39	4.8	4.01		

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	MAMMA1002892	1.35	2.45	4.98	6.64	6.24	5.84	*	+
	MAMMA1002893	4.52	3.58	5.4	7.6	8.03	8.43	**	+
	MAMMA1002895	1.43	1.31	3.28	1.81	3.89	1.64		
5	MAMMA1002898	0.53	1.67	4.15	2.69	4.72	1.42		
	MAMMA1002905	1.32	1.58	2.51	4.1	5.01	3.87	**	+
	MAMMA1002906	15.12	10.76	15.42	19.47	13.76	15.58		
	MAMMA1002908	0.99	1.24	4.28	3.53	4.24	4.07		
	MAMMA1002909	1.92	2.64	5.67	6.82	8.18	6.57	*	+
10	MAMMA1002918	2.75	2.69	5.42	5.27	7.26	6.58		
	MAMMA1002925	92.88	85.77	163.7	127.31	122.97	178.98		
	MAMMA1002926	6.08	6.31	16.25	16.64	19.48	19.9		
	MAMMA1002930	1.21	1.59	5.67	4.88	8.91	4.21		
15	MAMMA1002937	4.91	3.87	30.71	40.45	75.17	61.59	*	+
	MAMMA1002938	1.67	1.86	2.42	2.35	3.2	3.56		
	MAMMA1002941	0.49	1.48	2.78	2.53	3.59	2.24		
	MAMMA1002947	2.24	2.59	4.55	6	6.8	7.94	*	+
	MAMMA1002964	1.73	2.9	5.91	6.91	7.24	7.16	*	+
20	MAMMA1002967	1.94	1.59	2.28	2.9	4.19	2.79		
	MAMMA1002970	2.72	1.77	6	7.59	7.28	8.96	*	+
	MAMMA1002971	1.52	1.6	2.9	2.51	7.27	3.93		
	MAMMA1002972	1	1.32	2.95	1.74	4.56	2.12		
	MAMMA1002973	1.38	2.45	6.73	4.36	6.72	6.78		
25	MAMMA1002979	55.6	60.16	121.72	134.02	101.19	107.19		
	MAMMA1002982	0.53	1.98	2.28	2.04	3.28	1.9		
	MAMMA1002987	1.56	2.11	5.56	3.14	5.55	4.14		
	MAMMA1003003	0.77	2.18	4.78	4.46	6.47	5.08		
	MAMMA1003004	1.65	1.86	3.7	3.64	3.59	3.16		
30	MAMMA1003007	0.69	1.16	2.73	1.88	3.7	2.32		
	MAMMA1003011	1.56	1.8	3.67	3.77	5.41	3.94		
	MAMMA1003013	3.67	5.57	39.41	47.56	59.11	54.29	*	+
	MAMMA1003015	1.16	1.8	2.21	2.54	2.9	2.19		
	MAMMA1003019	0.6	1.61	2.1	3.12	4.61	2.63		
35	MAMMA1003020	2.96	4.19	5.34	11.31	10.33	10.09	**	+
	MAMMA1003026	1.29	1.56	2.95	2.66	4.25	2.25		
	MAMMA1003031	0.61	1.71	5.64	4.13	5.85	5.89		
	MAMMA1003033	1.34	1.65	4.13	2.84	5.11	3.64		
	MAMMA1003035	1.66	2.5	5.44	5.12	7.03	4.9		
40	MAMMA1003039	0.95	0.75	3.31	2.15	4.73	2.48		
	MAMMA1003040	1.38	2.54	5.32	4.57	7.47	7.43		
	MAMMA1003044	2.36	2.96	6.52	4.29	6.41	5.99		
	MAMMA1003047	1.82	3.67	7.61	5.74	7.05	7.13		
45	MAMMA1003049	0.47	1.72	2.03	1.08	1.56	1.45		
	MAMMA1003055	1.24	1.67	4.92	3.77	5.14	3.44		
	MAMMA1003056	0.9	0.91	1.85	1.22	2.26	1.02		
	MAMMA1003057	2.53	3.34	6.76	7.25	9.2	5.01		
	MAMMA1003066	1.65	2.06	4.73	4.1	7.08	5.07		
50	MAMMA1003075	1.11	1.71	3.16	1.85	4.37	2.32		
	MAMMA1003089	1.69	2.11	7.13	7.85	8.66	7.43		
	MAMMA1003092	1.25	1.79	3.21	2.62	4.08	1.76		
	MAMMA1003095	2.27	3.33	5.4	7.24	8.57	5.34		
	MAMMA1003099	1.88	2.51	4.95	4.09	6.45	4.35		
55	MAMMA1003102	1.33	2.04	2.88	3.2	3.27	2.39		

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	MAMMA1003104	0.64	1.07	3.17	2.15	3.25	1.56		
	MAMMA1003113	4.22	4.21	6.98	9.22	7.02	7.07		
	MAMMA1003126	12.93	14.72	20.89	19.28	12	15.63		
5	MAMMA1003127	2.95	3.14	5.91	3.88	6.12	5.19		
	MAMMA1003131	2.82	3.51	4.86	3.82	5.91	5.88		
	MAMMA1003135	3.66	4.65	7.61	2.33	4.04	2.64		
	MAMMA1003140	0.73	2.01	3.59	2.3	3.32	1.89		
	MAMMA1003146	2.08	2.24	3.89	3.17	5.09	3.3		
10	MAMMA1003150	1.18	1.8	3.01	3.37	4.29	3.45	*	+
	MAMMA1003154	0.54	1.41	2.29	2.21	3.57	2.34		
	MAMMA1003155	8.08	9.18	20.88	21.41	17.68	20.56		
	MAMMA1003157	5.94	4.82	6.07	5.18	7.05	7.89		
	MAMMA1003163	1.74	1.69	4.23	2.55	5.46	3.08		
15	MAMMA1003164	2.94	4.56	6.23	4.08	9.9	8.18		
	MAMMA1003166	3.62	3.5	5.77	6.24	8.66	6.12		
	NB9N31000010	2.5	3.88	7.58	9.63	12.26	9.5	*	+
	NB9N31000016	0.73	2.8	5.21	4.04	4.41	3.15		
20	NB9N31000043	8.1	8.88	19.71	12.51	12.3	12.64		
	NB9N31000045	167.24	153.32	255.96	401.78	320.53	296.06	*	+
	NB9N31000054	7.29	4.42	11.75	11.15	11.87	13.43		
	NB9N31000076	2.31	1.94	3.51	4.5	6.35	4.44	*	+
	NB9N31000086	2.62	2.65	6.23	3.61	9.71	7.69		
25	NT2RM1000001	2.56	2.45	6.24	5.7	7.05	6.32		
	NT2RM1000018	3.84	4.69	10.6	6.58	9.09	6.92		
	NT2RM1000032	1.12	2.64	3.88	2.28	4.92	3.21		
	NT2RM1000035	1.72	3.68	5.53	5.44	5.21	5.98		
	NT2RM1000037	1.38	2.98	2.75	2.41	4.15	2.11		
30	NT2RM1000039	3.45	5.13	5.9	6.51	7.26	8.4	*	+
	NT2RM1000042	33.96	32.7	65.25	57.46	67.15	64.39		
	NT2RM1000055	0.85	1.74	3.34	1.16	3.55	1.16		
	NT2RM1000059	3.26	3.16	7.66	4.69	5.97	5.78		
	NT2RM1000062	1.13	1.21	1.9	3.47	4.33	2.46	*	+
35	NT2RM1000065	23.8	16.41	34.06	36.15	35.1	51.38		
	NT2RM1000066	4.13	4.31	8.98	7.23	10.95	9.81		
	NT2RM1000071	49.63	37.81	86.71	73.04	63.32	84.05		
	NT2RM1000080	1.37	2.04	3.8	5.1	5.94	4.5	*	+
	NT2RM1000086	4.04	4.65	4.08	5.01	6.23	5.58	*	+
40	NT2RM1000092	6.17	6.93	15.76	14.48	25.91	15.13		
	NT2RM1000118	0.63	1.12	1.22	0.63	1.7	0.44		
	NT2RM1000119	1.32	2.27	1.96	1.84	3.38	2.99		
	NT2RM1000121	1.13	1.84	1.76	2.92	3.84	2.78	*	+
	NT2RM1000122	3.5	3.78	7.34	5.5	8.86	9.57		
45	NT2RM1000127	0.69	1.34	1.47	2.14	3.36	3.32	*	+
	NT2RM1000131	0.71	1.7	1.47	1.36	3.02	2.53		
	NT2RM1000132	3.2	4.88	4.83	6.86	6.46	6.31	*	+
	NT2RM1000153	1.75	1.9	3.68	2.38	4.45	4.84		
50	NT2RM1000184	72.82	77.46	151.91	106.39	163.07	125.55		
	NT2RM1000186	1.55	1.46	4.32	2.67	4.72	3.94		
	NT2RM1000187	3.11	1.96	5.16	10.09	9.1	8.78	**	+
	NT2RM1000199	1.12	1.37	2.11	2.41	3.51	2.72	*	+
	NT2RM1000213	1.32	1.75	2.38	2.66	2.71	2.22		
55	NT2RM1000215	10.95	11.07	17.21	19.51	22.84	15.14		



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	NT2RM1000218	9.72	9.95	23.71	26.94	24.74	29.21		
	NT2RM1000224	8.8	8.63	15.2	15.51	21.29	17.61		
5	NT2RM1000236	30.38	24.19	61.14	72.86	82.44	71.5	*	+
	NT2RM1000242	0.23	1.17	1.32	0.39	2.27	0.12		
	NT2RM1000244	1.41	1.48	3.43	6.9	3.69	6.7	*	+
	NT2RM1000252	1.75	1.5	3.4	3.4	3.06	3.18		
	NT2RM1000256	7.88	5.89	9.46	26.12	29.45	36.8	**	+
10	NT2RM1000257	1.98	3.01	5.09	4.64	6.83	6.65		
	NT2RM1000260	7.9	7.01	13.32	9.18	12.49	11.77		
	NT2RM1000269	3.87	2.87	5.12	6.63	9.78	3.87		
	NT2RM1000271	0.71	0.8	1.87	0.46	2.47	0.51		
	NT2RM1000272	117.67	92.26	202.95	249.32	333.98	356.74	*	+
15	NT2RM1000273	10.03	9.45	20.12	22.32	16.68	15.76		
	NT2RM1000274	63.11	66.41	123.01	137.14	91.97	104.48		
	NT2RM1000280	3.95	4.18	8.18	6.71	8.72	7.93		
	NT2RM1000295	0.49	1	2.2	1.12	3.16	0.87		
	NT2RM1000300	1.51	1.87	2.78	3.63	5.75	3.09		
20	NT2RM1000304	58.38	98.72	161.87	187.58	185.55	204.78	*	+
	NT2RM1000314	1.8	2.12	3.6	3.84	4.07	4.33		
	NT2RM1000318	12.6	14.04	20.81	35.01	29.96	29.8	**	+
	NT2RM1000335	2.76	2.57	4.34	6.29	5.41	4.09		
	NT2RM1000341	0.46	1.27	1.95	1.41	2.33	0.99		
25	NT2RM1000350	3.04	3.47	5.52	7.32	5.63	6.44		
	NT2RM1000354	0.55	1.31	1.31	5.43	7.2	5.72	**	+
	NT2RM1000355	30.24	31.5	56.85	74.62	50.25	61.33		
	NT2RM1000361	3.63	3.87	7.23	14.39	20.29	18.78	**	+
	NT2RM1000365	0.58	1.08	1.71	1.27	1.82	0.52		
30	NT2RM1000372	14.99	19.56	30.06	42.71	46.67	45.44	**	+
	NT2RM1000377	2.04	2.18	9.66	13.38	14.74	13.48	*	+
	NT2RM1000388	0.35	1.57	3.01	2.2	3.8	2.42		
	NT2RM1000394	0.45	1.31	1.87	1.43	2.72	0.69		
	NT2RM1000399	0.53	1.57	3.25	1.98	3.2	1.81		
35	NT2RM1000407	1.13	1.52	2.17	1.02	2.7	1.51		
	NT2RM1000421	0.84	0.57	2.78	1.06	1.77	1.13		
	NT2RM1000422	20.65	23.31	54.69	87.5	82.91	79.47	*	+
	NT2RM1000430	1.22	1.57	2.01	3.2	3.67	2.95	**	+
	NT2RM1000462	1.55	2.33	7.32	5.59	7.28	8.16		
40	NT2RM1000499	1.36	2.09	4.74	5	6.16	6.37	*	+
	NT2RM1000512	12.49	13.22	19.22	10.54	14.15	19.84		
	NT2RM1000519	33.96	37.54	55.78	31.14	29.25	47.55		
	NT2RM1000527	7.97	8.92	37.68	55.15	60.19	46.68	*	+
	NT2RM1000539	3.45	3.59	12.93	15.52	17.01	18.1	*	+
45	NT2RM1000542	0.85	1.05	2.99	1.17	2.35	1.02		
	NT2RM1000553	3.7	2.42	22.32	42.83	42.96	34.5	*	+
	NT2RM1000555	11.3	11.6	23.97	34.11	29.67	22.76		
	NT2RM1000558	2.09	5.34	9.74	9.56	16.24	14.29		
	NT2RM1000563	1.47	2.42	3.36	4.07	5.58	3.95	*	+
50	NT2RM1000566	0.88	1.57	3.5	3.62	6.01	2.79		
	NT2RM1000570	96.92	77.32	137.63	167.35	105.47	174.1		
	NT2RM1000571	13.21	11.87	22.51	43.87	40.18	28.45	*	+
	NT2RM1000574	0.84	2.15	2.55	2.15	3.07	1.67		
55	NT2RM1000580	1.37	2.18	4.07	5.15	7.98	2.96		

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	NT2RM1000620	2.61	2.95	8.2	8.35	9.58	7.26		
	NT2RM1000623	1.25	1.2	2.38	1.75	2.81	0.62		
	NT2RM1000630	0.79	2.28	2.39	1.68	3.51	1.67		
5	NT2RM1000633	30.97	39.36	36.34	54.43	44.6	43.59	*	+
	NT2RM1000634	1.91	4.16	8.12	2.56	7.05	5.57		
	NT2RM1000642	3.85	5.37	8.13	8.21	8.56	8.52		
	NT2RM1000647	41.3	39.09	62.11	57.72	68.29	62.69		
10	NT2RM1000648	2.49	2.65	4.61	6.14	5.63	4.51		
	NT2RM1000650	2.46	3.05	7.6	5.4	6.07	6		
	NT2RM1000661	4.48	5.7	15.82	15.48	13.45	13.18		
	NT2RM1000666	1	1.77	1.99	1.37	2.8	0.71		
	NT2RM1000669	3.51	2.76	4.67	3.63	5.42	3.28		
15	NT2RM1000672	2.23	3.95	7.81	3.98	8.47	7.22		
	NT2RM1000681	99.53	86.09	118.7	105.41	90.59	124.14		
	NT2RM1000691	2.02	2.61	5.74	3.61	7.69	3.76		
	NT2RM1000698	1.11	1.43	4	6.42	6.29	4.11	*	+
	NT2RM1000699	1.85	2.86	3.17	3.67	4.35	4.15	*	+
20	NT2RM1000702	3.71	4.64	9.47	9.31	9.72	11.4		
	NT2RM1000703	11.56	12.36	25.24	26.72	20.42	21.06		
	NT2RM1000704	24.48	23	32.91	46.54	24.13	40.82		
	NT2RM1000725	60.92	59.45	88.28	94.89	82.36	105.67		
25	NT2RM1000726	1.85	2.02	5.75	1.97	4.8	4		
	NT2RM1000731	1.11	2.24	4.98	2.45	3.47	3.43		
	NT2RM1000741	1.38	1.87	3.16	2.69	4.15	2.9		
	NT2RM1000742	2.61	4.6	7.41	9.55	10.94	9.84	*	+
	NT2RM1000744	2.1	3.61	7.14	4.05	5.24	5.05		
30	NT2RM1000746	2.25	2.47	2.95	2.22	4.01	3.89		
	NT2RM1000747	23.34	23.92	46.23	44.66	50.12	55.15		
	NT2RM1000752	3.83	2.36	4.62	3.95	4.88	3.46		
	NT2RM1000767	4.14	7.27	35.27	25.27	38.02	28.81		
	NT2RM1000770	2.97	3.08	6.36	4.71	6.71	5.67		
35	NT2RM1000772	0.76	0.7	1.07	1.34	1.69	0.44		
	NT2RM1000779	13.03	12.11	42.22	53.91	45.61	66.73	*	+
	NT2RM1000780	1.16	2.9	3.74	3.09	4.32	3.01		
	NT2RM1000781	1.07	0.98	1.71	2.58	4.4	1.93		
	NT2RM1000789	5.28	5.15	29.74	29.63	46.72	36.53		
40	NT2RM1000800	2.87	2.63	6.37	5.66	9.57	6.96		
	NT2RM1000802	2.44	2.99	7.5	4.34	5.47	4.82		
	NT2RM1000811	1.78	1.6	2.13	2.26	4.96	2.76		
	NT2RM1000826	6.06	6.36	13.34	14.42	20.73	20.98	*	+
	NT2RM1000829	3.91	2.87	6.39	6.73	8.48	8.41	*	+
45	NT2RM1000831	81.54	64.45	185.14	182.43	179.79	197.27		
	NT2RM1000833	14.58	13.33	42.25	76.74	73.25	67.48	**	+
	NT2RM1000834	4.06	3.09	6.2	8.49	9.42	10.49	**	+
	NT2RM1000841	12.34	10.01	21.15	34.98	36.63	30.81	**	+
	NT2RM1000848	4.79	4.42	6.44	9.36	12.74	10.45	**	+
50	NT2RM1000850	2.66	3.42	13.41	8.55	11.79	9.74		
	NT2RM1000852	1.34	1.94	3.23	3.01	5.76	2.61		
	NT2RM1000853	1.19	2.85	2.15	3.11	3.26	3.23		
	NT2RM1000855	29.27	24.82	45.19	52.48	45.32	58.45		
	NT2RM1000857	4.63	5	10.67	8.76	11.3	10.76		
55	NT2RM1000858	7.3	7.6	15.86	9.09	11.56	10.93		

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	NT2RM1000867	19.42	15.85	28.1	32.52	35.03	24.06		
	NT2RM1000874	3.15	2.65	7.03	5.17	9.62	5.31		
5	NT2RM1000882	2.36	1.37	3.71	5.39	9.31	5.45	*	+
	NT2RM1000883	5.21	3.34	7.42	5.18	11.3	7.9		
	NT2RM1000885	3.86	4.43	9.4	7.59	8.15	9.8		
	NT2RM1000893	3.15	3.41	8.14	7.73	6.17	8.39		
	NT2RM1000894	3.29	4.4	6.18	8.14	6.11	6.61		
10	NT2RM1000898	3.72	7.33	10.02	13.4	17.51	12.41	*	+
	NT2RM1000899	1.02	2.22	3.07	3.68	7.49	4.69		
	NT2RM1000905	11.92	17.41	30.36	37.19	45.16	37.3	*	+
	NT2RM1000910	7.5	8.78	20.16	36.37	36.98	37.5	**	+
	NT2RM1000914	6.46	7.69	19.74	14.28	17.33	17.77		
15	NT2RM1000919	6.1	3.92	9.91	14.61	17.49	15.37	**	+
	NT2RM1000921	0.72	1.9	3.69	2.79	4.27	3.32		
	NT2RM1000922	4.7	6.11	8.09	9.03	5.21	6.36		
	NT2RM1000924	0.89	3.03	3.04	3.08	2.89	3		
	NT2RM1000927	1.35	1.78	2.85	3.07	4.72	3.46		
20	NT2RM1000951	7.95	11.33	26.73	32.33	34.46	31.18	*	+
	NT2RM1000956	7.91	6.36	13.35	23.61	27.46	21.91	**	+
	NT2RM1000960	12.48	10.27	29.06	34.95	37.47	38.96	*	+
	NT2RM1000961	3.28	3.61	7.45	9.44	13.18	8.11		
	NT2RM1000962	4.14	3.5	8.18	7.59	10.15	9.86		
25	NT2RM1000973	16.71	15.79	29.32	31.15	11.56	27.73		
	NT2RM1000978	0.57	1.46	1.58	0.95	2.64	0.44		
	NT2RM1000982	2.34	2.29	3.52	3.57	4.94	4.54	*	+
	NT2RM1000991	1.61	1.78	4.25	3.88	5.56	5.23		
30	NT2RM1000994	6.36	6.16	12.57	16.52	16.64	14.53	*	+
	NT2RM1001002	5.11	6.69	15.34	21.78	22.69	22.28	*	+
	NT2RM1001003	5.42	5.15	11.98	16.24	9.06	8.46		
	NT2RM1001008	1.4	2.22	2.48	1.83	4.34	4.33		
	NT2RM1001011	6.29	5.43	7.86	14.4	10.46	14.72	*	+
35	NT2RM1001013	2.9	2.75	4.75	8.29	7.96	5.81	*	+
	NT2RM1001017	1	1.82	3.44	3.28	4.86	3.92		
	NT2RM1001018	65.15	74.45	146.86	134.65	125.46	113.93		
	NT2RM1001026	1.37	2.64	3.17	2.99	4.61	3.31		
	NT2RM1001028	0.98	1.73	2.91	1.74	1.89	0.76		
40	NT2RM1001043	4.47	3.64	8.42	11.43	12.7	8.01		
	NT2RM1001044	2.23	3.17	4.92	5.03	5.51	3.93		
	NT2RM1001059	1.47	3.72	4.12	4.05	6.11	3.02		
	NT2RM1001063	4.11	3.29	6.1	4.22	5.64	5.6		
	NT2RM1001066	0.86	1.85	2.44	2.23	3.99	2.85		
45	NT2RM1001072	1.8	2.8	4.33	1.94	3.74	1.52		
	NT2RM1001074	1.66	2.38	5.18	5.18	4.19	2.67		
	NT2RM1001076	1.39	2.2	4.94	3.43	4.42	1.72		
	NT2RM1001082	1.79	2.6	5.23	5.31	5.92	4.57		
	NT2RM1001085	1.25	1.65	2.81	1.16	3.27	1.17		
50	NT2RM1001092	3.82	4.2	5.57	9.34	7.94	9.82	**	+
	NT2RM1001102	1.7	2.3	4.4	2.49	5.94	4.64		
	NT2RM1001103	4.37	3.88	7.18	6.25	10.28	8.08		
	NT2RM1001105	1.77	2.02	4.63	2.49	5.11	3.51		
	NT2RM1001112	2.68	2.66	3.69	3.85	4.75	2.43		
55	NT2RM1001115	1.44	1.57	4.72	3	6.46	3.73		

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	NT2RM1001122	2.84	3.35	7.3	9.43	9.75	9.54	*	+
	NT2RM1001136	0.88	1.41	2.71	2.31	3.87	1.59		
5	NT2RM1001139	3.9	3.7	5.38	5.33	11.18	6.77		
	NT2RM2000003	2.45	3.33	2.4	4.5	6.29	4.88	*	+
	NT2RM2000006	2.34	2.95	7.25	5.12	7.11	6.24		
	NT2RM2000010	12.79	13.03	22.53	20.2	17.11	21.83		
	NT2RM2000013	8.1	9.44	50.36	68.75	95.32	74.36	*	+
10	NT2RM2000030	4.8	2.21	23.41	26.33	32.15	28.69		
	NT2RM2000032	2.76	2.92	8.53	10.01	12.19	10.67	*	+
	NT2RM2000039	3.94	4.67	4.75	6.42	5.78	4.99		
	NT2RM2000042	3.5	4.9	11.69	17.71	17.4	15.02	*	+
	NT2RM2000092	1	2.38	1.98	1.29	4.69	2.25		
15	NT2RM2000093	8.37	6.63	11.41	9.02	12.23	10.18		
	NT2RM2000101	9.2	9.94	40	61.09	76.38	69.62	*	+
	NT2RM2000104	6.82	8.02	46.75	51.34	68.83	43.48		
	NT2RM2000124	1.54	2.23	6.33	7.73	8.84	8.47	*	+
20	NT2RM2000155	5.08	3.77	5.8	9.45	11.58	12.51	**	+
	NT2RM2000191	3.33	5.68	28.62	26.54	34.38	31.6		
	NT2RM2000192	1.03	1.29	2.45	6.3	4.75	3.83	*	+
	NT2RM2000239	1.92	2.79	3.09	2.85	5.02	3.1		
	NT2RM2000240	32.78	29.59	74.35	61.15	60.54	61.71		
25	NT2RM2000241	4.49	5.9	6.35	8.24	11.72	6.78		
	NT2RM2000250	1.29	1.54	4.16	2.09	5.05	2.54		
	NT2RM2000259	3.06	3.42	3.59	6.38	8.44	6.74	**	+
	NT2RM2000260	2.53	2.05	3.12	4.23	4.07	5.79	*	+
	NT2RM2000265	0.91	1.55	0.99	1.43	2.4	1.09		
30	NT2RM2000287	4.7	4.23	10.82	10.69	11.54	14.73		
	NT2RM2000306	12.24	9.36	10.48	23.63	14	20.79	*	+
	NT2RM2000312	19.4	17.81	25.01	38.39	31.27	24.8		
	NT2RM2000322	1.93	1.82	4.48	3.79	7.05	3.32		
	NT2RM2000343	7.74	8.38	41.34	63.81	79.6	71.12	*	+
35	NT2RM2000359	3.67	2.86	4.95	4.93	9.55	4.72		
	NT2RM2000362	20.09	18.2	62.29	94.88	111.25	95.66	*	+
	NT2RM2000363	1.08	1.89	2.97	4.2	4.32	3.33	*	+
	NT2RM2000368	2.84	2.4	4.74	6.15	5.98	5.29	*	+
	NT2RM2000371	76.64	65.68	119.32	135.82	125	44.64		
40	NT2RM2000374	1.68	1.92	5.75	3.34	4.8	3.58		
	NT2RM2000387	8.98	9.83	11.92	20.02	25.18	17.11	*	+
	NT2RM2000393	1.7	1.63	3.75	3.31	7.65	3.28		
	NT2RM2000395	1.07	1.51	1.98	1.72	4.34	2.23		
	NT2RM2000402	12.38	11	15.78	25.15	18.31	22.51	*	+
45	NT2RM2000405	1.33	1.25	2.2	1.52	3.08	3.16		
	NT2RM2000407	0.76	1.78	2.49	1.89	2.72	2.89		
	NT2RM2000410	0.79	1.94	2.23	1.98	2.84	2.09		
	NT2RM2000420	3.09	2.52	4.43	4.24	4.5	3.26		
50	NT2RM2000422	3.22	2.44	5.81	3.61	6.17	2.87		
	NT2RM2000423	1.91	1.96	5.69	3.89	7.64	4.18		
	NT2RM2000452	3.46	3.18	4.31	7.35	8.65	9.57	**	+
	NT2RM2000469	3.28	3.28	4.44	1.87	2.33	2.46	*	-
	NT2RM2000490	6.03	6.03	9.18	5.55	6.16	6.9		
55	NT2RM2000497	3.29	3.29	4.59	3.15	5.48	2.43		
	NT2RM2000502	4.69	4.69	10.24	5.87	7.08	7.02		

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	NT2RM2000504	7.37	7.37	12.93	10.83	4.49	11.2	
	NT2RM2000514	2.75	2.75	6.23	3.11	3.32	3.8	
5	NT2RM2000522	1.9	1.9	3.27	1.94	1.18	1.13	
	NT2RM2000540	6.02	6.02	9.53	9.12	8.96	8.14	
	NT2RM2000556	2.09	2.09	2.8	1.24	2.33	0.93	
	NT2RM2000565	3.35	3.35	6.02	3.27	4.14	3.72	
	NT2RM2000566	6.59	6.59	15.8	9.09	9.21	9.57	
10	NT2RM2000567	2.16	2.16	5.64	2	5.67	3.82	
	NT2RM2000569	4.69	4.69	7.93	5.77	8.18	4.7	
	NT2RM2000577	11.08	11.08	15.39	11.79	14.95	14.48	
	NT2RM2000581	4.64	4.64	6.49	5.98	7.97	6.85	
	NT2RM2000582	5.23	5.23	10.34	8.34	9.14	7.19	
15	NT2RM2000588	21.84	21.84	65.91	40.15	44.01	45.21	
	NT2RM2000589	3.98	3.98	11.35	7.96	7.6	8.64	
	NT2RM2000594	1.87	1.87	4.38	1.62	2.71	1.92	
	NT2RM2000599	6.34	6.34	16.12	17.82	14.5	15.44	
20	NT2RM2000609	4.61	4.61	6.77	3.76	5.81	5.48	
	NT2RM2000612	3.52	3.52	6.4	5.93	7.47	4.55	
	NT2RM2000622	16.6	16.6	56.24	53.07	75.02	55.48	
	NT2RM2000623	2.66	2.66	7.1	7.92	6.03	5.58	
	NT2RM2000624	4.18	4.18	10.6	7.33	14.39	7.56	
25	NT2RM2000632	2.8	2.8	6.73	4.1	6.4	4.73	
	NT2RM2000635	3.42	3.42	8.09	5.41	6.29	5.31	
	NT2RM2000636	2.61	2.61	6.28	3.99	4.39	3.72	
	NT2RM2000639	3.73	3.73	8.26	5.42	7.79	5.99	
	NT2RM2000649	6.03	6.03	9.69	9.4	9.17	8.05	
30	NT2RM2000658	6.49	6.49	13.18	15.17	14.66	15.83	* +
	NT2RM2000660	11.45	11.45	18.34	17.03	7.1	20.16	
	NT2RM2000669	3.6	3.6	6.51	5.28	4.28	6.69	
	NT2RM2000689	31.07	31.07	59.7	37.03	16.51	70.9	
	NT2RM2000691	2.09	2.09	5.73	4.83	7.13	4.27	
35	NT2RM2000714	3.41	3.41	10.97	11.46	14.54	11.3	
	NT2RM2000718	4.08	4.08	7.15	2.88	5.42	4.33	
	NT2RM2000732	5.38	5.38	14.81	9.49	14.18	8.25	
	NT2RM2000735	3.72	3.72	6.16	4.27	6.55	6.49	
	NT2RM2000740	2.26	2.26	6.2	4.27	3.01	3.71	
40	NT2RM2000743	2.26	2.26	7.89	5.65	3.24	3.89	
	NT2RM2000772	6.43	6.43	8.48	5.24	6.72	9.47	
	NT2RM2000773	8.17	8.17	19.56	19.18	17.96	18.29	
	NT2RM2000776	13.96	13.96	17.16	24.24	9.95	26.76	
	NT2RM2000784	6.64	6.64	8.8	8.74	9.02	10.5	
45	NT2RM2000795	4.35	4.35	13.56	7.44	8.66	10.45	
	NT2RM2000796	2.27	2.27	4.64	1.71	2.31	1.38	
	NT2RM2000798	25.81	25.81	160.08	158.19	136.83	188.99	
	NT2RM2000801	45.09	45.09	161.29	160.44	152.13	189.56	
50	NT2RM2000821	7.53	7.53	12.33	7.37	7.77	11.87	
	NT2RM2000829	5.76	5.76	13.01	8.05	10.13	11.75	
	NT2RM2000837	3.29	3.29	7.28	4.27	6.08	4.18	
	NT2RM2000924	9.96	9.96	36.74	43.24	57.8	35.84	
	NT2RM2000930	10.64	10.64	18.29	24.45	27.78	28.34	** +
55	NT2RM2000937	4.35	4.35	8.62	5.08	6.66	6.56	
	NT2RM2000939	1.12	1.12	2.37	2.67	1.84	1.82	

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	NT2RM2000942	124.8	124.8	253.61	161.4	118.61	210.11		
	NT2RM2000951	1.01	1.01	2.6	2.13	3.12	1.6		
5	NT2RM2000952	2.53	2.53	5.31	5.98	6.41	6.86	*	+
	NT2RM2000966	19.69	19.69	111.88	95.61	137.32	135.9		
	NT2RM2000973	23.45	23.45	16.81	39.12	39.51	33.8	**	+
	NT2RM2000983	10.07	10.07	18.59	30.68	39.13	27.52	*	+
	NT2RM2000984	6.48	6.48	7.71	4.88	5.64	5.26	*	-
10	NT2RM2000994	8.27	8.27	16.47	13.2	8.36	21.81		
	NT2RM2001004	6.01	6.01	48.58	47.51	54.15	46.8		
	NT2RM2001022	101.09	101.09	350.92	239.63	304.37	490.04		
	NT2RM2001035	10.75	10.75	24.98	24.17	24.54	34.51		
	NT2RM2001038	5.77	5.77	9.86	10.48	11.75	7.9		
15	NT2RM2001043	4.45	4.45	10.02	5.1	7.41	6.74		
	NT2RM2001050	2.71	2.71	6.89	4.72	5.83	4.03		
	NT2RM2001055	3.78	3.78	5.89	4.24	6.31	4.7		
	NT2RM2001065	6.17	6.17	15.91	8.51	12.12	14.21		
	NT2RM2001075	39.81	39.81	188.21	154.65	156.72	168.68		
20	NT2RM2001083	2.23	2.23	5.57	4.01	5.8	3.01		
	NT2RM2001100	10.38	10.38	93.67	95.8	113.9	97.52		
	NT2RM2001105	6.34	6.34	8.27	11.35	5.34	11.8		
	NT2RM2001109	6.81	6.81	9.4	11.88	12.47	14.53	*	+
	NT2RM2001110	7.67	7.67	21.63	21.2	30.71	23.29		
25	NT2RM2001126	6.1	6.1	6.53	5.32	6.44	7.27		
	NT2RM2001131	5.52	5.52	40.22	21.93	29.37	20.14		
	NT2RM2001141	1.64	1.64	6.84	7.09	6.4	5.45		
	NT2RM2001152	1.63	1.63	3.27	4.42	5.77	3.02		
	NT2RM2001177	3.42	3.42	7.23	10.28	7.25	8.24		
30	NT2RM2001194	2.74	2.74	7.51	6.68	5.77	8.17		
	NT2RM2001195	3.7	3.7	8.8	6.37	7.13	6.89		
	NT2RM2001196	5.24	5.24	6.35	5.19	6.46	4.64		
	NT2RM2001201	14.45	14.45	25.36	20.02	21.68	22.38		
35	NT2RM2001221	4.22	4.22	8.61	11.69	13.61	16.63	*	+
	NT2RM2001238	2.87	2.87	5.65	3.91	3.88	1.96		
	NT2RM2001243	5.39	5.39	8.98	9.81	6.13	6.53		
	NT2RM2001244	3.91	3.91	10.63	6.58	9.24	6.41		
	NT2RM2001247	14.94	14.94	121.59	110.47	140.27	118.79		
40	NT2RM2001256	3.84	3.84	5.23	3.15	3.26	2.96		
	NT2RM2001269	4.4	4.4	5.98	4.8	5.63	4.74		
	NT2RM2001278	5.28	5.28	7.37	8.45	8.56	5.35		
	NT2RM2001291	3.05	3.05	5.18	3.24	4.62	2.9		
	NT2RM2001294	12.47	12.47	24.39	20.08	15.43	17.81		
45	NT2RM2001295	2.56	2.56	8.82	4.54	4.43	4.99		
	NT2RM2001302	2.38	2.38	4.55	2.3	4.5	2.81		
	NT2RM2001306	3.51	3.51	7.62	4.1	4.46	5.14		
	NT2RM2001312	2.34	2.34	3.72	1.92	2.84	1.68		
	NT2RM2001319	2.76	2.76	3.93	3.61	5.29	4.11		
50	NT2RM2001324	3.73	3.73	8.29	5.48	4.9	5.71		
	NT2RM2001345	8.53	8.53	10.01	6.83	11.12	14.14		
	NT2RM2001360	4.02	4.02	6.36	5.67	5.9	5.46		
	NT2RM2001370	5.75	5.75	14.53	8.56	9.86	11.69		
	NT2RM2001391	1.79	1.79	6.07	1.85	5.04	1.65		
55	NT2RM2001393	4.49	4.49	6.39	5.12	7.91	7.14		

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	NT2RM2001420	2.94	2.94	4.61	2.61	3.62	3.14		
	NT2RM2001423	5.44	5.44	9.53	8.64	11.95	11.36		
	NT2RM2001424	5.88	5.88	15.09	11.77	10.31	11.63		
5	NT2RM2001482	2.24	2.24	6.48	3.5	6.06	3.63		
	NT2RM2001499	1.4	1.4	5.81	2.84	4.3	2.17		
	NT2RM2001504	3.63	3.63	6.99	3.2	4.54	1.68		
	NT2RM2001524	2.51	2.51	5.81	2.34	2.22	3.51		
10	NT2RM2001530	2.56	2.56	4.42	2.68	4.35	3.52		
	NT2RM2001533	5.06	5.06	9.09	8.2	9.18	7.84		
	NT2RM2001540	5.77	5.77	8.36	14.57	17.99	27.1	*	+
	NT2RM2001544	2.4	2.4	6.12	3.7	3.72	2.31		
	NT2RM2001547	6.6	6.6	15.29	8.44	7.61	8.24		
15	NT2RM2001558	1.53	1.53	3.44	1.76	4.87	1.71		
	NT2RM2001575	2.45	2.45	4.57	3.36	4.38	2.29		
	NT2RM2001582	2.99	2.99	4.98	2.2	5.16	3.06		
	NT2RM2001588	3.69	3.69	8.8	6.39	9.14	6.6		
	NT2RM2001592	2.66	2.66	6.2	3.1	5.24	4.64		
20	NT2RM2001603	4.74	4.74	8.7	10.42	12.03	11.77	*	+
	NT2RM2001605	1.74	1.74	4.52	3.08	1.51	2.39		
	NT2RM2001611	2.28	2.28	8.63	3.74	3.34	3.51		
	NT2RM2001613	14.91	14.91	32.53	21.51	13.13	27.42		
25	NT2RM2001626	2.45	2.45	3.08	2.1	4.28	2.06		
	NT2RM2001632	4.93	4.93	7.07	4.67	4.88	5.42		
	NT2RM2001633	4.45	4.45	10.39	3.74	5.15	5.43		
	NT2RM2001635	4.33	4.33	9.54	4.3	5.81	4.7		
	NT2RM2001636	4.88	4.88	7.35	12.75	18.11	13.34	**	+
	NT2RM2001637	1.25	1.25	6.48	4.18	3.68	2.51		
30	NT2RM2001639	3.98	3.98	9.32	4.67	4.33	3.29		
	NT2RM2001641	1.63	1.63	4.69	4.84	6.02	2.71		
	NT2RM2001643	2.78	2.78	7.46	4.79	4.4	2.83		
	NT2RM2001648	12.97	12.97	18.91	20.13	17.07	25.5		
35	NT2RM2001652	6.32	6.32	5.65	4.29	8.13	4.46		
	NT2RM2001659	5.78	5.78	9.17	5.73	5.28	6.95		
	NT2RM2001660	3.44	3.44	3.86	2.08	2.29	2.63	**	-
	NT2RM2001664	1.24	1.24	6.12	4.51	4.89	4.8		
	NT2RM2001668	3.72	3.72	8.16	7.66	5.72	7.02		
40	NT2RM2001670	1.62	1.62	4.11	2.88	3.96	3.56		
	NT2RM2001671	2.67	2.67	5.57	3.9	6.46	4.85		
	NT2RM2001675	1.94	1.94	4.28	1.97	3.73	0.64		
	NT2RM2001681	2.47	2.47	5.91	3.13	4.64	3.39		
	NT2RM2001685	4.58	4.58	5.68	1.29	2.72	1.14	**	-
45	NT2RM2001688	5.46	5.46	4.14	3.11	3.82	2.46	*	-
	NT2RM2001695	15.09	15.09	35.18	17.41	19.26	34.51		
	NT2RM2001696	2.74	2.74	6.64	7.15	6.7	6.8		
	NT2RM2001698	1.44	1.44	3	4.06	3.49	1.65		
	NT2RM2001699	1.63	1.63	5.03	4.19	3.75	5.48		
50	NT2RM2001700	1.65	1.65	4.13	2.56	3.37	3.91		
	NT2RM2001704	2.68	2.68	5.46	3.89	3.85	3.99		
	NT2RM2001706	4.29	4.29	6.77	3.33	3.13	3.32		
	NT2RM2001714	6.48	6.48	6.64	5.62	7.33	5.18		
	NT2RM2001716	0.97	0.97	3.7	3.03	5.49	2.92		
55	NT2RM2001718	1.91	1.91	3.47	5	3.5	3		

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	NT2RM2001723	2.09	2.09	5.48	5.1	5.21	5.71		
	NT2RM2001727	3.08	3.08	6.25	7.51	7.28	5.7		
5	NT2RM2001730	3.52	3.52	7.15	5.04	5.43	3.85		
	NT2RM2001738	4.56	4.56	6.2	6.71	10.25	9.08	*	+
	NT2RM2001743	2.95	2.95	5.81	4.39	5.02	4.46		
	NT2RM2001753	5.98	5.98	7.55	5.72	6.09	4.54		
	NT2RM2001755	0.89	0.89	2.82	2.4	2.83	2.67		
10	NT2RM2001760	14.77	14.77	33.17	27.49	25.48	36.23		
	NT2RM2001765	1.35	1.35	1.71	2.45	3.12	2.03	*	+
	NT2RM2001767	12.04	12.04	120.66	148.84	168.4	146.29	*	+
	NT2RM2001768	2.1	2.1	3.59	3.41	4.21	3.05		
	NT2RM2001771	4.82	4.82	5.65	7.15	5.97	5.05		
15	NT2RM2001778	2.89	2.89	4.09	2.34	3.24	1.48		
	NT2RM2001782	5.32	5.32	7.32	4.96	7.71	7.57		
	NT2RM2001784	0.84	0.84	2.19	2.81	2.5	1.41		
	NT2RM2001785	1.35	1.35	4.11	5.5	5.02	2.76		
20	NT2RM2001792	6.03	6.03	8.53	5.49	5.54	5.76		
	NT2RM2001795	3.97	3.97	6.15	7.62	5.96	8.9		
	NT2RM2001797	2.82	2.82	3.78	5	5.94	2.71		
	NT2RM2001800	3.46	3.46	4.26	5.01	4.03	5.24		
	NT2RM2001803	3.5	3.5	6.61	4.46	7.34	2.44		
25	NT2RM2001805	3.65	3.65	3.21	2.53	4.2	1.71		
	NT2RM2001806	7.34	7.34	17.96	15.62	15.23	21.11		
	NT2RM2001813	1.54	1.54	2.05	2.54	1.88	2.32		
	NT2RM2001814	2.46	2.46	4.71	3.52	2.89	4.42		
	NT2RM2001818	1.21	1.21	2.66	0.97	1.48	0.27		
30	NT2RM2001823	1.4	1.4	3.24	1.87	2.46	1.37		
	NT2RM2001825	14.79	14.79	36.08	34.68	34.2	35.81		
	NT2RM2001832	5.93	5.93	6.1	5.19	5.48	2.93		
	NT2RM2001839	67.48	67.48	123.46	152.63	157.11	121.35		
	NT2RM2001840	3.04	3.04	7.13	4.61	5.11	5.37		
35	NT2RM2001851	3.92	3.92	7.61	3.78	4.74	6.49		
	NT2RM2001855	8.21	8.21	11.51	10.22	12.06	15.41		
	NT2RM2001867	2.82	2.82	5.01	2.83	5.62	3.74		
	NT2RM2001869	60.8	60.8	90.58	101.19	79.67	105.32		
	NT2RM2001879	3.01	3.01	6.99	2.55	3.19	2.66		
40	NT2RM2001883	1.52	1.52	3.26	0.98	2.28	0.73		
	NT2RM2001886	1.57	1.57	4.56	2.48	3.51	2.42		
	NT2RM2001887	3.78	3.78	7.66	4.48	4.97	5.73		
	NT2RM2001896	274.2	274.2	378.57	325.68	216.52	497.31		
	NT2RM2001902	1.92	1.92	4.28	1.31	2.92	2.14		
45	NT2RM2001903	16.25	16.25	42.55	35.47	31.71	37.22		
	NT2RM2001930	2.11	2.11	6.3	2.3	5.86	5.44		
	NT2RM2001935	4.16	4.16	5.04	3.16	4.42	5.87		
	NT2RM2001936	2.81	2.81	4.9	2.99	3.44	4		
	NT2RM2001939	3.56	3.56	3.34	1.82	3.01	3.16		
50	NT2RM2001941	1.84	1.84	4.29	2.84	2.82	2.72		
	NT2RM2001950	4.66	4.66	10	6.01	6	8.69		
	NT2RM2001952	2.67	2.67	4.78	2.49	4.55	5.37		
	NT2RM2001976	11.48	11.48	18.2	14.58	11.46	35.27		
	NT2RM2001982	1.85	1.85	3.91	2.04	2.47	1.88		
55	NT2RM2001983	4.45	4.45	8.36	4.18	6.49	7.54		



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	NT2RM2001984	7.74	7.74	8.88	20.06	27.05	22.95	**	+
	NT2RM2001989	2.72	2.72	3.68	2.99	4.26	3.7		
	NT2RM2001996	7.51	7.51	8.09	4.8	8.01	5.29		
5	NT2RM2001997	3.65	3.65	7.29	3.18	5.09	6.78		
	NT2RM2001998	2.24	2.24	5.07	3.33	6.53	3.96		
	NT2RM2001999	4.86	4.86	7.69	6.88	6.02	4.01		
	NT2RM2002003	11.33	11.33	18.17	10.15	11	14.9		
	NT2RM2002004	1.99	1.99	5.79	2.51	2.09	1.9		
10	NT2RM2002009	5.35	5.35	9.03	9.85	11.04	11.09	*	+
	NT2RM2002014	2.62	2.62	3	3.65	4.47	4.03	**	+
	NT2RM2002019	25.1	25.1	38.52	19.47	14.2	16.35		
	NT2RM2002029	12.92	12.92	19.01	10.82	4.88	14.74		
15	NT2RM2002030	4.15	4.15	5.8	13.54	9.71	21.98	*	+
	NT2RM2002034	22.05	22.05	31.76	24.83	20.89	21.04		
	NT2RM2002049	7.4	7.4	12.12	9.76	10.42	13.22		
	NT2RM2002055	2.8	2.8	8.01	1.91	4.03	2.52		
	NT2RM2002072	9.26	9.26	12.88	12.28	19.12	12.82		
20	NT2RM2002088	4.82	4.82	13.85	11.35	11.7	15.28		
	NT2RM2002091	4.98	4.98	8.44	5.92	3.82	4.61		
	NT2RM2002100	3.26	3.26	6.05	4.82	4.24	3.19		
	NT2RM2002109	1.31	1.31	3.57	2.57	4.88	4.92		
	NT2RM2002126	21.41	21.41	32.24	35.28	22.31	31.52		
25	NT2RM2002128	3.7	3.7	5.17	2.74	3.86	2.41		
	NT2RM2002129	6.43	6.43	11.48	8.53	13.03	10.66		
	NT2RM2002142	5.72	5.72	9.74	5.26	8.91	6.4		
	NT2RM2002144	3.27	3.27	3.76	1.85	1.73	1.62	**	-
	NT2RM2002145	2.63	2.63	8.69	6.1	5.18	5.98		
30	NT2RM2002153	2.61	2.61	6.37	6.31	7.62	5.75		
	NT2RM2002163	0.97	0.97	3.41	1.87	3.4	0.64		
	NT2RM2002170	3.28	3.28	7.03	6.62	7.5	7.65		
	NT2RM2002178	3.99	3.99	3.67	3.5	5.48	2.9		
	NT2RM2002179	7.82	7.82	8.69	6.17	8.15	6.02		
35	NT2RM2002270	4.51	4.51	4.56	2.28	1.76	1.67	**	-
	NT2RM2002326	2.47	2.47	3.86	2.13	3.69	2.34		
	NT2RM2002337	1.88	1.88	3.97	5.4	4.22	4.79	*	+
	NT2RM2002339	2.83	2.83	6.29	5.26	5.22	3.85		
	NT2RM2002345	5.16	5.16	6.03	4.04	4.2	4.21	*	-
40	NT2RM2002368	2.43	2.43	5.86	6.05	7.01	4.96		
	NT2RM2002381	2.23	2.23	5.16	3.47	3.65	2.8		
	NT2RM2002424	4.64	4.64	7.1	6.69	8.5	6.3		
	NT2RM2002450	4.17	4.17	3.87	2.29	2.39	1.87	**	-
45	NT2RM2002482	3.93	3.93	4.65	2.66	3.2	3.79		
	NT2RM2002492	9.39	9.39	24.31	29.13	24.65	29.29		
	NT2RM2002575	3.26	3.26	5.23	5.99	6.03	5.07		
	NT2RM2002580	4.23	4.23	4.68	4.82	7.79	7.42		
	NT2RM2002592	7.7	7.7	12.59	13.07	15.28	14.69	*	+
50	NT2RM2002608	27.33	27.33	45.49	57.07	65.96	48.3	*	+
	NT2RM2002615	6.01	6.01	9.38	13.15	20.32	14.42	*	+
	NT2RM2002622	14.35	14.35	16.22	18.38	24.99	13.44		
	NT2RM2002630	4.86	4.86	6.63	8.05	7.37	6.7		
	NT2RM2002634	1.72	1.72	4.66	4.71	4.6	3.94		
55	NT2RM2002645	27.02	27.02	68.46	30.66	14.59	31.46		

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	NT2RM2002646	12.09	12.09	25.03	29.45	22.88	34.8		
	NT2RM2002647	7.68	7.68	17.56	19.5	17.74	23.44		
5	NT2RM2002652	5.11	5.11	4.71	4.3	6.43	3.73		
	NT2RM2002692	4.59	4.59	4.48	2.5	2.86	2.02	**	-
	NT2RM2002721	30.26	30.26	46.01	62.71	84.18	61.02	*	+
	NT2RM2002748	18.37	18.37	43.62	87.35	119.27	102.35	**	+
	NT2RM2002764	2.28	2.28	5.3	5.05	5.95	4.07		
10	NT2RM2002772	3.15	3.15	9.32	9.66	7.81	5.44		
	NT2RM2002811	5.79	5.79	12.3	14.01	9.18	10.45		
	NT2RM2002818	2.03	2.03	7.94	5.86	5.42	7.13		
	NT2RM2002879	4.21	4.21	7.17	8.39	7.87	9.11	*	+
	NT2RM2002979	11.79	11.79	19.66	24.49	23.23	21.79	*	+
15	NT2RM2002981	4.42	4.42	3.78	3.58	4.95	2.63		
	NT2RM2002995	5.13	5.13	3.29	3.42	3.74	3.5		
	NT2RM2003031	1.37	1.37	2.63	3	2.58	1.9		
	NT2RM2003042	4.1	4.1	10.77	10.59	6.02	6.07		
20	NT2RM2003044	1.88	1.88	4.11	2.13	5.11	1.2		
	NT2RM2003090	4.4	4.4	7.64	9.36	7.91	10.68	*	+
	NT2RM2003095	11.98	11.98	25.25	15.63	16.43	19.04		
	NT2RM2003116	11.16	11.16	16.09	17.96	21.43	22.08	*	+
	NT2RM2003222	3.98	3.98	3.63	2.67	3.64	2.35		
25	NT2RM2003224	11.29	11.29	15.33	24.29	29.77	20.76	*	+
	NT2RM2003250	14.18	14.18	86.06	85.79	96.6	94.15		
	NT2RM2003258	4.59	4.59	6.32	6.54	5.11	5.69		
	NT2RM2003262	5.07	5.07	7.33	5.06	7.76	5.72		
	NT2RM4000023	2.15	2.15	7.02	3.57	4.91	4.29		
30	NT2RM4000024	2.28	2.28	6.78	3.17	4.98	4.33		
	NT2RM4000027	4.74	4.74	7.77	4.85	6.94	11.32		
	NT2RM4000030	2.95	2.95	5.73	3.16	4.9	2.64		
	NT2RM4000033	2.51	2.51	4.77	2.36	3.89	4.61		
	NT2RM4000034	1.93	1.93	5.35	3.74	4.84	6.09		
35	NT2RM4000046	1.37	1.37	3.79	1.57	3.5	2.32		
	NT2RM4000052	1.82	1.82	3.55	1.72	2.96	1.98		
	NT2RM4000054	10.43	10.43	13.85	12.07	12.83	24.7		
	NT2RM4000061	1.65	1.65	4.17	1.66	4.54	0.83		
	NT2RM4000074	15.83	15.83	43.57	27.9	34.24	30.79		
40	NT2RM4000085	5.35	5.35	10.1	8.41	10.19	10.17		
	NT2RM4000086	3.06	3.06	4.5	3.84	5.25	3.71		
	NT2RM4000100	6.62	6.62	15.05	12.74	15.6	14.84		
	NT2RM4000101	3.77	3.77	9.11	7.17	7.71	8.78		
	NT2RM4000102	32.35	32.35	42.47	27.24	19.34	70.54		
45	NT2RM4000104	2.78	2.78	7.13	3.41	5.12	4.3		
	NT2RM4000115	2.87	2.87	6.1	3.91	5.86	4.08		
	NT2RM4000129	2.17	2.17	4.75	2.62	3.48	2.18		
	NT2RM4000139	3.17	3.17	3.31	3.58	4.82	6.49		
	NT2RM4000149	2.74	2.74	1.49	2.41	2.55	7.32		
50	NT2RM4000155	2.73	2.73	5.5	2.13	4.51	3.71		
	NT2RM4000156	5.94	5.94	16.74	20.45	21	21.96	*	+
	NT2RM4000167	1.36	1.36	2.58	2.61	4.34	1.75		
	NT2RM4000169	9.95	9.95	36.53	29.12	24.89	23.57		
	NT2RM4000191	4.29	4.29	7.56	5.49	5.57	5.66		
55	NT2RM4000197	2.73	2.73	4.78	1.83	3.86	2.2		

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	NT2RM4000198	3.38	3.38	7.42	5.26	5.45	4.21		
	NT2RM4000199	2	2	3.51	2.8	4	3.76		
5	NT2RM4000200	0.67	0.67	3.19	2.25	1.84	1.2		
	NT2RM4000202	1	1	3.24	2.11	2.42	1.84		
	NT2RM4000210	1.46	1.46	3.72	2.41	3.08	2.21		
	NT2RM4000215	2.54	2.54	5.43	3.3	4.09	3.06		
	NT2RM4000220	6.42	6.42	10.52	8.68	11.08	15.14		
10	NT2RM4000229	3.26	3.26	6.62	1.46	2.34	1.76		
	NT2RM4000231	6.37	6.37	7.06	6.13	7.85	6.24		
	NT2RM4000233	4.83	4.83	17.3	11.9	14.34	13.4		
	NT2RM4000244	2.35	2.35	5.22	3.86	4.14	5.17		
	NT2RM4000251	3.85	3.85	10.97	4.82	6.52	4.59		
15	NT2RM4000255	2.28	2.28	4.7	3.79	4.89	1.42		
	NT2RM4000265	2.23	2.23	5.69	4.29	8.21	1.99		
	NT2RM4000283	18.14	18.14	26.21	37.17	39.88	44.79	**	+
	NT2RM4000284	13.85	13.85	33.72	31.96	42.88	40.67		
	NT2RM4000290	6.31	6.31	7.76	3.77	4.92	4	*	-
20	NT2RM4000295	2.36	2.36	2.16	2.32	2.13	0.88		
	NT2RM4000306	3.79	3.79	7.76	7.1	6.14	5.02		
	NT2RM4000307	5.04	5.04	9.13	9.95	9.99	11.72	*	+
	NT2RM4000309	2.48	2.48	5.34	3.92	6.52	5.52		
	NT2RM4000313	3.92	3.92	9.61	5.75	7.77	8.52		
25	NT2RM4000318	3.38	3.38	6.87	4.35	6.36	3.28		
	NT2RM4000324	4.93	4.93	5.93	2.79	4.98	2.12		
	NT2RM4000326	5.32	5.32	4.61	2.59	2.45	2.01	**	-
	NT2RM4000327	4.97	4.97	10.95	7.94	10.32	7.71		
	NT2RM4000344	5.46	5.46	16.67	11.16	10.17	19.18		
30	NT2RM4000349	3.68	3.68	9.99	11.87	10.88	13.8	*	+
	NT2RM4000354	1.65	1.65	3.13	4.2	4.31	3.1		
	NT2RM4000356	1.5	1.5	3.11	2.5	4.07	1.64		
	NT2RM4000366	15.75	15.75	44.48	38.81	44.07	58.06		
	NT2RM4000368	3.04	3.04	5.9	4.36	5.48	3.48		
35	NT2RM4000373	6.49	6.49	12.29	12.72	15.96	16.47	*	+
	NT2RM4000386	4.92	4.92	4.71	3.81	4.57	4.6		
	NT2RM4000395	2.7	2.7	4.69	6.36	6.51	5.68	*	+
	NT2RM4000414	1	1	2.76	2.38	2.9	2.19		
	NT2RM4000417	1.66	1.66	2.83	3.9	3.95	3.25	*	+
40	NT2RM4000421	2.99	2.99	5.17	4.96	5.47	4.13		
	NT2RM4000425	10.56	10.56	26.8	26.49	31.48	45.28		
	NT2RM4000433	2.78	2.78	5.39	1.67	2.21	1.79		
	NT2RM4000436	3.8	3.8	9.47	11.84	16.75	16.38	*	+
45	NT2RM4000444	4.51	4.51	12.97	7.29	8.54	7.38		
	NT2RM4000457	3.35	3.35	8.69	13.35	12.38	13.25	*	+
	NT2RM4000471	1.73	1.73	4.01	4.17	4.87	2.49		
	NT2RM4000472	2.2	2.2	7.62	6.64	7.61	5.39		
	NT2RM4000486	2.98	2.98	5.92	6.85	7.54	6		
50	NT2RM4000490	3.85	3.85	6.41	7.16	5.1	5.86		
	NT2RM4000496	3.68	3.68	3.86	2.16	2.36	2.04	**	-
	NT2RM4000505	26.85	26.85	60.33	68.9	80.59	70.67	*	+
	NT2RM4000511	22.8	22.8	45.35	64.6	89.95	75.97	*	+
	NT2RM4000514	2.61	2.61	6.75	10.47	7.53	9.25	*	+
55	NT2RM4000515	3.75	3.75	8.81	7.27	7.94	4.66		

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	NT2RM4000517	34.51	34.51	74.2	76.45	53.07	79.47	
	NT2RM4000520	2.24	2.24	3.08	3.21	3.3	5.49	
	NT2RM4000531	2.76	2.76	5.71	4.41	5.5	4.22	
5	NT2RM4000532	3.03	3.03	5.56	2.72	3.54	2.39	
	NT2RM4000533	3.55	3.55	5.43	4.73	6.98	3.23	
	NT2RM4000534	5.17	5.17	2.92	2.73	4.62	1.94	
	NT2RM4000563	5.21	5.21	16.69	17.05	16.8	19.36	
	NT2RM4000566	1.79	1.79	4.6	7.14	5.27	7.91	* +
10	NT2RM4000568	10.48	10.48	19.4	28.18	22.91	33.06	* +
	NT2RM4000585	1.97	1.97	2.52	0.82	1.99	1.26	
	NT2RM4000587	3.88	3.88	6.15	6.66	5.75	5.15	
	NT2RM4000590	3.73	3.73	4.12	1.64	2.48	2.3	** -
	NT2RM4000593	4.46	4.46	7.83	10.21	12.36	7.45	
15	NT2RM4000595	3.94	3.94	3.91	2.27	4.36	2.45	
	NT2RM4000603	4.18	4.18	6.98	6.95	7.23	7.26	
	NT2RM4000611	9.81	9.81	18.02	17.1	17.38	25.49	
	NT2RM4000616	2.05	2.05	6.19	2.73	4.14	4.53	
20	NT2RM4000621	26.04	26.04	70.86	57.5	62.2	59.07	
	NT2RM4000648	2.78	2.78	7.83	2.66	2.67	3.88	
	NT2RM4000649	5.53	5.53	11.03	7.34	8.4	13.12	
	NT2RM4000658	3.22	3.22	8.18	4.22	6.14	8.14	
	NT2RM4000661	57.68	57.68	140.68	141.09	135.49	177.49	
25	NT2RM4000673	3.02	3.02	5.72	3.69	3.8	4.59	
	NT2RM4000674	2.23	2.23	4.27	2.89	2.63	2.99	
	NT2RM4000689	3.81	3.81	6.47	5.34	6.36	7.74	
	NT2RM4000698	14.85	14.85	20.92	25.12	23.66	26.39	* +
	NT2RM4000700	2.39	2.39	5.53	2.41	6.95	5.61	
30	NT2RM4000701	10.07	10.07	54.36	61.81	67.75	63.17	
	NT2RM4000712	3.5	3.5	7.9	5.97	8.03	9.55	
	NT2RM4000717	2.14	2.14	6.66	3.67	2.94	4.3	
	NT2RM4000733	4.37	4.37	7.8	4.16	6.93	11.03	
	NT2RM4000734	2.17	2.17	5.92	2.35	5.23	4.7	
35	NT2RM4000741	2.14	2.14	6.11	3.59	4.75	4.66	
	NT2RM4000744	1.76	1.76	7.05	2.76	4.4	10.18	
	NT2RM4000749	15.53	15.53	23.13	26.26	27.8	34.67	* +
	NT2RM4000751	2.88	2.88	6.54	6.23	6.11	5.94	
	NT2RM4000752	4.11	4.11	4.88	4.78	5.12	38.58	
40	NT2RM4000760	3.5	3.5	9.69	4.54	6.31	5.26	
	NT2RM4000761	237.9	237.9	478.3	219.65	302.54	336.34	
	NT2RM4000764	66.05	66.05	178	212.33	205.98	232.75	* +
	NT2RM4000768	6.11	6.11	11.21	15.56	10.14	21.17	
45	NT2RM4000778	1.6	1.6	4.7	4.27	5.18	6.18	
	NT2RM4000779	4.52	4.52	8.28	6.87	7.19	7.33	
	NT2RM4000787	2.55	2.55	7.49	3.64	4.9	4.53	
	NT2RM4000790	2.99	2.99	5.03	5.47	5.82	12.06	
	NT2RM4000795	1.99	1.99	3.67	2.36	1.2	2.51	
50	NT2RM4000796	3.26	3.26	5.86	4.29	3.48	4.28	
	NT2RM4000798	1.77	1.77	5.53	3.72	3.08	3.47	
	NT2RM4000800	4.15	4.15	8.16	8.7	9.44	9.06	
	NT2RM4000813	3.31	3.31	8.79	7.14	7.95	10.09	
	NT2RM4000820	4.89	4.89	9.14	5.39	6.27	5.44	
55	NT2RM4000827	7.1	7.1	18.55	16.3	15.8	17.88	

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	NT2RM4000830	3.27	3.27	7.35	5.28	7.8	8.38	
	NT2RM4000833	2.51	2.51	6.84	4.48	3.35	4.87	
	NT2RM4000841	4	4	15	10.57	8.84	10.1	
5	NT2RM4000846	1.66	1.66	8.83	4.74	6.83	5.09	
	NT2RM4000848	2.61	2.61	5.75	4.15	6.32	3.12	
	NT2RM4000852	3.89	3.89	9.81	8.16	8.67	8.29	
	NT2RM4000855	5.12	5.12	7.64	5.99	6.08	7.19	
10	NT2RM4000859	11.18	11.18	16.28	16.48	19.12	17.62	
	NT2RM4000868	3.06	3.06	6.47	5.23	6.91	7.05	
	NT2RM4000870	4	4	9.82	7.06	3.87	6.59	
	NT2RM4000879	1.67	1.67	6	4.15	3.31	3.11	
	NT2RM4000882	18.99	18.99	28.36	20.33	16.5	12.55	
15	NT2RM4000887	2.16	2.16	6.01	3.53	4.91	1.6	
	NT2RM4000895	2.33	2.33	5.33	3.16	5.9	3.08	
	NT2RM4000897	5.78	5.78	6.99	8.89	9.73	7.02	
	NT2RM4000901	5.22	5.22	6.41	4.37	6.2	6.12	
	NT2RM4000950	4.04	4.04	5.09	3.57	4.06	2.91	
20	NT2RM4000965	2.89	2.89	4.54	5.98	4.04	6.18	
	NT2RM4000971	2.49	2.49	4.78	4.84	4.29	7.62	
	NT2RM4000979	5.16	5.16	12.71	10.23	10.46	7.87	
	NT2RM4000987	1.9	1.9	4.59	3.64	4.22	3.21	
	NT2RM4000989	2.51	2.51	5.17	4.2	5.16	4.99	
25	NT2RM4000991	3.1	3.1	4.83	2.87	3.53	8.73	
	NT2RM4000992	3.39	3.39	5.41	3.6	4.54	3.19	
	NT2RM4000996	6.22	6.22	7.86	7.14	8	7.28	
	NT2RM4000997	3.53	3.53	13.96	9.81	10.96	10.89	
	NT2RM4001001	26.06	26.06	55.43	37.67	34.22	54.29	
30	NT2RM4001002	5.13	5.13	11.03	11.54	11.33	19.44	
	NT2RM4001016	1.63	1.63	2.73	4.07	5.31	3.76	*
	NT2RM4001025	65.77	65.77	133.97	148.39	181.87	171.5	* +
	NT2RM4001027	2.49	2.49	3.66	1.67	1.77	4.31	
	NT2RM4001032	2.55	2.55	6.74	4.94	5.46	3.84	
35	NT2RM4001047	3.87	3.87	3.7	2.61	2.73	2.7	** -
	NT2RM4001049	3.97	3.97	10.12	18.29	20.63	26.25	** +
	NT2RM4001051	2.72	2.72	12.54	11.17	10.12	13.68	
	NT2RM4001052	14.95	14.95	72.14	75.49	75.01	79.12	
	NT2RM4001053	14.96	14.96	39.3	41.36	28.95	25.87	
40	NT2RM4001054	3.13	3.13	5.17	5.34	5.69	5.01	
	NT2RM4001059	3.65	3.65	6.37	4.91	3.52	4.48	
	NT2RM4001071	4.03	4.03	7.35	6.8	7.34	6.55	
	NT2RM4001084	8.04	8.04	6.52	9.49	10.53	9.53	* +
45	NT2RM4001092	12.61	12.61	109.97	76.93	98.78	73.14	
	NT2RM4001100	6.72	6.72	20.93	22.35	15.18	18.98	
	NT2RM4001116	1.17	1.17	2.5	2.77	2.96	2.16	
	NT2RM4001119	1.74	1.74	4.82	4.72	4.22	4.15	
	NT2RM4001140	2.65	2.65	7.49	8.27	7.78	9.03	
50	NT2RM4001148	6.59	6.59	13.68	12.1	12.92	15.83	
	NT2RM4001151	3.7	3.7	4.31	1.94	3.65	1.68	
	NT2RM4001155	5.51	5.51	6.36	3.55	5.37	4.63	
	NT2RM4001157	1.68	1.68	4.95	4.86	2.81	3.82	
	NT2RM4001160	1.57	1.57	3.39	2.99	1.9	2.41	
55	NT2RM4001163	42.35	42.35	86.27	106.63	52.13	98.56	

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	NT2RM4001187	2.64	2.64	7.25	3.96	4.87	5.2
	NT2RM4001191	3.2	3.2	9.95	8.59	6.36	8.72
5	NT2RM4001200	3.83	3.83	6.35	5.52	4.41	4.11
	NT2RM4001203	9.93	9.93	20.29	22.65	25.36	21.82
	NT2RM4001204	3.23	3.23	3.59	3.17	2.83	2.6
	NT2RM4001217	4.62	4.62	12.16	11.26	13.39	13.72
	NT2RM4001245	7.31	7.31	17.14	13.76	14.49	17.16
10	NT2RM4001247	3.23	3.23	9.1	5.73	6.57	5.03
	NT2RM4001256	2.51	2.51	6.39	3.57	5.48	4.14
	NT2RM4001258	8.2	8.2	24.68	25.02	24.16	22.89
	NT2RM4001267	3.43	3.43	4.83	3.93	4.3	8.08
	NT2RM4001273	4.23	4.23	8.38	7.39	6.96	8.77
15	NT2RM4001281	4	4	10.54	10.15	9.05	10
	NT2RM4001286	345.27	345.27	526.77	215.2	220.51	552.53
	NT2RM4001290	23.51	23.51	61.5	56.51	48.6	59.58
	NT2RM4001309	2.64	2.64	6.81	3.17	5.42	4.05
	NT2RM4001313	2.63	2.63	8.62	3.81	6.36	7.03
20	NT2RM4001316	3.14	3.14	6.12	3.39	3.85	5.25
	NT2RM4001320	2.4	2.4	6.43	2.83	3.16	5.6
	NT2RM4001321	3.98	3.98	8.62	6.17	7.03	6.24
	NT2RM4001325	2.54	2.54	5.2	4.76	2.93	5.25
	NT2RM4001333	8.65	8.65	18.06	8.57	10.76	9.51
25	NT2RM4001340	4.81	4.81	12.27	6.99	7.72	11.24
	NT2RM4001344	4.09	4.09	4.69	3.04	3.44	4.93
	NT2RM4001347	6.49	6.49	9.8	10.53	9.72	17.71
	NT2RM4001357	7.59	7.59	12.09	8.58	11.68	9.37
	NT2RM4001360	2.79	2.79	5.11	3.82	2.85	3.07
30	NT2RM4001371	4.71	4.71	8.57	6.58	13.16	12.93
	NT2RM4001377	8.01	8.01	13.74	8.66	9.23	10.58
	NT2RM4001382	17.31	17.31	56.74	35.57	28.32	38.22
	NT2RM4001384	2.17	2.17	4.11	2.35	3.34	3.75
	NT2RM4001400	3.78	3.78	5.76	4.87	4.66	5.07
35	NT2RM4001409	2.55	2.55	6.82	4.82	4.63	5.27
	NT2RM4001410	5.48	5.48	21.69	17.34	21.09	18.91
	NT2RM4001411	2.66	2.66	6.5	5.86	6.64	6.77
	NT2RM4001412	1.75	1.75	3.33	2.39	2.52	2.79
	NT2RM4001414	2.18	2.18	4.83	2.45	2.4	3.77
40	NT2RM4001436	8.35	8.35	16.65	10.45	10.13	15.55
	NT2RM4001437	2.77	2.77	8.85	8.31	11.26	7.67
	NT2RM4001444	11.57	11.57	25.93	21.1	18.36	18.42
	NT2RM4001454	3.62	3.62	7.89	6.16	5.03	4.79
45	NT2RM4001455	5.85	5.85	22.19	18.03	25.08	26.16
	NT2RM4001483	4.37	4.37	8.77	4.97	5.43	6.46
	NT2RM4001489	3.12	3.12	7.04	3.64	4.19	5.46
	NT2RM4001495	1.35	1.35	5.13	2.85	3.29	3.37
	NT2RM4001499	1.74	1.74	4.98	3.65	2.77	3.3
50	NT2RM4001515	0.95	0.95	3.38	2.65	5.38	3.41
	NT2RM4001519	1.86	1.86	4.6	2.24	4.38	2.85
	NT2RM4001522	3.8	3.8	7.66	5.36	7.42	9.13
	NT2RM4001523	5.46	5.46	9.11	4.82	7.58	5.79
	NT2RM4001550	11.9	11.9	17.38	16.49	16.76	15.01
55	NT2RM4001553	7.88	7.88	13.4	23.26	23.53	23.87 ** +

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	NT2RM4001554	0.86	0.86	1.74	1.85	1.11	2.2		
	NT2RM4001557	2.5	2.5	6.33	5.05	3.36	4.89		
	NT2RM4001565	1.87	1.87	4.05	2.46	3.34	3.23		
5	NT2RM4001566	3.23	3.23	8.57	8.91	10.49	11.42		
	NT2RM4001569	1.47	1.47	5.4	3.35	4.15	1.56		
	NT2RM4001579	6.57	6.57	16.69	19.23	23.83	18.22		
	NT2RM4001582	4.06	4.06	5.97	2.16	3.17	2.67	*	-
10	NT2RM4001589	21.51	21.51	37.16	42.45	55.76	47.57	*	+
	NT2RM4001592	1.37	1.37	2.96	3.02	2.14	3.71		
	NT2RM4001594	1.98	1.98	4.09	5.4	5.24	5.67	*	+
	NT2RM4001597	2.65	2.65	5.64	5.17	4.97	4.33		
	NT2RM4001605	2.7	2.7	6.18	5.71	5.92	5.93		
15	NT2RM4001609	23.65	23.65	45	61.08	78.89	77.31	*	+
	NT2RM4001610	48.1	48.1	69.16	132.54	132.39	115.22	**	+
	NT2RM4001611	3.31	3.31	4.56	2.33	2.32	2.02	*	-
	NT2RM4001618	7.05	7.05	7.95	6.68	8.98	12.95		
	NT2RM4001622	13.53	13.53	19.88	14.67	24.67	28.46		
20	NT2RM4001624	1.6	1.6	3.02	3.92	2.66	4.43		
	NT2RM4001625	4.89	4.89	39.6	41.63	47.1	46.46		
	NT2RM4001629	3.82	3.82	8.82	12.09	12.08	13.38	*	+
	NT2RM4001632	15.28	15.28	24.55	31.07	26.16	25.6		
	NT2RM4001642	3.29	3.29	4.17	2.89	3.62	2.1		
25	NT2RM4001647	4.44	4.44	6.83	4.04	5.48	4.67		
	NT2RM4001650	4.96	4.96	4.94	2.66	2.87	3.79	**	-
	NT2RM4001662	2.18	2.18	5.47	8.31	6.54	9.39	*	+
	NT2RM4001666	2.28	2.28	6.5	6.24	6.17	8.14		
30	NT2RM4001670	3.52	3.52	10.77	11.16	10.82	14.91		
	NT2RM4001682	12.66	12.66	31.6	33.03	26.04	37.07		
	NT2RM4001710	6.7	6.7	38.5	40.58	58.41	40.31		
	NT2RM4001712	4.06	4.06	7.61	10.19	10.7	9.98	*	+
	NT2RM4001714	10.88	10.88	19.37	18.67	19.3	17.65		
35	NT2RM4001715	10.77	10.77	11.6	13.55	16.86	12.99		
	NT2RM4001727	3.41	3.41	5.92	4.83	5.89	7.6		
	NT2RM4001731	2.6	2.6	10.72	13.46	11.23	11.73		
	NT2RM4001735	12.84	12.84	21.53	22.01	20.88	34.93		
	NT2RM4001739	2.46	2.46	7.3	8.13	5.17	7.14		
40	NT2RM4001741	14.41	14.41	29.88	26.98	27.21	32.35		
	NT2RM4001746	3.65	3.65	6.76	6.89	6.5	5.33		
	NT2RM4001754	3.16	3.16	4.17	3.39	3.62	3.84		
	NT2RM4001757	5.02	5.02	5.78	4.7	6.31	7.97		
	NT2RM4001758	1	1	0.76	1.98	0.65	1.46		
45	NT2RM4001768	4.83	4.83	10.19	8.48	6.91	7.83		
	NT2RM4001775	3.23	3.23	2.76	1.9	1.85	1.71	**	-
	NT2RM4001776	2.56	2.56	4.77	2.47	2.68	2.69		
	NT2RM4001783	2.88	2.88	3.22	3.12	3.48	3.68		
	NT2RM4001793	4.67	4.67	11.44	12.02	9.6	10.75		
50	NT2RM4001810	3.31	3.31	4.46	3.33	3.63	3.11		
	NT2RM4001813	3.9	3.9	4.15	4.71	4.19	5.36		
	NT2RM4001818	4.06	4.06	11.34	10.43	8.67	10.53		
	NT2RM4001819	2.35	2.35	5.6	2.37	3.02	4.58		
	NT2RM4001823	1.76	1.76	4.48	2.47	4.04	4.27		
55	NT2RM4001828	5.01	5.01	11.49	5.67	7.54	7.51		

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	NT2RM4001835	9.75	9.75	18.65	21.12	16.5	26.55		
	NT2RM4001836	3.27	3.27	8.32	3.65	3.54	5.58		
5	NT2RM4001841	7.94	7.94	15.82	20.15	20.96	23.33	*	+
	NT2RM4001842	2.1	2.1	4.44	3.5	3.35	4.85		
	NT2RM4001843	5.65	5.65	14.54	13.34	12.25	14.94		
	NT2RM4001856	4.42	4.42	7.16	7.65	4.71	16.83		
	NT2RM4001858	5.91	5.91	15.86	16.09	17.03	16.93		
10	NT2RM4001861	2.91	2.91	9.57	6.31	8.66	9.28		
	NT2RM4001863	8.06	8.06	9.5	15.16	15.68	11.77	*	+
	NT2RM4001865	5.04	5.04	11.25	7.44	10.24	9.03		
	NT2RM4001869	5.1	5.1	5.96	5.22	8.45	21.88		
	NT2RM4001873	9.62	9.62	18.43	13.33	15.49	19.21		
15	NT2RM4001876	2.24	2.24	6.94	3.65	4.39	7.25		
	NT2RM4001880	3.6	3.6	8.57	5.13	5.41	7.67		
	NT2RM4001885	5.71	5.71	11.11	7.11	6.56	11.98		
	NT2RM4001889	10.25	10.25	18.24	16.31	15.85	21.33		
	NT2RM4001894	2.61	2.61	6.07	3.58	3.65	3.49		
20	NT2RM4001897	7.87	7.87	20.24	18.41	20.4	23.46		
	NT2RM4001899	3.36	3.36	7.43	4.92	8.19	8.54		
	NT2RM4001905	3	3	4.84	3.3	4.53	7.1		
	NT2RM4001922	2.55	2.55	6.05	3.97	4.84	5.11		
25	NT2RM4001930	2.64	2.64	8.9	2.88	6.53	6.38		
	NT2RM4001938	2.65	2.65	4.91	5.09	5.65	6.43		
	NT2RM4001940	2.73	2.73	6.17	5.91	4.46	5.48		
	NT2RM4001942	37.36	37.36	32.02	53.86	59.28	82.77	*	+
	NT2RM4001953	4.65	4.65	9.68	5.04	6.79	4.91		
	NT2RM4001965	4.96	4.96	8.82	10.18	8.54	8.39		
30	NT2RM4001966	3	3	5.14	6.3	7.45	8.19	*	+
	NT2RM4001969	2.22	2.22	7.29	5.01	2.95	4.5		
	NT2RM4001974	1.19	1.19	4.61	1.89	2.96	4.83		
	NT2RM4001979	2.09	2.09	6.37	3.39	4.65	7.36		
35	NT2RM4001980	4.3	4.3	7.59	7.58	8.02	9.33		
	NT2RM4001984	2.31	2.31	5.36	2.68	3.49	4.57		
	NT2RM4001987	3.36	3.36	9.66	2.92	4.6	5.01		
	NT2RM4002013	6.62	6.62	15.13	13.47	17.16	19.8		
	NT2RM4002018	2.31	2.31	5.15	4.09	5.53	7.1		
40	NT2RM4002033	3.19	3.19	8.16	4.91	3.27	5.93		
	NT2RM4002034	1.89	1.89	6.19	4.82	4.38	4.03		
	NT2RM4002044	7.71	7.71	17.9	18.75	12.3	18.5		
	NT2RM4002047	3.88	3.88	5.19	2.68	5.38	9.2		
	NT2RM4002054	4.54	4.54	6.97	2.56	4.3	3.89		
45	NT2RM4002055	13.72	13.72	74.75	60.51	91.27	61.53		
	NT2RM4002059	23.73	23.73	31.85	48.05	63.09	52.61	**	+
	NT2RM4002061	3.72	3.72	5.32	3.59	3.69	4.81		
	NT2RM4002062	1.9	1.9	5.41	3.66	2.84	4.26		
	NT2RM4002063	2.21	2.21	8.1	7.64	7.35	3.79		
50	NT2RM4002066	2.07	2.07	5.29	4.42	6.32	4.07		
	NT2RM4002067	2.51	2.51	4.27	3.07	5.19	4.41		
	NT2RM4002073	3.73	3.73	7.24	5.51	7.69	5.16		
	NT2RM4002074	5.19	5.19	7.35	5.67	7.47	4.49		
	NT2RM4002075	5.13	5.13	5.9	3.16	3.18	2.91	**	-
55	NT2RM4002076	3.13	3.13	3.05	1.94	2.52	1.71	*	-



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	NT2RM4002078	10.3	10.3	28.06	23.95	20.81	26.64		
	NT2RM4002081	10.47	10.47	30.87	19.18	17.8	18.22		
	NT2RM4002082	1.25	1.25	3.02	3.85	2.58	1.23		
5	NT2RM4002093	2.82	2.82	3.9	4.79	4.66	4.79	*	+
	NT2RM4002109	4.42	4.42	11.51	13.95	15.12	15.21	*	+
	NT2RM4002115	2.86	2.86	4.51	4.81	4.8	2.52		
	NT2RM4002118	4.48	4.48	6.14	4.3	4.86	4.27		
10	NT2RM4002128	3.78	3.78	4.57	2.84	3.31	3.13	*	-
	NT2RM4002137	3.96	3.96	8.14	10.27	7.51	8.92		
	NT2RM4002139	3.78	3.78	8.98	7.03	7.84	7.87		
	NT2RM4002140	4.04	4.04	9.45	8.87	7.81	10.17		
	NT2RM4002145	5.99	5.99	17.51	25.81	31.07	24.47	*	+
15	NT2RM4002146	4.51	4.51	8.23	8.56	9	8.92		
	NT2RM4002161	2.33	2.33	4.97	1.38	3.15	5.3		
	NT2RM4002174	4.86	4.86	8.02	3.12	4.53	6.15		
	NT2RM4002178	7.3	7.3	24.43	28.61	33.13	29.27	*	+
	NT2RM4002180	3.47	3.47	11.93	9.27	10.02	11.28		
20	NT2RM4002185	5.94	5.94	35.51	31.59	32.34	31.69		
	NT2RM4002189	1.6	1.6	3.24	3.68	5.59	4.91	*	+
	NT2RM4002194	9.3	9.3	25.94	37.2	29.64	38.23	*	+
	NT2RM4002198	6.09	6.09	7.61	9.37	8.4	10.04	*	+
	NT2RM4002205	4.01	4.01	9.05	6.76	7.86	8.76		
25	NT2RM4002213	5.36	5.36	8.79	8.05	11.99	14.41		
	NT2RM4002216	7.35	7.35	12.58	16.58	23.93	18.16	*	+
	NT2RM4002226	3.84	3.84	9.71	20.85	16.65	16.5	**	+
	NT2RM4002237	4.19	4.19	10.13	10.37	7.64	13.22		
	NT2RM4002240	1.96	1.96	3.64	3.73	3.71	7.59		
30	NT2RM4002251	2.11	2.11	6.2	7.87	5.48	5.17		
	NT2RM4002256	4.38	4.38	10.68	10.7	9.46	9.64		
	NT2RM4002262	2.85	2.85	6.25	3.34	4.43	9.66		
	NT2RM4002266	3.93	3.93	4.76	2.76	3.55	4.47		
	NT2RM4002276	11.23	11.23	15.55	16.5	28.25	20.64		
35	NT2RM4002278	1.89	1.89	4.59	4.33	3.99	5.11		
	NT2RM4002281	17.71	17.71	59.08	62.68	51.19	59.89		
	NT2RM4002287	2.08	2.08	3.84	2.46	4.21	3.32		
	NT2RM4002294	3.19	3.19	6.99	6.28	6.09	8.69		
	NT2RM4002298	18.59	18.59	60.14	86.09	89.9	88.75	*	+
40	NT2RM4002301	3.2	3.2	6.85	4.63	5.94	4.02		
	NT2RM4002306	4.71	4.71	8.24	4.99	5.31	4.2		
	NT2RM4002323	3.9	3.9	4.06	4.11	4.39	3.11		
	NT2RM4002334	11.54	11.54	20.76	17.92	20.72	16.95		
45	NT2RM4002339	1.78	1.78	3.52	1.33	1.3	1.38		
	NT2RM4002344	2.36	2.36	5.74	2.87	3.57	7.92		
	NT2RM4002345	3.56	3.56	10.59	5.06	4.63	7.5		
	NT2RM4002352	2.04	2.04	7.67	3.99	5.14	3.74		
	NT2RM4002362	20.38	20.38	24.92	11.23	14.32	15.17	*	-
50	NT2RM4002373	2.1	2.1	3.96	3.21	2.55	3.63		
	NT2RM4002374	2.28	2.28	4.39	2.29	3.58	4.3		
	NT2RM4002376	4.02	4.02	6.03	3.31	2.97	5.52		
	NT2RM4002383	2.8	2.8	8.49	4.76	5.79	4.28		
	NT2RM4002390	3.03	3.03	6.01	4.06	5.27	7.37		
55	NT2RM4002398	5.16	5.16	43.18	33.97	50.73	30.41		

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	NT2RM4002409	2.11	2.11	5.93	3.37	4.29	1.9	
	NT2RM4002414	4.73	4.73	6.21	7.37	9.12	14.53	
5	NT2RM4002438	2.07	2.07	5.28	3.03	4.38	7.18	
	NT2RM4002440	2.99	2.99	6.92	5.78	5.32	9.49	
	NT2RM4002446	2.23	2.23	6.08	2.95	4.45	5.7	
	NT2RM4002450	3.36	3.36	10.01	6.15	7.75	7.24	
	NT2RM4002452	2.13	2.13	6.3	3.67	5.15	7.23	
10	NT2RM4002457	2.68	2.68	4.44	2.66	3.26	4.52	
	NT2RM4002458	3.06	3.06	5.77	3.32	5.34	4.04	
	NT2RM4002460	2.43	2.43	3.68	1.57	2.45	1.43	
	NT2RM4002464	5.4	5.4	12.62	14.39	13.72	14.3	
	NT2RM4002479	4.66	4.66	6.69	4.91	7.98	11.54	
15	NT2RM4002482	4.26	4.26	16.18	10.19	11.5	12.2	
	NT2RM4002489	6.74	6.74	16.91	8.79	5.81	11.68	
	NT2RM4002493	1.35	1.35	3.22	1.96	3.51	2.73	
	NT2RM4002499	34.96	34.96	72.9	59.42	52.07	54.3	
	NT2RM4002504	5.15	5.15	10.68	10.57	13.51	9.8	
20	NT2RM4002506	4.77	4.77	9.4	4.93	7.59	8.53	
	NT2RM4002510	2.03	2.03	3.27	1.66	2.97	2.48	
	NT2RM4002527	1.57	1.57	3.14	1.83	2.31	4.47	
	NT2RM4002532	2.45	2.45	7.75	5.88	3.37	5.19	
	NT2RM4002534	1.79	1.79	4.8	2.1	3.45	2.94	
25	NT2RM4002535	2.5	2.5	6.51	5.89	8.1	6.37	
	NT2RM4002554	3.29	3.29	5.31	3.31	5.47	3.12	
	NT2RM4002558	6.91	6.91	32.57	32.58	41.54	25.61	
	NT2RM4002565	5.38	5.38	13.6	8.22	9.85	10.53	
	NT2RM4002567	3.34	3.34	5.43	4.21	4.49	7.22	
30	NT2RM4002571	4.48	4.48	15.61	11.95	16.47	15.24	
	NT2RM4002572	5.57	5.57	17.2	13.7	9.59	13.48	
	NT2RM4002577	7.76	7.76	15.25	6.59	5.87	5.65	
	NT2RM4002583	1.08	1.08	3.58	2.28	4.83	2.44	
	NT2RM4002584	1.64	1.64	5.67	3.24	5.74	5.56	
35	NT2RM4002593	3.29	3.29	5.17	2.75	3.91	4.61	
	NT2RM4002594	11.26	11.26	46.5	38.21	55.32	43.58	
	NT2RM4002604	4.83	4.83	4.64	1.77	2.03	2.89	** -
	NT2RM4002614	3.48	3.48	3.48	2.52	3.66	2.81	
40	NT2RM4002616	1.07	1.07	2.73	2.88	2.71	2.38	
	NT2RM4002623	1.39	1.39	4.89	3.92	3.72	5.06	
	NT2RM4002634	1.41	1.41	4.38	3.42	4.91	2.96	
	NT2RM4002636	2.22	2.22	3.93	3.92	4.18	4.12	
	NT2RP1000002	8.82	8.82	52.94	75.1	92.89	81.45	* +
45	NT2RP1000006	4.68	4.68	6.28	4.25	4.48	2.56	
	NT2RP1000015	4.86	4.86	5.27	2.74	1.99	2.28	** -
	NT2RP1000018	5.45	5.45	5	5.55	4.83	4.96	
	NT2RP1000034	18.22	18.22	49.95	38.04	30.76	50.07	
	NT2RP1000035	1.93	1.93	3.2	5.26	3.23	3.96	
50	NT2RP1000040	1.77	1.77	3.33	2.93	3.28	4.28	
	NT2RP1000042	1.3	1.3	3.44	1.99	3.22	2.38	
	NT2RP1000048	3.6	3.6	10.24	7.25	9.9	9	
	NT2RP1000050	2.21	2.21	4.71	2.89	4	3.57	
	NT2RP1000056	4.03	4.03	3.74	1.09	0.61	1.96	** -
55	NT2RP1000058	3.49	3.49	2.03	1.84	2.07	2.48	

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	NT2RP1000063	1.77	1.77	3.65	4.09	4	3.83		
	NT2RP1000068	1.89	1.89	3.99	3.12	3.33	2.43		
	NT2RP1000072	22.9	22.9	74.07	82.91	66.26	95.85		
5	NT2RP1000073	2.18	2.18	2.45	2.68	3.69	3.86	*	+
	NT2RP1000078	2.72	2.72	3.17	2.93	2.3	3.13		
	NT2RP1000079	4.13	4.13	5.32	3.6	4.48	2.5		
	NT2RP1000080	4.99	4.99	8.13	9.46	12.46	9.46	*	+
	NT2RP1000086	4.15	4.15	3.63	1.31	2.1	3.75		
10	NT2RP1000087	1.3	1.3	4.36	3.51	3.21	3.45		
	NT2RP1000089	4.5	4.5	9.98	12.69	11.3	14.93	*	+
	NT2RP1000090	45.76	45.76	96.6	94.37	53.44	93.42		
	NT2RP1000100	2.17	2.17	4.05	5.23	4.13	3.66		
	NT2RP1000101	3.44	3.44	5.22	4.41	2.88	4.81		
15	NT2RP1000111	3.24	3.24	5.56	4.51	3.9	3.69		
	NT2RP1000112	3.29	3.29	4.08	1.85	3.33	3		
	NT2RP1000124	5.57	5.57	4.96	3.11	5.73	5.5		
	NT2RP1000125	7.28	7.28	19.39	13.69	10.68	16.86		
20	NT2RP1000129	1.81	1.81	4.35	5.14	3.91	4.27		
	NT2RP1000130	2.31	2.31	4.11	5.31	5.62	16.86		
	NT2RP1000154	7.5	7.5	15.63	17.16	12.72	16.37		
	NT2RP1000163	2.42	2.42	3.51	2.72	2.99	3.59		
	NT2RP1000170	3.42	3.42	4.2	4.96	5.17	5.85	*	+
25	NT2RP1000174	3.5	3.5	3.42	1.3	2.38	2.12	**	-
	NT2RP1000181	6.14	6.14	7.22	10.97	14.98	9.38	*	+
	NT2RP1000191	1.08	1.08	5.61	4.94	3.59	5.71		
	NT2RP1000202	1.06	1.06	1.66	2.02	1.2	2.24		
	NT2RP1000239	1.53	1.53	4.1	2.15	0.94	2.07		
30	NT2RP1000243	2.37	2.37	2.04	1.31	1.14	1.64	**	-
	NT2RP1000255	1.94	1.94	3.02	2.11	2.26	1.78		
	NT2RP1000259	5.27	5.27	9.55	5.53	6.33	4.29		
	NT2RP1000261	2.76	2.76	4.4	2.07	1.64	2.64		
	NT2RP1000269	5.16	5.16	5.01	7.7	10.51	7.39	*	+
35	NT2RP1000271	7.79	7.79	15.88	13.16	15.11	18.48		
	NT2RP1000272	7.71	7.71	13.07	10.72	11.74	11.3		
	NT2RP1000279	2.19	2.19	5.24	2.23	3.91	2.62		
	NT2RP1000290	6.61	6.61	9.02	12.65	13.52	9.92	*	+
	NT2RP1000293	6.86	6.86	10.91	9.75	8.45	10.92		
40	NT2RP1000300	12.42	12.42	11.93	9.96	11.37	10.2	*	-
	NT2RP1000324	5.16	5.16	6	4.69	5.92	6.97		
	NT2RP1000325	54.42	54.42	101.4	70.46	57.52	78.6		
	NT2RP1000326	4.01	4.01	7.67	3.82	4.56	7.85		
	NT2RP1000331	12.16	12.16	24.08	12.19	10.5	20.1		
45	NT2RP1000333	4.18	4.18	7.52	6.66	6.53	6.98		
	NT2RP1000336	1.45	1.45	4.45	1.35	3.76	1.78		
	NT2RP1000347	3.05	3.05	8.75	7.26	8.31	6.38		
	NT2RP1000348	2.11	2.11	4.14	2.76	3	2.75		
	NT2RP1000349	2.12	2.12	3.92	3	4.39	4.11		
50	NT2RP1000353	40.87	40.87	83.5	51.49	47.8	66.02		
	NT2RP1000356	39.53	39.53	93.37	50.3	56.48	74.42		
	NT2RP1000357	3.89	3.89	9.63	8.43	8.7	8.72		
	NT2RP1000358	2.85	2.85	6.11	4.23	3.04	5.09		
55	NT2RP1000360	11.04	11.04	19.39	12.08	18.42	19.44		

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	NT2RP1000363	13.09	13.09	15.39	13.13	13.38	10.01		
	NT2RP1000376	1.81	1.81	3.8	2.09	1.9	2.24		
5	NT2RP1000386	118	118	191.31	146.98	187.97	155.47		
	NT2RP1000407	0.72	0.72	3.16	0.58	0.89	1.2		
	NT2RP1000409	2.05	2.05	5.39	2.84	6.59	3.83		
	NT2RP1000413	4.78	4.78	8.03	5.86	8.89	10.19		
	NT2RP1000416	1.5	1.5	2.01	0.93	3.17	0.7		
10	NT2RP1000418	2.27	2.27	6.69	5.08	6.67	4.85		
	NT2RP1000420	1.77	1.77	5.19	7.32	7.64	3.7		
	NT2RP1000434	1.48	1.48	4.39	1.27	3.12	1		
	NT2RP1000439	5.02	5.02	9.31	20.62	28.73	24.75	**	+
	NT2RP1000443	1.8	1.8	3.46	2.24	1.61	1.63		
15	NT2RP1000447	2.21	2.21	5.57	2.49	2.87	3.1		
	NT2RP1000448	1.39	1.39	3.58	3.09	4.4	1.41		
	NT2RP1000451	4.2	4.2	6.37	5.72	7.27	7.04		
	NT2RP1000458	15.1	15.1	10.53	19.73	8.72	23.03		
	NT2RP1000460	7.55	7.55	13.82	8.76	11.49	8.62		
20	NT2RP1000465	4.58	4.58	20.97	20.41	19.98	22.46		
	NT2RP1000468	3.25	3.25	4.64	3.82	4.1	4.45		
	NT2RP1000470	2.38	2.38	5.67	3.99	2.35	3.8		
	NT2RP1000477	1.11	1.11	3.81	1.1	0.84	0.83		
	NT2RP1000478	4.53	4.53	12.55	19.87	18.75	20.39	*	+
25	NT2RP1000481	1.23	1.23	3.89	2.48	4.09	1.2		
	NT2RP1000493	2.44	2.44	3.8	1.74	3.83	0.87		
	NT2RP1000513	13.07	13.07	16.37	17.06	17.57	18.97	*	+
	NT2RP1000522	6.13	6.13	12.69	13.13	13.08	10.32		
	NT2RP1000533	3.72	3.72	6.17	2.92	4.49	2.17		
30	NT2RP1000544	1.53	1.53	2.45	1.38	1.24	1.44		
	NT2RP1000547	0.88	0.88	2.45	2	1.63	1.23		
	NT2RP1000551	1.7	1.7	2.62	2.13	3.2	1.1		
	NT2RP1000567	1.66	1.66	4.29	2.54	4.29	1.77		
	NT2RP1000574	1.99	1.99	4.28	1.5	3.43	1.38		
35	NT2RP1000577	3.14	3.14	6.01	3.16	5.31	2.05		
	NT2RP1000579	4.64	4.64	6.24	3.27	3.97	2.04		
	NT2RP1000581	5.22	5.22	3.58	2.07	1.61	0.93	**	-
	NT2RP1000593	1.74	1.74	4.39	2.48	3.28	2.3		
	NT2RP1000604	3.85	3.85	7.75	17.25	13.78	16.39	**	+
40	NT2RP1000609	1.15	1.15	2.21	2.84	2.61	1.55		
	NT2RP1000613	1.12	1.12	2.56	1.82	4.29	0.82		
	NT2RP1000622	5.94	5.94	15.9	14.91	19.42	15.46		
	NT2RP1000627	9.18	9.18	18.96	23.88	21.9	14.86		
45	NT2RP1000629	4.18	4.18	5.9	5.92	5.32	3.17		
	NT2RP1000630	6.54	6.54	7.84	7.21	7.67	7.92		
	NT2RP1000639	0.64	0.64	0.31	1.53	2.04	0.28		
	NT2RP1000640	130.14	130.14	307.77	227.5	176.05	232.29		
	NT2RP1000646	4.14	4.14	9.59	10.19	11.87	12.15	*	+
50	NT2RP1000659	2.65	2.65	7	8.91	7.99	6.04		
	NT2RP1000674	13.48	13.48	28.08	43.62	45.82	56.95	**	+
	NT2RP1000677	3.9	3.9	10.76	11.84	10.19	9.87		
	NT2RP1000679	2.38	2.38	3.76	2.3	2.35	1.05		
	NT2RP1000688	4.72	4.72	3.34	2.76	2.73	1.83	*	-
55	NT2RP1000689	1.44	1.44	1.86	2.03	1.22	1.13		

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	NT2RP1000695	1.11	1.11	2.5	2.09	2.44	1.52		
	NT2RP1000701	0.89	0.89	1.08	2.62	2.74	1.71	*	+
	NT2RP1000702	1.12	1.12	2.28	3.74	4.07	3.15	*	+
5	NT2RP1000713	2.29	2.29	2.79	2.8	3.56	2.38		
	NT2RP1000721	4.14	4.14	4.49	4.48	3.92	3.78		
	NT2RP1000730	3.5	3.5	4.83	2.61	4.5	2.41		
	NT2RP1000733	6.08	6.08	6.56	4.91	8.12	5.65		
10	NT2RP1000738	3.18	3.18	8.04	5.16	5.71	7.11		
	NT2RP1000739	1.11	1.11	2.65	4.02	3.09	2.86		
	NT2RP1000740	1.41	1.41	3.13	3.63	3.57	3.77	*	+
	NT2RP1000746	1.15	1.15	3.58	2.28	3.74	1.37		
	NT2RP1000750	4	4	8.31	10.25	10.72	9.39	*	+
15	NT2RP1000751	33.15	33.15	59.65	67.84	64.22	66.55		
	NT2RP1000767	3.8	3.8	3.64	1.7	2.62	0.62	*	-
	NT2RP1000769	9.31	9.31	13.98	7.42	8.59	7.19		
	NT2RP1000780	0.86	0.86	1.01	1.87	1.13	0.89		
	NT2RP1000782	4.25	4.25	12.21	10.24	7.96	9.13		
20	NT2RP1000796	3.17	3.17	2.69	4.23	2.99	2.86		
	NT2RP1000797	12.31	12.31	22.78	19.44	18.64	21.78		
	NT2RP1000800	1.13	1.13	3.74	2.46	2.66	1.46		
	NT2RP1000825	2.38	2.38	2.91	1.04	1.88	0.87	*	-
	NT2RP1000833	2.5	2.5	2.85	0.92	2.39	1.26		
25	NT2RP1000834	35.44	35.44	66.57	73.98	90.28	71.45		
	NT2RP1000836	1.83	1.83	3.43	1.01	2.39	1.04		
	NT2RP1000837	3.36	3.36	6.66	3.22	4.71	3.67		
	NT2RP1000846	1.29	1.29	5.48	1.67	2.84	1.4		
	NT2RP1000847	1.99	1.99	5.49	2.15	5.12	1.64		
30	NT2RP1000851	4.67	4.67	9.32	6.18	7.94	6.72		
	NT2RP1000856	14.31	14.31	17.46	20.38	23.22	19.37	*	+
	NT2RP1000860	2.09	2.09	4.54	4.02	2.74	4.04		
	NT2RP1000902	5.31	5.31	11.6	6.94	9.91	7.34		
	NT2RP1000903	2.45	2.45	6.26	4.04	3.42	4.24		
35	NT2RP1000905	1.76	1.76	4.87	5.36	5.66	10		
	NT2RP1000915	5.51	5.51	10.01	6.72	8.59	9.91		
	NT2RP1000916	2.31	2.31	5.51	1.78	3.82	2.09		
	NT2RP1000921	9.38	9.38	8.73	8.23	9.13	7.92		
	NT2RP1000943	5.14	5.14	10.76	8.51	8.55	7.2		
40	NT2RP1000944	1.59	1.59	2.21	1.78	1.74	1.15		
	NT2RP1000947	8.5	8.5	14.91	16.51	15.04	14.22		
	NT2RP1000954	2.11	2.11	4.96	2.74	5.55	3.04		
	NT2RP1000958	6.48	6.48	14.73	4.54	10.17	10.21		
	NT2RP1000959	124.81	124.81	209.45	128.43	72.65	206.1		
45	NT2RP1000966	9.96	9.96	12.96	14.28	15.36	21.39		
	NT2RP1000974	2.46	2.46	5.38	3.98	6.08	3.71		
	NT2RP1000980	3.07	3.07	5.5	4.04	4.53	4.02		
	NT2RP1000981	4.3	4.3	8.09	5.68	7.26	5.27		
	NT2RP1000988	6.45	6.45	10.46	9.62	6.44	7.87		
50	NT2RP1001002	2.8	2.8	7.36	3.94	4.57	4.3		
	NT2RP1001004	4.72	4.72	8.25	3.65	4.9	5.37		
	NT2RP1001007	1.42	1.42	3.42	1.69	3.84	2.03		
	NT2RP1001011	1.94	1.94	5.93	3.82	5.46	4.83		
55	NT2RP1001013	4.45	4.45	9.41	5.92	8.62	5.04		

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	NT2RP1001014	2.21	2.21	5.89	3.76	6.64	3.49	
	NT2RP1001020	1.87	1.87	4.11	2.08	3.75	2.36	
	NT2RP1001023	62.79	62.79	145.09	101.48	105.86	143.96	
5	NT2RP1001027	18.11	18.11	82.66	51.63	59.05	68.9	
	NT2RP1001031	1.83	1.83	3.31	2.05	3.53	2.25	
	NT2RP1001033	2.43	2.43	6.09	5.68	5.98	4.27	
	NT2RP1001042	2.94	2.94	6.47	2.99	3.85	2.04	
10	NT2RP1001045	15.95	15.95	23.24	40.66	47.04	44.53	** +
	NT2RP1001073	6.64	6.64	10.57	8.32	10.46	7.33	
	NT2RP1001079	2.91	2.91	6.37	2.16	2.58	1.48	
	NT2RP1001080	2.16	2.16	4.89	6.88	4.2	4.56	
	NT2RP1001113	1.07	1.07	3.64	3.55	3.94	3.26	
15	NT2RP1001159	21.42	21.42	43.84	22.89	23.31	34.25	
	NT2RP1001173	1.7	1.7	3.07	1.38	4.28	1.52	
	NT2RP1001176	7.4	7.4	10.13	13	9.31	13.95	
	NT2RP1001177	5.31	5.31	5.75	3.01	5.5	2.02	
	NT2RP1001185	6.42	6.42	9.37	3.79	4.63	2.73	* -
20	NT2RP1001199	3.9	3.9	7.67	6.93	5.22	3.28	
	NT2RP1001205	7.78	7.78	19.46	16.66	12.64	23.28	
	NT2RP1001215	1.82	1.82	5.02	3.79	4.12	3.15	
	NT2RP1001225	4.54	4.54	7.96	7.56	8.77	6.31	
25	NT2RP1001245	7.27	7.27	10.86	19.68	21.03	22.13	** +
	NT2RP1001247	2.04	2.04	4.01	1.77	2.89	1.67	
	NT2RP1001248	2.81	2.81	6.79	3.94	4.63	2.4	
	NT2RP1001253	5.02	5.02	6.39	4.48	4.38	3.32	
	NT2RP1001286	6.18	6.18	7.69	3.79	3.88	4.12	** -
30	NT2RP1001294	2.4	2.4	4.47	3.6	2.73	4.18	
	NT2RP1001302	2.46	2.46	4.51	4.89	2.9	5.39	
	NT2RP1001310	15.54	15.54	34.01	21.13	20.75	27.15	
	NT2RP1001311	1.9	1.9	3.22	2.66	3.16	2.38	
	NT2RP1001313	2.6	2.6	7.72	5.45	7.85	5.78	
35	NT2RP1001324	2.47	2.47	5.3	3.34	4.17	2.35	
	NT2RP1001349	3.3	3.3	6.29	3.63	3.92	2.14	
	NT2RP1001361	19.41	19.41	18.28	23.28	28.33	24.16	* +
	NT2RP1001379	3.82	3.82	9.52	4.97	7.97	7.06	
	NT2RP1001385	2.06	2.06	4.51	4.09	3.89	4.4	
40	NT2RP1001395	4.96	4.96	7.86	6.01	6.32	8.13	
	NT2RP1001410	8.75	8.75	20.39	15.74	15.66	9.94	
	NT2RP1001424	2.39	2.39	3.34	3	3	1.73	
	NT2RP1001432	4.33	4.33	3.86	2.19	1.76	2.05	** -
	NT2RP1001449	6.23	6.23	7.5	6.29	8.21	4.63	
45	NT2RP1001457	4.09	4.09	4.21	2.11	2.26	2.63	** -
	NT2RP1001459	21.54	21.54	132.97	90.96	107.97	81.08	
	NT2RP1001466	5.73	5.73	14.97	11.31	9.39	10.99	
	NT2RP1001475	2.45	2.45	6.31	5.98	6.67	3.9	
	NT2RP1001482	3.93	3.93	9.18	15.88	13.03	8.2	
50	NT2RP1001494	1.61	1.61	4.6	4.34	4.18	2.25	
	NT2RP1001500	3.39	3.39	8.13	8.09	8.65	7.42	
	NT2RP1001517	5.11	5.11	7.37	4.41	5.38	2.36	
	NT2RP1001540	4.74	4.74	5.03	4.6	4.86	3.11	
	NT2RP1001543	1.02	1.02	1.83	1.49	1.12	0.98	
55	NT2RP1001546	22.51	22.51	51.51	34.99	22.76	33.42	

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	NT2RP1001550	9.33	9.33	21.4	14.35	12.21	13.42		
	NT2RP1001553	2.07	2.07	6.07	5.69	6.04	4.45		
	NT2RP1001555	36.28	36.28	58.55	41.1	53.63	54.35		
5	NT2RP1001563	2.28	2.28	3.44	2.07	2.24	1.31		
	NT2RP1001569	9.43	9.43	16	17.31	18.21	13.04		
	NT2RP1001584	15.6	15.6	19.66	28.1	32.53	25.83	**	+
	NT2RP1001599	1.18	1.18	1.95	1.27	1.19	1.24		
	NT2RP1001616	5	5	11.95	9.49	6.7	8.95		
10	NT2RP1001654	11.78	11.78	18.07	16.27	16.54	18.38		
	NT2RP1001665	2.77	2.77	4.72	2.73	2.05	2.05		
	NT2RP1001679	76.31	76.31	195.7	199.2	240.87	222.46		
	NT2RP1001681	10.11	10.11	15.1	20.39	21.03	23.99	**	+
	NT2RP1001694	3.58	3.58	3.82	2.45	2.38	1.97	**	-
15	NT2RP2000001	5.23	5.23	5.53	4.17	4.54	3.74	**	-
	NT2RP2000006	3.49	3.49	7.32	4.12	3.88	3.4		
	NT2RP2000007	3.18	3.18	6.56	4.68	5.66	4.92		
	NT2RP2000008	2.77	2.77	6.72	3.66	5.3	4.9		
20	NT2RP2000010	2.89	2.89	5.59	2.99	5.06	2.5		
	NT2RP2000011	7.08	7.08	17.96	14.55	14.74	15.15		
	NT2RP2000027	2.28	2.28	7.42	4.52	4.89	3.61		
	NT2RP2000028	22.93	22.93	62.54	46.48	51.47	53.47		
	NT2RP2000032	2.5	2.5	5.85	3.11	3.71	6.42		
25	NT2RP2000040	11.57	11.57	23.92	14.38	14.5	23.1		
	NT2RP2000042	5.28	5.28	10.32	6.89	7.21	12.64		
	NT2RP2000045	5.7	5.7	9.42	5.27	6.45	6.3		
	NT2RP2000051	3.16	3.16	6.29	9.23	9.96	9.53	**	+
	NT2RP2000054	2.55	2.55	6.42	3.81	5.42	2.53		
30	NT2RP2000056	3.68	3.68	6.23	5.67	6.89	5.8		
	NT2RP2000057	60.79	60.79	174.83	212.63	239.81	221.98	*	+
	NT2RP2000067	3.1	3.1	3.86	2.98	4.36	5.72		
	NT2RP2000070	2.91	2.91	6.27	5.7	5.95	8.21		
	NT2RP2000076	1.66	1.66	4.45	2.98	3.58	3.23		
35	NT2RP2000077	1.67	1.67	4.73	2.43	4.94	3.14		
	NT2RP2000079	3.76	3.76	9.24	5.15	4.81	5.47		
	NT2RP2000088	2.9	2.9	5.22	2.18	3.07	2.21		
	NT2RP2000091	5.84	5.84	6.54	6.62	8.28	6.72		
	NT2RP2000092	4.37	4.37	6.7	6.06	7.67	5.65		
40	NT2RP2000097	2.74	2.74	3.39	3.4	4.13	4.13	*	+
	NT2RP2000098	3.44	3.44	6.83	6.69	9.01	6.27		
	NT2RP2000108	1.93	1.93	7.24	4.8	6.31	6.68		
	NT2RP2000114	1.95	1.95	3.65	2.58	4.41	2.9		
	NT2RP2000116	3.17	3.17	7.36	5.35	3.85	9.42		
45	NT2RP2000119	3.14	3.14	7.16	4.58	7.96	5.6		
	NT2RP2000120	3.91	3.91	7.62	5.57	8.5	5.8		
	NT2RP2000126	2.86	2.86	4.86	3.88	5.1	3.44		
	NT2RP2000133	1.83	1.83	3.66	3.13	4.05	2.01		
50	NT2RP2000147	6.28	6.28	12.88	11.64	6.51	8.58		
	NT2RP2000153	4.61	4.61	9.55	10.57	6.49	12.05		
	NT2RP2000156	3.27	3.27	8.24	5.59	6.55	4.07		
	NT2RP2000157	3.7	3.7	6.33	6.57	5.02	4.15		
	NT2RP2000161	4.45	4.45	8.82	7.52	7.5	6.02		
55	NT2RP2000168	4.22	4.22	12.63	3.94	6.03	3.88		

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	NT2RP2000173	12.56	12.56	81.37	72.12	92.12	78.68	
	NT2RP2000175	1.9	1.9	3.78	2.03	3.33	4.43	
5	NT2RP2000178	2.06	2.06	6.06	3.23	3.01	3.81	
	NT2RP2000183	1.64	1.64	7.82	5.82	6.21	6.03	
	NT2RP2000195	3.1	3.1	6.65	6	6.71	3.22	
	NT2RP2000204	73.6	73.6	93.43	102.95	40.16	62.34	
	NT2RP2000205	4	4	6.56	3.91	5.74	4.5	
10	NT2RP2000208	3.06	3.06	9.42	4.23	6.77	3.36	
	NT2RP2000224	13.3	13.3	31.75	18.34	21.15	20.93	
	NT2RP2000230	9.96	9.96	18.99	12.16	16.4	11.95	
	NT2RP2000231	4.3	4.3	7.41	4.24	3.43	4.54	
	NT2RP2000232	1.08	1.08	2.75	1.53	2.45	0.74	
15	NT2RP2000233	8.04	8.04	60.44	47.2	64.72	52.31	
	NT2RP2000239	3	3	4.7	8.93	8.93	7.01	** +
	NT2RP2000240	2.01	2.01	5.25	2.49	3.41	1.45	
	NT2RP2000248	4.29	4.29	6.09	2.82	2.39	0.96	* -
	NT2RP2000256	5.7	5.7	8.25	5.62	6.22	5.44	
20	NT2RP2000257	3.47	3.47	6.92	4.86	6.52	4.34	
	NT2RP2000258	1.53	1.53	3.83	3.88	2.93	3.02	
	NT2RP2000261	2.95	2.95	3.94	4.47	3.59	2.91	
	NT2RP2000270	3.12	3.12	6.26	6.66	4.06	4.3	
	NT2RP2000274	1.78	1.78	3.87	3.48	5.16	2.56	
25	NT2RP2000277	2.18	2.18	6.13	3.19	4.02	2.98	
	NT2RP2000279	2.26	2.26	4.92	2.43	2.52	2.17	
	NT2RP2000283	5.75	5.75	27.65	21.53	27.32	24.78	
	NT2RP2000288	6.29	6.29	7.46	8.9	10.89	8.64	* +
	NT2RP2000289	1.12	1.12	2.79	3.09	2.77	1.93	
30	NT2RP2000297	2.57	2.57	5.7	4.8	4.53	6.09	
	NT2RP2000298	3.61	3.61	9.64	8.51	7.66	8.24	
	NT2RP2000310	1.43	1.43	2.3	2.46	3.41	1.7	
	NT2RP2000327	2.12	2.12	3.96	3.13	3.49	1.57	
	NT2RP2000328	6.95	6.95	11.56	13.43	16.7	14.68	* +
35	NT2RP2000329	10.73	10.73	10.17	17.55	23.92	18.52	** +
	NT2RP2000333	6.35	6.35	6.4	6.83	7.17	4.64	
	NT2RP2000337	2.05	2.05	5.16	4.43	5.32	5.31	
	NT2RP2000346	2.55	2.55	5.18	7.2	5.63	4.95	
	NT2RP2000357	1.57	1.57	6.87	5.48	5.14	5.35	
40	NT2RP2000358	2.09	2.09	4.52	5.03	4.9	4.01	
	NT2RP2000366	3.23	3.23	4.08	4.16	4.25	2.32	
	NT2RP2000369	7.22	7.22	9.94	44.13	45.2	44.34	** +
	NT2RP2000376	26.92	26.92	108.62	84.48	134.63	85.95	
	NT2RP2000394	6.49	6.49	5.92	5.08	8.52	4.21	
45	NT2RP2000396	2.71	2.71	6.55	7.52	6.8	5.02	
	NT2RP2000412	4.48	4.48	23.45	21.42	24.93	20.49	
	NT2RP2000414	8.03	8.03	18.69	23.83	18.98	23.37	
	NT2RP2000420	1.12	1.12	4.11	3.54	3.25	1.97	
	NT2RP2000422	6.41	6.41	13.18	17.56	17.88	18.67	* +
50	NT2RP2000426	21.59	21.59	80.94	87.94	110.97	74.98	
	NT2RP2000428	24.92	24.92	43.91	34.21	35.59	30.95	
	NT2RP2000438	5.06	5.06	5.17	5.62	6.94	5.11	
	NT2RP2000447	4.14	4.14	9.68	7.3	7.08	7.16	
55	NT2RP2000448	3.03	3.03	4.63	4.57	3.57	3.17	



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	NT2RP2000459	2.47	2.47	4.93	2.82	3.15	2.09		
	NT2RP2000479	3.3	3.3	7.51	5.33	5.71	5.06		
	NT2RP2000498	3.07	3.07	6.25	4.48	5.09	3.9		
5	NT2RP2000503	2.47	2.47	4.46	2.54	2.82	1.52		
	NT2RP2000510	4.01	4.01	6.19	5.08	6.45	3.7		
	NT2RP2000514	2.65	2.65	2.51	1.94	2.25	1.63	*	-
	NT2RP2000516	4.72	4.72	9.77	4.92	5.29	5.18		
10	NT2RP2000523	2.21	2.21	3.17	1.92	2.44	2.63		
	NT2RP2000533	17.82	17.82	29.05	22.57	27.56	30.78		
	NT2RP2000540	1.98	1.98	4.66	3.01	5.41	5.18		
	NT2RP2000547	3.1	3.1	5.26	4.38	5.27	3.71		
	NT2RP2000557	4.26	4.26	6.96	4.34	6.5	3.32		
15	NT2RP2000558	3.43	3.43	7.17	6.43	7.11	8.26		
	NT2RP2000564	3.04	3.04	7.2	3.49	8.03	4.77		
	NT2RP2000565	4.54	4.54	11.07	7.64	9.24	9.98		
	NT2RP2000583	14.8	14.8	44.9	49.6	34.93	49.08		
	NT2RP2000591	0.81	0.81	3.81	1.53	2.61	1.21		
20	NT2RP2000599	1.85	1.85	4.1	1.97	3.43	2.36		
	NT2RP2000601	1.78	1.78	4.67	1.28	2.48	1.3		
	NT2RP2000603	2.58	2.58	4.44	2.54	2.84	2.98		
	NT2RP2000610	3.77	3.77	7.23	6.32	7.62	5.53		
	NT2RP2000614	75.85	75.85	129.42	130.63	184.38	188.58	*	+
25	NT2RP2000616	1.81	1.81	4.89	3.9	5.1	3.83		
	NT2RP2000617	2.17	2.17	6.73	5.78	6.82	6.26		
	NT2RP2000623	3.1	3.1	5.36	3.46	5.1	3.49		
	NT2RP2000634	1.56	1.56	3.92	2.29	3.34	2.02		
	NT2RP2000636	3.78	3.78	8.64	6.27	7.6	6.62		
30	NT2RP2000638	4.37	4.37	8.91	4.57	7.41	5.69		
	NT2RP2000644	2.22	2.22	5.47	3.41	4.16	3.45		
	NT2RP2000649	8.96	8.96	15.76	13.65	17.22	13.07		
	NT2RP2000652	3.35	3.35	4.58	3.57	4.36	2.72		
	NT2RP2000656	3.73	3.73	6.93	4.83	3.91	4.08		
35	NT2RP2000658	1.08	1.08	2.64	1.51	3.18	1.43		
	NT2RP2000663	4.23	4.23	6.9	5.98	7.21	5.9		
	NT2RP2000664	4.24	4.24	10.24	12.72	12.54	16.44	*	+
	NT2RP2000668	7.49	7.49	26.84	16.92	20.41	17.17		
	NT2RP2000678	1.77	1.77	3.19	1.77	2.09	1.13		
40	NT2RP2000694	4.89	4.89	8.39	11.06	13	13.36	**	+
	NT2RP2000704	1.8	1.8	5.63	2.99	3.13	3.67		
	NT2RP2000710	4.51	4.51	9.96	6.72	8.08	7.23		
	NT2RP2000712	1.43	1.43	5.35	3.39	3.57	2.95		
	NT2RP2000715	3.42	3.42	7.43	6.04	7.56	4.49		
45	NT2RP2000720	4.92	4.92	11.76	7.24	8	7.11		
	NT2RP2000731	3.92	3.92	9.15	3.7	4.5	2.61		
	NT2RP2000739	3.23	3.23	5.67	2.62	3.32	5.65		
	NT2RP2000748	1.59	1.59	4.2	1.42	1.81	1.62		
50	NT2RP2000749	11.84	11.84	21.88	14.4	8.47	13.91		
	NT2RP2000758	1.6	1.6	3.17	2.65	6	1.17		
	NT2RP2000764	1.51	1.51	5.74	2.95	5.22	1.95		
	NT2RP2000766	9.08	9.08	52.24	46.37	59.37	52.89		
	NT2RP2000777	12.28	12.28	18.43	26.91	28.56	24.47	**	+
55	NT2RP2000786	21.32	21.32	73.91	55.85	67.59	58.16		

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	NT2RP2000793	5.32	5.32	6.9	4.32	3.57	4.38	*	-
	NT2RP2000796	5.32	5.32	7.41	7.38	9.17	6.66		
5	NT2RP2000809	3.25	3.25	8.3	6.46	4.69	5.45		
	NT2RP2000812	6.65	6.65	17.51	16.43	14.35	16.89		
	NT2RP2000814	4.16	4.16	4.97	3.75	4.6	3.29		
	NT2RP2000816	1.84	1.84	5.64	4.64	5.19	3.58		
	NT2RP2000818	3.28	3.28	5.19	3.18	3.66	1.95		
10	NT2RP2000819	2.76	2.76	5.79	3.03	3.05	1.94		
	NT2RP2000841	4.35	4.35	4.51	2.17	2.48	1.65	**	-
	NT2RP2000842	7.8	7.8	9.57	13.62	14.25	12.66	**	+
	NT2RP2000845	2.52	2.52	8.31	7.51	6.76	6.93		
	NT2RP2000863	2.45	2.45	3.48	3.82	3.37	2.47		
15	NT2RP2000880	5.96	5.96	11.61	9.5	11.13	10.25		
	NT2RP2000892	4.3	4.3	6.43	6.54	6.97	5.01		
	NT2RP2000894	5.59	5.59	11.88	5.41	5.59	2.16		
	NT2RP2000903	5.71	5.71	9.12	10.73	11.92	7.44		
20	NT2RP2000906	4.56	4.56	5.39	2.63	3.78	2.19	*	-
	NT2RP2000910	4.34	4.34	4.26	2.9	2.7	1.68	**	-
	NT2RP2000931	10.97	10.97	18.36	20.51	19.28	24.6		
	NT2RP2000932	2.86	2.86	5.43	4.8	4.72	4.21		
	NT2RP2000938	18.41	18.41	42.99	35.71	30.01	43.52		
25	NT2RP2000943	7.02	7.02	14.98	18.7	14.88	14.48		
	NT2RP2000957	3.19	3.19	4.11	4.26	3.66	2.71		
	NT2RP2000958	7	7	6.84	10.43	12.36	7.8		
	NT2RP2000959	9.88	9.88	14.99	13.92	17.38	10.69		
	NT2RP2000965	5.05	5.05	7.82	15.73	18.97	16.02	**	+
30	NT2RP2000970	2.31	2.31	6.72	5.14	5	4.62		
	NT2RP2000973	0.9	0.9	1.47	2.56	2.64	1.57	*	+
	NT2RP2000985	2.69	2.69	6	9.28	6.29	13.98		
	NT2RP2000987	1.89	1.89	3.31	4.54	3.17	1.66		
	NT2RP2000997	13.83	13.83	23.99	38.12	29.73	40.96	*	+
35	NT2RP2001024	2.86	2.86	5.34	3.61	3.12	2.36		
	NT2RP2001028	4.66	4.66	4.2	2.65	4.09	0.99		
	NT2RP2001036	5.14	5.14	8.86	6.16	6.44	4.91		
	NT2RP2001039	1.08	1.08	3.18	3.47	1.14	2.24		
	NT2RP2001044	1.13	1.13	2.5	2.53	1.89	2.8		
40	NT2RP2001056	4.97	4.97	28.32	20.16	26.9	18.16		
	NT2RP2001065	2.38	2.38	6.24	7.45	7.4	5.69		
	NT2RP2001067	2.98	2.98	5.38	4.12	5.29	2.41		
	NT2RP2001070	3.3	3.3	7.63	4.72	6.17	3.58		
	NT2RP2001081	2.91	2.91	8.19	4.8	6.68	3.9		
45	NT2RP2001087	3.93	3.93	2.36	2.06	2.92	1.61		
	NT2RP2001094	0.69	0.69	1.37	1.25	1.15	1.04		
	NT2RP2001119	2.02	2.02	6.11	5.86	4.44	4.35		
	NT2RP2001127	1.53	1.53	4.04	2.69	1.85	2.1		
	NT2RP2001133	2.45	2.45	4.73	4.06	3.61	3.6		
50	NT2RP2001137	2.68	2.68	4.07	2.3	2.82	2.9		
	NT2RP2001142	3.88	3.88	7.47	3.37	2.83	2.42		
	NT2RP2001149	2.7	2.7	2.98	2.11	3.39	1.32		
	NT2RP2001168	6	6	7.81	6.8	7.01	5.75		
	NT2RP2001173	4.15	4.15	7.88	3.98	3.09	5.44		
55	NT2RP2001174	9.23	9.23	14.98	14.12	15.45	18.01		

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	NT2RP2001184	2.78	2.78	5.46	4.21	7.18	4.64	
	NT2RP2001196	1.62	1.62	5.93	3.14	3.28	2.94	
5	NT2RP2001200	3.85	3.85	9.36	5.02	4.25	7.88	
	NT2RP2001218	2.29	2.29	5.69	2.55	3.89	3.6	
	NT2RP2001223	2.65	2.65	5.03	1.95	3.69	3.31	
	NT2RP2001226	4.34	4.34	10.19	6.95	5.72	7.35	
	NT2RP2001227	4.45	4.45	6.12	3.2	3.62	6.01	
10	NT2RP2001232	6.44	6.44	13.95	7.13	9.79	13.66	
	NT2RP2001233	4.02	4.02	10.57	7.04	7.77	8.01	
	NT2RP2001245	4.21	4.21	8.03	9.47	11.82	11.16	* +
	NT2RP2001246	6.3	6.3	9.84	9	11.28	11.57	
	NT2RP2001268	6.19	6.19	18.1	17.61	16.26	18.55	
15	NT2RP2001270	4.78	4.78	9.11	5.68	8.7	10.04	
	NT2RP2001276	4.92	4.92	13.29	12.73	10.92	12.73	
	NT2RP2001277	3.11	3.11	7.02	4.91	6.22	10.82	
	NT2RP2001290	2.71	2.71	6.46	4.42	5.61	6.01	
	NT2RP2001295	5.46	5.46	9.44	5.13	5.98	7.92	
20	NT2RP2001297	118.17	118.17	120.73	139.11	97.16	145.76	
	NT2RP2001301	9.12	9.12	18.56	15.89	19.62	14.24	
	NT2RP2001312	2.7	2.7	5.68	5.6	4.59	6.04	
	NT2RP2001327	4.73	4.73	5.69	6.39	8.53	11.86	
	NT2RP2001328	8.44	8.44	20.87	16.32	23.25	23.16	
25	NT2RP2001341	4.59	4.59	9.22	3.06	7.65	7.21	
	NT2RP2001347	3.09	3.09	8.54	5.54	9.55	6.9	
	NT2RP2001366	10.33	10.33	48.06	54.83	51.5	52.33	
	NT2RP2001378	2.33	2.33	3.77	3.74	4.64	5.02	
	NT2RP2001381	2.82	2.82	6.86	5.79	6.62	8.37	
30	NT2RP2001388	3.25	3.25	6.71	4.54	5.11	5.2	
	NT2RP2001391	443.52	443.52	734.13	742.83	990.71	747.95	
	NT2RP2001392	2.98	2.98	6.43	4.58	3.16	4.18	
	NT2RP2001394	3.3	3.3	8.55	8.35	6.09	10.15	
	NT2RP2001397	5.04	5.04	6.79	7.33	5.68	12.2	
35	NT2RP2001400	3.1	3.1	6.4	3.43	6.25	2.92	
	NT2RP2001408	3.31	3.31	6.13	4.02	5.97	5.62	
	NT2RP2001420	5.63	5.63	12.09	8.09	9.97	9.17	
	NT2RP2001423	4.71	4.71	9.71	6.21	8.29	7.19	
40	NT2RP2001427	2.68	2.68	5.32	3.69	4.61	5.49	
	NT2RP2001428	2.71	2.71	7.13	5.49	3.78	3.03	
	NT2RP2001436	4.27	4.27	8.85	5.84	2.85	4.84	
	NT2RP2001440	2.89	2.89	7.34	10.24	10.15	11.98	* +
	NT2RP2001445	2.43	2.43	6.75	5.86	5.55	5.89	
45	NT2RP2001449	4.37	4.37	6.41	5	4.74	5.02	
	NT2RP2001450	3.19	3.19	6.75	2.26	5.4	8.59	
	NT2RP2001467	4.53	4.53	10.28	5.32	4.72	6.5	
	NT2RP2001469	4.74	4.74	6.79	8.22	11.04	7.18	
	NT2RP2001480	6.54	6.54	26.68	14.98	12.63	15.42	
50	NT2RP2001495	5.86	5.86	11.96	3.16	9.04	10.39	
	NT2RP2001499	8.25	8.25	16.78	10.05	14.46	9.66	
	NT2RP2001506	2.79	2.79	7.24	5.32	8.19	5.33	
	NT2RP2001508	10.59	10.59	13.66	18.74	20.49	21.92	** +
	NT2RP2001511	6.41	6.41	9.74	6.08	8.63	6.53	
55	NT2RP2001514	7.04	7.04	7.02	7.24	6.44	6.38	

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	NT2RP2001520	2.93	2.93	4.84	2.6	3.19	2.87		
	NT2RP2001526	3.88	3.88	8.49	7.01	5.27	3.83		
5	NT2RP2001529	9.87	9.87	53.78	44.74	55.72	60.88		
	NT2RP2001536	1.63	1.63	4.17	3.81	4.52	4.71		
	NT2RP2001538	83.44	83.44	178.68	132.75	146.73	155.87		
	NT2RP2001547	4.96	4.96	14.87	16.77	19.21	17.77	*	+
	NT2RP2001560	6.28	6.28	21.64	25.41	28.19	27.75	*	+
10	NT2RP2001562	5.56	5.56	5.57	5.94	6.75	4.64		
	NT2RP2001566	7.96	7.96	9.24	8.22	7.91	8.56		
	NT2RP2001569	4.26	4.26	8.71	6.09	5.65	8.28		
	NT2RP2001576	3.95	3.95	11.58	13.42	9	12.82		
	NT2RP2001581	47.15	47.15	130.15	121.19	112.28	129.54		
15	NT2RP2001597	3.73	3.73	7.88	8.57	8.3	13.3		
	NT2RP2001601	2.37	2.37	4.81	3.67	4.81	3.34		
	NT2RP2001613	2.74	2.74	4.87	2.83	2.72	4.15		
	NT2RP2001628	3.42	3.42	3.97	3.14	3.04	7.84		
	NT2RP2001634	8.64	8.64	13.94	16.57	23.67	17.67	*	+
20	NT2RP2001635	2.51	2.51	5.92	5.63	5.53	4.72		
	NT2RP2001660	4.27	4.27	16.91	5.9	5.54	10.06		
	NT2RP2001662	1.49	1.49	4.07	4.5	4.44	3.47		
	NT2RP2001663	2.82	2.82	5.09	10.37	8.21	9.74	**	+
	NT2RP2001672	3.28	3.28	3.82	3.88	4.09	4	*	+
25	NT2RP2001675	4.1	4.1	5.01	5.23	4.73	5.06		
	NT2RP2001677	9.58	9.58	18.2	20.9	26.67	19.74	*	+
	NT2RP2001678	4.84	4.84	6.73	4.6	4.83	4.5		
	NT2RP2001683	1.89	1.89	3.12	4.6	4.72	2.78		
	NT2RP2001699	3.15	3.15	6.16	6.5	5.84	4.88		
30	NT2RP2001707	1.24	1.24	3.19	3.42	4.13	4.8	*	+
	NT2RP2001720	1.47	1.47	3.6	3.91	3	2.72		
	NT2RP2001721	2.26	2.26	4.57	5.53	3.96	3.66		
	NT2RP2001740	12	12	60.21	52.38	79.71	54.73		
35	NT2RP2001748	6.43	6.43	10.8	8.75	10.25	8.55		
	NT2RP2001755	5.51	5.51	4.96	3.71	4.62	2.69	*	-
	NT2RP2001762	1.25	1.25	2.01	3.87	2.56	3.52	*	+
	NT2RP2001768	1.91	1.91	4.7	6.7	5.55	4.55		
	NT2RP2001769	3.06	3.06	5.86	10.42	5.06	11.86		
	NT2RP2001784	3.62	3.62	6.23	7.06	6.02	6.91		
40	NT2RP2001805	2.33	2.33	5.61	6.02	4.93	6.6		
	NT2RP2001813	2.75	2.75	3.73	1.84	1.98	1.94	*	-
	NT2RP2001817	3.16	3.16	4.49	4.03	5.32	3.45		
	NT2RP2001818	2.72	2.72	2.45	2.35	3.62	2.66		
45	NT2RP2001837	5.13	5.13	13.43	10.29	10.16	12.33		
	NT2RP2001839	17.02	17.02	83.84	60.14	71.06	82.26		
	NT2RP2001861	2	2	6.37	3.16	3.52	3.87		
	NT2RP2001869	2.64	2.64	6.54	4.35	5.77	8.84		
	NT2RP2001876	12.15	12.15	27.71	24.54	24.93	23.67		
50	NT2RP2001878	2.32	2.32	3.96	2.95	3.32	4.95		
	NT2RP2001881	3.72	3.72	5.4	9.67	12.64	12.16	**	+
	NT2RP2001883	2.63	2.63	6.8	4.33	5.42	6.35		
	NT2RP2001884	13.59	13.59	23.56	15.33	10.54	23.6		
	NT2RP2001885	3.27	3.27	5.49	2.88	4.39	4.82		
55	NT2RP2001898	10.76	10.76	80.37	69.48	88.43	73.46		

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	NT2RP2001900	3.38	3.38	4.03	2.61	4.93	10.26	
	NT2RP2001903	3.73	3.73	7.71	5.57	5.7	8.2	
	NT2RP2001907	3.1	3.1	8.56	5.05	7.56	6.72	
5	NT2RP2001915	2.89	2.89	5.06	4.06	3.08	7.19	
	NT2RP2001921	4.04	4.04	10.3	13.02	12.45	19.33	* +
	NT2RP2001926	2.75	2.75	8.25	3.55	5.3	5.64	
	NT2RP2001933	5.65	5.65	52.55	43.62	43.55	48.58	
	NT2RP2001936	1.54	1.54	5.03	2.8	2.96	3.8	
10	NT2RP2001943	25.33	25.33	49.4	47.71	40.48	51.65	
	NT2RP2001946	3.05	3.05	4.3	3.41	4.51	6.1	
	NT2RP2001947	3.18	3.18	3.44	3.93	3.21	6.88	
	NT2RP2001948	3.59	3.59	10.79	5.71	7.29	19.72	
	NT2RP2001956	5.24	5.24	12.73	11.54	9.42	9.89	
15	NT2RP2001969	4.05	4.05	7.82	3.24	5.7	6	
	NT2RP2001976	2.9	2.9	6.39	5.68	6.95	6.41	
	NT2RP2001978	3.26	3.26	6.08	4.18	4.83	6.03	
	NT2RP2001985	2.14	2.14	3.8	2.56	4.63	2.51	
	NT2RP2001991	3.34	3.34	5.7	1.53	4.62	5.19	
20	NT2RP2001997	3.16	3.16	8.43	5.31	7.47	6.98	
	NT2RP2002015	136.21	136.21	265.98	266.8	340.89	272.43	
	NT2RP2002017	3.24	3.24	6.06	2.06	3.3	2.57	
	NT2RP2002025	6.08	6.08	51.73	31.83	26.94	37.84	
25	NT2RP2002030	6.06	6.06	11.95	9.77	8.07	8.76	
	NT2RP2002032	2.31	2.31	4.95	2.39	3.81	2.55	
	NT2RP2002033	3	3	6.71	3.53	7.57	8.05	
	NT2RP2002041	3.5	3.5	6.37	2.76	3.15	9	
	NT2RP2002046	3	3	6.88	2.99	7.4	6.01	
30	NT2RP2002047	2.71	2.71	3.86	2.06	3.87	3.83	
	NT2RP2002050	7.67	7.67	11.66	9.78	6.47	7.77	
	NT2RP2002052	3.77	3.77	8.39	6.6	3.99	6.28	
	NT2RP2002058	2.07	2.07	4.11	3.1	4.82	3.39	
	NT2RP2002060	1.48	1.48	3.44	2.1	5.9	3.18	
35	NT2RP2002063	3.61	3.61	5.83	3.3	5.2	6.65	
	NT2RP2002066	10.11	10.11	13.47	5.47	9.88	9.73	
	NT2RP2002070	3.74	3.74	6.3	2.15	3.1	3.83	
	NT2RP2002076	3.72	3.72	5.1	3.35	5.58	3.63	
	NT2RP2002078	13.09	13.09	105.74	73.87	88.51	76.08	
40	NT2RP2002079	5.76	5.76	36.34	31.87	32.66	36.54	
	NT2RP2002099	4.19	4.19	5.82	4.7	6.75	6.03	
	NT2RP2002105	2.66	2.66	12.25	11.41	14.04	11.23	
	NT2RP2002115	1.63	1.63	5.21	1.98	3.42	1.52	
	NT2RP2002124	3.66	3.66	6	4.56	5.38	3.88	
45	NT2RP2002137	3.99	3.99	4.83	2.21	2.1	1.76	** -
	NT2RP2002139	24.08	24.08	45.74	51.88	77.99	62.3	* +
	NT2RP2002154	1.37	1.37	4.13	3.56	2.36	3.2	
	NT2RP2002155	351.63	351.63	869.83	623.53	501.61	620.68	
	NT2RP2002172	1.5	1.5	3.33	2.78	3.53	5.13	
50	NT2RP2002185	3.29	3.29	7.65	7.3	8.56	8.12	
	NT2RP2002188	1.74	1.74	5.95	4.15	4.31	4.95	
	NT2RP2002192	2.9	2.9	7.6	6.65	6.42	5.83	
	NT2RP2002193	5.21	5.21	5.22	4.76	4.95	5.75	
55	NT2RP2002208	5.96	5.96	7.31	4.7	5.67	5.14	

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	NT2RP2002219	2.2	2.2	1.8	2.22	3.2	2.26		
	NT2RP2002231	1.72	1.72	3.1	4.11	2.76	5.76		
	NT2RP2002232	2.59	2.59	5.17	3.93	4.7	6.08		
5	NT2RP2002235	5.62	5.62	15.07	16.26	16.18	15.18		
	NT2RP2002239	37.02	37.02	67.99	72.09	67.21	63.77		
	NT2RP2002252	2.64	2.64	3.66	2.63	2.76	2.94		
	NT2RP2002256	4.62	4.62	15.3	11.37	16.99	12.91		
10	NT2RP2002257	7.01	7.01	22.77	18.65	25.09	20.6		
	NT2RP2002259	1.58	1.58	13.91	9.9	12.15	10.49		
	NT2RP2002264	0.6	0.6	3.14	3.2	3.12	3.92		
	NT2RP2002267	3.66	3.66	8.75	8.95	8.3	11.16		
	NT2RP2002270	4.26	4.26	8.23	16.09	10.47	14.71	*	+
15	NT2RP2002281	2.85	2.85	5.66	8.18	6.48	6.54	*	+
	NT2RP2002288	4.32	4.32	6.6	5.33	5.56	4.23		
	NT2RP2002292	5.42	5.42	8.4	6.64	8.08	6.95		
	NT2RP2002299	9.6	9.6	9.22	11.75	19.42	15.97	*	+
	NT2RP2002304	1.37	1.37	4.78	6.99	5.08	5.52		
20	NT2RP2002312	1.21	1.21	2.33	3.78	5.3	3.28	*	+
	NT2RP2002316	3.28	3.28	5.43	7.57	7.21	8.2	**	+
	NT2RP2002325	1.95	1.95	3.46	2.79	2.22	4.95		
	NT2RP2002333	2.13	2.13	3.03	3.53	4.86	5.69	*	+
	NT2RP2002371	5.43	5.43	9.14	9.72	12.07	11.65	*	+
25	NT2RP2002373	10.65	10.65	40.1	36.72	58.84	33.58		
	NT2RP2002381	4.68	4.68	2.35	2.66	3.19	3.71		
	NT2RP2002385	5.71	5.71	11.84	9.95	11.34	9.47		
	NT2RP2002394	0.94	0.94	1.52	1.24	0.96	1.26		
30	NT2RP2002408	2.7	2.7	5.08	3.89	3.12	4.29		
	NT2RP2002409	3.73	3.73	10.81	10.78	7.95	8.35		
	NT2RP2002424	2.98	2.98	4.22	5.84	6.22	7.85	*	+
	NT2RP2002426	6.44	6.44	11.38	7.59	8.46	8.93		
	NT2RP2002429	17.2	17.2	24.73	27.87	33.96	20.83		
35	NT2RP2002437	4.61	4.61	5.98	4.83	6.47	4.79		
	NT2RP2002439	3.83	3.83	6.69	2.68	3.22	4		
	NT2RP2002442	13.63	13.63	71.65	57.78	63.05	78.84		
	NT2RP2002457	3.27	3.27	5.31	4.35	4.87	5.82		
	NT2RP2002464	2.17	2.17	5.34	3.29	4.59	4.24		
40	NT2RP2002475	3.11	3.11	7.88	5.3	2.83	5.43		
	NT2RP2002479	3.09	3.09	4.25	1.95	2.99	1.93		
	NT2RP2002487	1.73	1.73	5.15	1.98	2.1	3.04		
	NT2RP2002498	1.52	1.52	2.2	2.62	2.82	4.47		
	NT2RP2002503	7.63	7.63	31.85	29.32	32.02	31.84		
45	NT2RP2002504	3.81	3.81	5.73	6	7.23	11.28		
	NT2RP2002510	2.65	2.65	8.92	4.68	6.59	6.85		
	NT2RP2002520	3.57	3.57	7.17	6.26	8.86	6.61		
	NT2RP2002527	5.18	5.18	6.02	9	12.37	11.22	**	+
	NT2RP2002533	3.34	3.34	6.27	4.83	6.94	5.88		
50	NT2RP2002537	3.22	3.22	4.02	4.09	5.91	10.08		
	NT2RP2002542	4.81	4.81	4.64	5.99	5.93	9.73		
	NT2RP2002546	4.31	4.31	5.85	6.5	4.91	5.24		
	NT2RP2002549	4.06	4.06	9.33	7.68	10.49	11.65		
	NT2RP2002564	4.11	4.11	11.18	10.67	9.21	9.29		
55	NT2RP2002591	2.45	2.45	7.03	3.31	4.79	5.79		

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	NT2RP2002595	9.67	9.67	12.41	12.06	13.39	14.79		
	NT2RP2002602	4.19	4.19	7.53	5.68	8.96	10.42		
	NT2RP2002606	1.27	1.27	2.93	2.26	2.97	3.95		
5	NT2RP2002609	6.12	6.12	9.95	4.79	5.48	7.74		
	NT2RP2002618	2.74	2.74	6.83	4.2	6.34	5.44		
	NT2RP2002621	4.24	4.24	10.22	6.58	7.52	9.79		
	NT2RP2002643	1.79	1.79	4.84	3.11	5.98	3.94		
	NT2RP2002672	4.48	4.48	9.23	8.03	9.37	9.87		
10	NT2RP2002673	4.13	4.13	5.01	8	12.88	17.73	*	+
	NT2RP2002674	2.4	2.4	4.06	2.78	2.37	1.84		
	NT2RP2002686	2.73	2.73	4.61	3.17	5.19	6.49		
	NT2RP2002688	10.73	10.73	28.07	22.34	33.34	28.71		
	NT2RP2002695	2.62	2.62	7.03	5.26	4.34	5.52		
15	NT2RP2002701	7.29	7.29	13.37	11.85	5.18	10.04		
	NT2RP2002706	3.02	3.02	5.58	6.47	8.14	6.19	*	+
	NT2RP2002710	11.2	11.2	36.97	39.43	33.9	42.75		
	NT2RP2002721	5.53	5.53	9.42	7.33	7.34	8.45		
20	NT2RP2002727	3.56	3.56	6.87	2.17	3.96	3.52		
	NT2RP2002734	3.59	3.59	6.65	5.71	7.65	7.54		
	NT2RP2002736	5.25	5.25	13.13	13.17	13.59	17.58		
	NT2RP2002740	2	2	5.11	3.18	2.81	3.13		
	NT2RP2002741	2.12	2.12	4.8	4.68	5.39	5.78		
25	NT2RP2002750	2.5	2.5	9.22	7.73	9.57	8.18		
	NT2RP2002752	4.59	4.59	10.39	7.93	7.66	8.03		
	NT2RP2002753	4.49	4.49	9.91	8.66	9.04	14.67		
	NT2RP2002760	4.79	4.79	10.31	3.56	4.5	4.13		
	NT2RP2002769	4.42	4.42	6.06	3.89	5.67	6.43		
30	NT2RP2002778	4.13	4.13	10.59	6.8	8.2	9.12		
	NT2RP2002791	8.89	8.89	54.27	48.75	53.08	50.19		
	NT2RP2002800	1.66	1.66	4.52	4	5.19	5.38		
	NT2RP2002805	3.38	3.38	5.46	4.75	6.44	3.81		
	NT2RP2002811	3.27	3.27	8.23	5.87	8.13	10.61		
35	NT2RP2002824	18.29	18.29	25.05	29.95	34.29	25.05		
	NT2RP2002839	13.26	13.26	31.21	16.09	23.42	16.27		
	NT2RP2002845	5.87	5.87	7.93	4.61	6.12	5.5		
	NT2RP2002857	2.95	2.95	3.6	2.35	4.23	2.99		
	NT2RP2002862	4.56	4.56	12.49	12.55	9.84	11.34		
40	NT2RP2002880	5.27	5.27	13.89	13.5	11.56	11.1		
	NT2RP2002885	8.6	8.6	17.12	7.56	10.07	10.02		
	NT2RP2002891	1.9	1.9	7.78	4.65	6.63	7.56		
	NT2RP2002907	2.95	2.95	6.91	5.95	5.5	4.9		
	NT2RP2002925	5.67	5.67	6.73	10.04	11.6	8.45	*	+
45	NT2RP2002927	10.08	10.08	10.63	19.05	21.85	15.48	**	+
	NT2RP2002928	4.32	4.32	4.56	2.65	2.34	2.51	**	-
	NT2RP2002929	3.96	3.96	9.74	8.09	7.86	9.87		
	NT2RP2002934	1.5	1.5	1.4	2.81	3.01	2.49	**	+
50	NT2RP2002939	2.96	2.96	5.09	5.15	6.71	4.91		
	NT2RP2002942	2.4	2.4	5.06	4.35	5.07	10.81		
	NT2RP2002954	5.41	5.41	11.46	7.21	9.1	8.65		
	NT2RP2002959	8.15	8.15	12.55	13.81	16.28	16.69	*	+
	NT2RP2002974	5.03	5.03	6.53	4.7	3.45	4.54		
55	NT2RP2002976	6.92	6.92	17.08	11.84	14.66	12.42		

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	NT2RP2002979	4.41	4.41	8.12	7.03	8.66	7.6		
	NT2RP2002980	6.44	6.44	15.09	15.56	11	17.45		
	NT2RP2002986	3.87	3.87	7.6	6.68	7.4	7.39		
5	NT2RP2002987	3.52	3.52	8.23	11.1	9.18	9.4	*	+
	NT2RP2002988	14.96	14.96	22.92	30.07	31.87	31.36	**	+
	NT2RP2002993	2.97	2.97	4.18	3.8	3.84	2.84		
	NT2RP2003000	4.88	4.88	8.34	6.97	9.62	9.97		
10	NT2RP2003008	4.85	4.85	5.06	3.34	4.76	4.78		
	NT2RP2003020	4.45	4.45	44.26	28.35	46.52	34.33		
	NT2RP2003032	1.91	1.91	4.02	5.82	6.48	6.59	**	+
	NT2RP2003034	4.21	4.21	13.47	13.16	11.15	16.31		
	NT2RP2003042	2.15	2.15	3.81	4.57	3.65	4.92		
15	NT2RP2003050	2.32	2.32	3.56	2.55	2.17	1.83		
	NT2RP2003060	7.27	7.27	15.51	21.53	18.91	17.46	*	+
	NT2RP2003073	5.61	5.61	8.73	7.06	10.51	8.17		
	NT2RP2003099	5.05	5.05	3.67	3.21	3.73	2.84		
20	NT2RP2003108	3.6	3.6	4.23	5.29	3.91	6.62		
	NT2RP2003115	1.68	1.68	5	7.75	4.69	4.84		
	NT2RP2003117	2.71	2.71	5.69	3.6	4.66	4.13		
	NT2RP2003121	1.83	1.83	3.47	4.03	2.69	3.33		
	NT2RP2003125	4.13	4.13	11.44	15.42	12.55	13.66	*	+
25	NT2RP2003127	2.36	2.36	3.94	1.53	1.66	1.75		
	NT2RP2003129	3.43	3.43	7.09	6.08	6.05	5.42		
	NT2RP2003137	4.49	4.49	6.14	7.58	8.4	6.46	*	+
	NT2RP2003138	4.66	4.66	20.24	16.55	17.45	16.92		
	NT2RP2003146	6.2	6.2	24.78	18.5	23.25	25.96		
30	NT2RP2003148	3.09	3.09	6.73	3.06	4.6	4.04		
	NT2RP2003150	1.45	1.45	5.71	3.98	5.2	4.3		
	NT2RP2003157	6.93	6.93	34.27	34.29	31.85	32.84		
	NT2RP2003158	6.3	6.3	25.32	26.87	28.69	59.31		
	NT2RP2003161	2.73	2.73	3.36	2.51	2.82	6.12		
35	NT2RP2003164	1.96	1.96	2.1	1.28	1.87	2.46		
	NT2RP2003165	2.18	2.18	5.94	3.1	3.69	4.84		
	NT2RP2003177	1.63	1.63	4.37	2.79	3.03	4.42		
	NT2RP2003179	1.23	1.23	4.98	4.08	3.63	7.96		
	NT2RP2003194	4.04	4.04	7.2	5.73	6.29	14.77		
40	NT2RP2003206	1.59	1.59	4.47	1.64	3.52	1.44		
	NT2RP2003210	5.06	5.06	15.15	16.14	12.93	15.9		
	NT2RP2003227	1.62	1.62	3.97	2.04	3.66	6.28		
	NT2RP2003228	6.57	6.57	29.53	29.56	43.94	44.24		
	NT2RP2003230	3.51	3.51	7.91	4.49	8.04	8.46		
45	NT2RP2003231	2.22	2.22	5.59	2.46	3.23	3.83		
	NT2RP2003237	2.52	2.52	4.59	4.59	6.4	6.46	*	+
	NT2RP2003239	2.3	2.3	4.46	2.97	4.46	4.05		
	NT2RP2003243	2.16	2.16	4.13	2.38	3.28	3.98		
	NT2RP2003265	3.93	3.93	5.33	4.22	4.88	4.92		
50	NT2RP2003267	2.73	2.73	3.15	3.24	4.17	7.42		
	NT2RP2003272	6.03	6.03	14.8	16.93	23.85	32.58	*	+
	NT2RP2003277	3.85	3.85	11.29	5.53	8.39	6.39		
	NT2RP2003280	3.47	3.47	9.38	7.67	7.25	6.09		
	NT2RP2003286	2.18	2.18	4.23	4.13	5	9.61		
55	NT2RP2003293	2.98	2.98	6.9	5.66	7.05	7.94		



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	NT2RP2003295	4.67	4.67	8.45	8.73	12.39	6.35		
	NT2RP2003297	3.43	3.43	7.57	4.32	6.89	5.28		
5	NT2RP2003300	20.38	20.38	32.04	45.7	53.51	48.07	**	+
	NT2RP2003302	2.88	2.88	4.52	3.46	3.81	7.26		
	NT2RP2003307	0.57	0.57	2.62	1.43	1.49	1.38		
	NT2RP2003308	1.44	1.44	4.5	2.77	4.44	5.44		
	NT2RP2003311	4.18	4.18	5.83	7.35	4.25	8.2		
10	NT2RP2003329	2.99	2.99	4.41	2.63	3.89	4.44		
	NT2RP2003339	3.06	3.06	7.01	3.76	4.92	3.64		
	NT2RP2003345	4.15	4.15	8.38	2.77	3.97	6.33		
	NT2RP2003347	2.55	2.55	4.23	2.08	1.98	3.46		
	NT2RP2003367	2.15	2.15	4.65	2.7	1.98	1.44		
15	NT2RP2003369	1.34	1.34	4.71	2.16	2.36	0.89		
	NT2RP2003383	4.05	4.05	6.75	7.66	7.17	6.99		
	NT2RP2003390	9.1	9.1	17.93	16.66	14.27	12.94		
	NT2RP2003391	9.39	9.39	12.9	11.96	9.91	12.84		
	NT2RP2003393	4.23	4.23	6.99	6.14	5.03	9.44		
20	NT2RP2003394	8.67	8.67	16.21	17.56	21.75	17.23		
	NT2RP2003401	4.39	4.39	5.97	3.52	3.72	2.9		
	NT2RP2003403	3.42	3.42	7.64	6.62	8.55	7.79		
	NT2RP2003433	3.02	3.02	15.54	13.62	13.5	13.08		
	NT2RP2003445	3.2	3.2	4.74	4.08	3.5	3.93		
25	NT2RP2003446	2.67	2.67	6.23	5.06	6.05	4.47		
	NT2RP2003456	2.04	2.04	6.57	4.26	5.89	3.81		
	NT2RP2003466	3.56	3.56	20.09	17.34	25.96	23.53		
	NT2RP2003469	6.2	6.2	5.65	6.19	7.53	6.33		
	NT2RP2003470	5.64	5.64	6.47	5.06	6.11	6.44		
30	NT2RP2003471	2.72	2.72	3.88	3.22	2.78	3.38		
	NT2RP2003480	7.15	7.15	20.74	19.77	19.89	21.14		
	NT2RP2003495	3.99	3.99	6.03	8.07	7.24	10.72	*	+
	NT2RP2003499	1.52	1.52	4.58	3.67	4.05	2.75		
	NT2RP2003505	0.98	0.98	3.21	2.62	3.88	1.4		
35	NT2RP2003506	2.54	2.54	6.53	5.65	5.36	4.78		
	NT2RP2003511	3.67	3.67	5.57	4.22	3.1	2.96		
	NT2RP2003513	3.79	3.79	6.01	5.49	5.57	5.71		
	NT2RP2003517	2.9	2.9	2.52	1.32	1.11	0.85	**	-
	NT2RP2003522	11.08	11.08	19.77	10.55	11.42	16.52		
40	NT2RP2003525	5.12	5.12	14.93	12.19	10.72	11.79		
	NT2RP2003533	3.36	3.36	10.44	12.12	10.72	12.94		
	NT2RP2003541	6.72	6.72	11.29	12.02	13.42	11.7		
	NT2RP2003543	2.48	2.48	5.96	4.17	3.55	6.54		
	NT2RP2003545	2.59	2.59	4.85	2.22	3.6	1.85		
45	NT2RP2003559	4.92	4.92	4.81	3.97	3.84	3.37	**	-
	NT2RP2003564	4.46	4.46	3.93	2.53	1.97	2.42	**	-
	NT2RP2003565	4.94	4.94	50.48	41.12	48.32	37.82		
	NT2RP2003567	3.51	3.51	16.65	16.25	19.43	16.05		
	NT2RP2003575	4.44	4.44	18.78	19.56	22.63	20.7		
50	NT2RP2003576	102.12	102.12	203.44	206.62	128.42	171.89		
	NT2RP2003579	11.45	11.45	26.58	38.62	39.51	39.88	*	+
	NT2RP2003581	3.85	3.85	6.1	4.33	4.38	3.96		
	NT2RP2003587	8.37	8.37	11.47	13.35	14.11	12.14	*	+
55	NT2RP2003590	7.15	7.15	9.08	11.06	13.15	14.91	*	+

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	NT2RP2003593	1.58	1.58	4.57	7.84	4.43	8.59		
	NT2RP2003596	4.86	4.86	10.86	14.43	13.12	17.96	*	+
	NT2RP2003599	6.49	6.49	12.46	14.29	10.17	11.98		
5	NT2RP2003600	1.88	1.88	2.95	3.02	3.64	6.36		
	NT2RP2003604	7.09	7.09	8.97	16.39	13.03	16.68	**	+
	NT2RP2003629	3.72	3.72	5.25	3.11	4.56	2.38		
	NT2RP2003630	4.09	4.09	6.66	4.79	6.78	3.84		
	NT2RP2003643	5.49	5.49	4.88	7.15	9.8	8.51	*	+
10	NT2RP2003655	4.27	4.27	11.12	7.52	6.38	7.59		
	NT2RP2003664	12.29	12.29	24.31	17.9	18.07	17.11		
	NT2RP2003668	2.52	2.52	5.01	3.3	3.18	3.62		
	NT2RP2003687	1.61	1.61	2.77	1.63	2.42	1.71		
15	NT2RP2003691	3.03	3.03	5.07	3.7	4.21	4.57		
	NT2RP2003702	3.99	3.99	6.14	2.89	3.02	2.89		
	NT2RP2003704	3.31	3.31	4.12	2.65	3.84	1.99		
	NT2RP2003706	2.44	2.44	1.24	1.72	1.42	1.6		
	NT2RP2003713	4.11	4.11	5.49	4.16	3.89	3.87		
20	NT2RP2003714	3.39	3.39	7.8	5.19	5.31	5.32		
	NT2RP2003727	3.96	3.96	11.63	4.81	6.08	10.46		
	NT2RP2003737	2.52	2.52	8.58	4.88	6.47	4.6		
	NT2RP2003751	1.66	1.66	4.84	1.24	1.67	1.37		
	NT2RP2003760	2.52	2.52	5.47	3.87	4.19	5.45		
25	NT2RP2003764	2.1	2.1	2.81	1.44	1.87	4.62		
	NT2RP2003769	5.52	5.52	11.45	7.41	8.17	10.64		
	NT2RP2003770	7.43	7.43	12.42	7.17	5.67	12.82		
	NT2RP2003777	3.44	3.44	6.78	5.01	5.6	9.57		
	NT2RP2003781	4.93	4.93	15.85	13.04	11.91	13.48		
30	NT2RP2003785	9.69	9.69	13.44	11.1	10.68	8.99		
	NT2RP2003793	9.32	9.32	9.5	8.29	13.22	10.51		
	NT2RP2003806	5.6	5.6	12.03	8.54	8.75	12.97		
	NT2RP2003825	10.73	10.73	62.01	57.88	71.84	82.78		
	NT2RP2003840	3.19	3.19	6.07	3.86	4.44	4.71		
35	NT2RP2003857	4.02	4.02	4.94	3.15	4.61	6.12		
	NT2RP2003859	1.82	1.82	6	3.35	4.16	4.21		
	NT2RP2003871	5.22	5.22	9.43	5.1	4.59	7.79		
	NT2RP2003876	3.82	3.82	8.8	5.92	5.87	7.92		
	NT2RP2003878	3.38	3.38	6.49	3.8	4.9	4.11		
40	NT2RP2003885	2.46	2.46	3.09	1.66	3.29	2.37		
	NT2RP2003898	5.39	5.39	8.91	12.3	12.73	18.25	*	+
	NT2RP2003902	5.09	5.09	10.78	8.24	8.23	10.42		
	NT2RP2003912	3.83	3.83	14.48	5.91	7.43	6.74		
	NT2RP2003931	1.81	1.81	6.03	3.95	6.86	4.42		
45	NT2RP2003940	2.31	2.31	9.51	7.1	6.2	7.3		
	NT2RP2003950	2.81	2.81	5.48	3.84	5.57	2.98		
	NT2RP2003952	1.86	1.86	5.63	2.58	4.23	2.98		
	NT2RP2003968	4.82	4.82	7.38	9.86	11.76	13.51	*	+
50	NT2RP2003976	5.35	5.35	9.56	12.56	12.6	13.2	*	+
	NT2RP2003981	3.27	3.27	7.41	4.62	2.03	4.07		
	NT2RP2003984	5.57	5.57	15.87	10.21	4.25	10.34		
	NT2RP2003986	2.79	2.79	6.22	6.29	6.32	5.17		
	NT2RP2003988	2.36	2.36	6.84	4.51	7.42	5		
55	NT2RP2004013	8.46	8.46	13.75	14.68	13.19	17		

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	NT2RP2004014	4.24	4.24	10.07	4.06	5.12	4.08		
	NT2RP2004036	6.88	6.88	14.85	14.08	19.02	16.03		
	NT2RP2004041	2.77	2.77	5.02	3.96	4.43	5.19		
5	NT2RP2004042	1.99	1.99	4.6	4.41	2.02	4.09		
	NT2RP2004049	4.68	4.68	19.13	14.24	15.5	16.3		
	NT2RP2004060	5.7	5.7	10.41	7.09	8.67	10.84		
	NT2RP2004066	2.17	2.17	4.31	3.05	4.83	3.65		
10	NT2RP2004069	3.99	3.99	7.24	3.54	6	4.26		
	NT2RP2004076	3.73	3.73	5.82	1.92	4.2	3.61		
	NT2RP2004080	4.21	4.21	9.26	4.45	6.47	6.15		
	NT2RP2004081	3.27	3.27	5.39	3.51	3.71	4.5		
	NT2RP2004098	2.32	2.32	6.48	5.4	3.1	5.75		
15	NT2RP2004108	3.82	3.82	9.56	7.18	5.89	7.56		
	NT2RP2004124	3.13	3.13	5.9	3.68	5.82	3.92		
	NT2RP2004130	3.67	3.67	9.32	5.51	9.12	8.4		
	NT2RP2004133	2.05	2.05	6.41	3.69	6.54	6.25		
	NT2RP2004141	5.72	5.72	7.15	5.14	7.05	7.05		
20	NT2RP2004142	5.33	5.33	8.1	4.18	5.45	3.93		
	NT2RP2004152	3.34	3.34	4.78	5.7	7.49	4.39		
	NT2RP2004165	3.71	3.71	8.3	5.87	5.92	6.54		
	NT2RP2004170	1.86	1.86	5.97	5.37	4.17	4.94		
	NT2RP2004172	2.93	2.93	5.24	4.69	5.58	4.26		
25	NT2RP2004176	3.45	3.45	8.4	7.77	10.21	8.98		
	NT2RP2004179	4.01	4.01	9.17	3.94	5.07	4.15		
	NT2RP2004187	3.16	3.16	6.36	3.87	3.88	4.59		
	NT2RP2004190	5.1	5.1	5.46	5.49	7.33	9.98		
30	NT2RP2004194	7.54	7.54	14.57	18.5	23.44	19.83	*	+
	NT2RP2004196	4.28	4.28	13.77	10.02	7.87	14.61		
	NT2RP2004205	2.67	2.67	8.14	8.64	6.62	7.81		
	NT2RP2004207	2.57	2.57	4.38	4.15	4.97	3.59		
	NT2RP2004226	2.09	2.09	4.95	4.11	6.15	5.33		
35	NT2RP2004232	2.79	2.79	6.52	6	6.59	5.33		
	NT2RP2004239	3.57	3.57	4.49	2.71	3.97	5.6		
	NT2RP2004240	7.07	7.07	12.57	13	15.8	8.95		
	NT2RP2004242	3.87	3.87	6.52	5.77	6.94	7.27		
	NT2RP2004245	1.74	1.74	3.47	2.42	3.29	3.15		
40	NT2RP2004270	9.77	9.77	33.78	28.39	27.43	29.48		
	NT2RP2004300	2	2	5.22	4.34	4.52	3.26		
	NT2RP2004304	6.46	6.46	15.37	17.41	12.33	13.9		
	NT2RP2004313	3.17	3.17	3.78	5.51	4.18	4.63	*	+
	NT2RP2004316	3.46	3.46	5.84	4.9	4.96	4.04		
45	NT2RP2004321	4.71	4.71	6.06	6.79	7.43	6.29	*	+
	NT2RP2004336	4.19	4.19	4.97	2.73	4.28	4.53		
	NT2RP2004339	5.3	5.3	20.89	17.11	18.07	15.39		
	NT2RP2004347	1.39	1.39	3.99	4.78	5	4.19		
	NT2RP2004364	2.26	2.26	6.52	5.08	6.72	4.76		
50	NT2RP2004365	3.18	3.18	6.58	6.68	6.34	7.7		
	NT2RP2004366	2.49	2.49	6.06	4.49	4.71	3.08		
	NT2RP2004373	8.17	8.17	14.38	7.1	7.22	5.91		
	NT2RP2004375	9.27	9.27	13.98	20.89	26.85	20.68	**	+
	NT2RP2004389	5.25	5.25	5.62	5.01	6.26	5.61		
55	NT2RP2004392	8.88	8.88	23.7	13.04	19.48	20.89		

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	NT2RP2004396	1.98	1.98	6.27	6.65	4.98	6.17		
	NT2RP2004399	5.24	5.24	8.12	12.56	7.74	9.52		
	NT2RP2004400	2.07	2.07	3.55	2.36	3.47	2		
5	NT2RP2004404	15.79	15.79	46	45.56	40.89	41.74		
	NT2RP2004410	16.64	16.64	24.04	27.99	33.46	32.69	*	+
	NT2RP2004412	5.84	5.84	6.74	7.37	9.71	7.37		
	NT2RP2004414	4.27	4.27	5.09	3.81	4.89	3.8		
10	NT2RP2004425	3.71	3.71	6.53	3.73	3.18	4.04		
	NT2RP2004447	1.93	1.93	5.68	2.75	5.22	3.56		
	NT2RP2004463	13.57	13.57	16.23	16.84	16.25	20.26		
	NT2RP2004476	9.11	9.11	12.69	11.89	12.66	15.87		
	NT2RP2004488	3.82	3.82	8.52	4.59	6.02	5.37		
15	NT2RP2004490	2.88	2.88	3.86	2.31	2.96	4.1		
	NT2RP2004495	35.59	35.59	88.76	96.31	109.31	123.5	*	+
	NT2RP2004512	4.25	4.25	7.62	5.84	6.41	7.12		
	NT2RP2004523	5.18	5.18	11.04	8.44	7.56	10.21		
	NT2RP2004524	2.19	2.19	6.33	4.97	5.32	5.56		
20	NT2RP2004536	8.99	8.99	16.96	14.1	14.51	17.51		
	NT2RP2004538	8.03	8.03	24.44	20.15	25.59	22.24		
	NT2RP2004548	4.45	4.45	9.92	7.39	9.1	10.51		
	NT2RP2004551	4.95	4.95	5.62	7.17	9.98	6.21		
25	NT2RP2004556	83.73	83.73	210.17	226.48	298.92	241.84		
	NT2RP2004568	5.19	5.19	11.18	6.52	9.16	9.99		
	NT2RP2004580	3.98	3.98	7.71	5.71	7.88	7.04		
	NT2RP2004585	11.28	11.28	49.82	36.69	46.91	64.56		
	NT2RP2004587	1.85	1.85	4.16	2.07	2.89	3		
30	NT2RP2004594	4.56	4.56	9.24	11.47	12.21	28.18		
	NT2RP2004600	3.49	3.49	5.76	2.22	3.22	3.09		
	NT2RP2004602	4.62	4.62	6.32	6	8.49	6.26		
	NT2RP2004606	392.21	392.21	581.19	612.4	897.5	764.63	*	+
	NT2RP2004614	2.92	2.92	4.73	2.69	3.63	3.81		
35	NT2RP2004648	2.52	2.52	4.96	3.24	5.01	4.12		
	NT2RP2004655	5.69	5.69	10.1	8.37	6.76	9.46		
	NT2RP2004664	3.64	3.64	5.35	3.59	4.62	5.97		
	NT2RP2004670	1.98	1.98	3.81	1.98	3.71	4.27		
	NT2RP2004675	3.37	3.37	9.29	4.08	5.87	5.33		
40	NT2RP2004681	3.46	3.46	7.56	5.72	8.92	7.55		
	NT2RP2004689	2.63	2.63	5.75	5.75	4.73	7.87		
	NT2RP2004709	3.93	3.93	7.79	4.46	2.89	5.25		
	NT2RP2004710	3.15	3.15	8.37	5.63	4.61	6.88		
	NT2RP2004721	1.79	1.79	5.99	3.39	4.41	2.78		
45	NT2RP2004736	3.26	3.26	5.81	6.11	4.79	4.63		
	NT2RP2004743	4.94	4.94	7.96	5.94	6.67	7.36		
	NT2RP2004750	6.21	6.21	17.46	11.9	15.49	11.01		
	NT2RP2004755	11.65	11.65	19.9	14.84	22.87	19.91		
	NT2RP2004767	3.54	3.54	9	4.05	5.8	4.81		
50	NT2RP2004768	3.48	3.48	29.51	18.48	18.73	19.6		
	NT2RP2004775	4.68	4.68	5.68	7.71	5.62	8.26		
	NT2RP2004791	7.23	7.23	16.58	9.33	10.24	11.68		
	NT2RP2004794	14.01	14.01	25.74	23.04	16.86	22.78		
	NT2RP2004795	5.15	5.15	7.97	6.96	5.67	11.2		
55	NT2RP2004799	6.74	6.74	10.99	5.35	8.58	6.3		

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	NT2RP2004802	6.35	6.35	11.79	6.1	7.62	6.24	
	NT2RP2004810	3.44	3.44	8.83	7.37	7.84	6.03	
	NT2RP2004816	5.58	5.58	12.1	11.22	8.76	11.15	
5	NT2RP2004837	4.13	4.13	9.89	10.43	7.23	12.98	
	NT2RP2004841	0.91	0.91	2.86	3.69	4.03	8.87	
	NT2RP2004847	3.25	3.25	13.75	13.82	13.87	17.16	
	NT2RP2004861	2.3	2.3	5.23	2.33	4.23	2.46	
10	NT2RP2004897	3.35	3.35	6.43	4.26	3.27	3.35	
	NT2RP2004932	6.64	6.64	10.16	7.96	8.53	6.91	
	NT2RP2004933	4.63	4.63	3.41	2.98	2.93	3.2	*
	NT2RP2004936	3.69	3.69	6.41	4.56	4.42	7.53	
	NT2RP2004951	2.98	2.98	10.48	5.09	5.22	19.28	
15	NT2RP2004959	3.13	3.13	6.61	6.43	6.26	6.5	
	NT2RP2004961	2.1	2.1	4.79	4.89	6.49	5.44	
	NT2RP2004962	2.27	2.27	7.28	4.5	5.57	4.47	
	NT2RP2004966	2.26	2.26	6.07	4.1	4.1	2.97	
	NT2RP2004967	3.87	3.87	6.16	4.07	4.82	3.26	
20	NT2RP2004974	5.27	5.27	5.43	3.59	3.47	3.89	**
	NT2RP2004978	2.68	2.68	5.26	4.17	6.39	5.09	
	NT2RP2004982	0.57	0.57	1.82	2.2	1.94	1.72	
	NT2RP2004985	16.03	16.03	45.34	44.65	46.12	54.4	
	NT2RP2004999	2.21	2.21	5.64	4.27	8.86	10.34	
25	NT2RP2005000	3.62	3.62	5.76	4.33	4.76	4.65	
	NT2RP2005001	5.41	5.41	7.91	8.26	9.15	8.32	
	NT2RP2005003	3.8	3.8	7.2	6.11	7.91	6.2	
	NT2RP2005012	6.61	6.61	20.14	18.41	20.96	17.87	
	NT2RP2005018	1.9	1.9	4.24	3.29	2.24	2.91	
30	NT2RP2005020	6.12	6.12	23.58	19.97	19.94	22.96	
	NT2RP2005022	1.65	1.65	5.01	5.09	7.24	4.77	
	NT2RP2005027	5.96	5.96	38.61	42.51	40.08	33.77	
	NT2RP2005031	1.54	1.54	4.99	3.94	4.53	3.92	
	NT2RP2005035	44.19	44.19	94.82	116.52	107.36	106.69	* +
35	NT2RP2005037	4.28	4.28	5.87	7.91	10.26	7.09	*
	NT2RP2005038	4.86	4.86	4.84	1.85	2.29	3.1	**
	NT2RP2005048	9.92	9.92	30.91	30.14	33.38	32.48	
	NT2RP2005069	16.01	16.01	34.88	21.99	20.63	27.64	
40	NT2RP2005073	7.36	7.36	30.35	29.36	28.24	30.33	
	NT2RP2005097	2.39	2.39	5.6	5.27	5.2	4.6	
	NT2RP2005108	1.76	1.76	3.95	2.84	4.21	7.12	
	NT2RP2005116	3.53	3.53	5.96	6.27	5.42	5.89	
	NT2RP2005126	5.88	5.88	8.31	8.9	14.96	8.51	
45	NT2RP2005135	5.08	5.08	5.22	4.65	6.59	5.47	
	NT2RP2005139	1.94	1.94	2.77	1.87	1.81	2.45	
	NT2RP2005140	3.82	3.82	4.86	12.39	6.72	8.55	* +
	NT2RP2005144	4.04	4.04	6.31	6.69	5.97	9.7	
	NT2RP2005147	2.23	2.23	5.49	5.61	6.15	6.25	
50	NT2RP2005148	2.86	2.86	5.63	3.83	6.65	4.83	
	NT2RP2005159	3.92	3.92	5.6	4.94	6.38	7.41	
	NT2RP2005162	3.23	3.23	5.56	4.57	5.4	4.21	
	NT2RP2005163	9.15	9.15	20.61	24.53	28.92	23.77	* +
	NT2RP2005168	2.87	2.87	6.14	5.24	4.79	4.88	
55	NT2RP2005181	2.64	2.64	5.42	3.4	2.11	1.98	

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	NT2RP2005204	5.4	5.4	7.81	9.08	11.94	11.81	*	+
	NT2RP2005219	4.61	4.61	9.64	7.09	10.28	8.7		
	NT2RP2005227	3.59	3.59	10.43	7.55	5.36	9.97		
5	NT2RP2005237	26.49	26.49	94.81	86.96	105.8	93.92		
	NT2RP2005239	2.24	2.24	6.07	2.62	4.27	4.34		
	NT2RP2005247	10.63	10.63	37.59	35.58	46.1	46.95		
	NT2RP2005254	4.35	4.35	9.14	5.7	6.44	6.93		
	NT2RP2005270	9.06	9.06	17.44	10.82	9.28	17.11		
10	NT2RP2005276	7.19	7.19	11.53	10.88	11.68	15.71		
	NT2RP2005287	7.98	7.98	11.97	8.37	7.7	13.36		
	NT2RP2005288	2.51	2.51	5.14	2.89	5.59	5.22		
	NT2RP2005289	4.26	4.26	8.48	6.68	9.08	7.49		
15	NT2RP2005293	5	5	6.93	13.68	14.37	15.66	**	+
	NT2RP2005315	5.79	5.79	10.64	8.04	12.95	16.68		
	NT2RP2005322	5.05	5.05	15.42	18.91	11.33	22.43		
	NT2RP2005325	8.45	8.45	18.4	15.57	13.63	20.01		
	NT2RP2005336	1.71	1.71	6.68	4.18	5.74	5.3		
20	NT2RP2005343	2.44	2.44	7.48	3.91	4.11	5.89		
	NT2RP2005344	3.39	3.39	4.83	2.37	2.67	3.32		
	NT2RP2005347	3.14	3.14	3.61	3.34	2.96	3.53		
	NT2RP2005354	6.49	6.49	11.79	10.37	13	11.38		
	NT2RP2005358	35.87	35.87	109.04	101.37	134.72	117.96		
25	NT2RP2005360	2.93	2.93	5	3.59	4.97	3.84		
	NT2RP2005378	5.27	5.27	13.12	7.54	8.7	13.93		
	NT2RP2005391	3.06	3.06	5.41	4.21	6.76	7.72		
	NT2RP2005393	1.61	1.61	6.34	4.86	6.16	4.07		
	NT2RP2005407	2.59	2.59	5.71	4.28	5.65	4.64		
30	NT2RP2005419	2.65	2.65	9.05	6.37	8.5	6.77		
	NT2RP2005425	5.63	5.63	18.38	15.27	18.89	15.46		
	NT2RP2005429	3.23	3.23	5.85	5.41	6.65	5.64		
	NT2RP2005436	4.65	4.65	10.5	7.02	4.28	4.97		
	NT2RP2005441	2.28	2.28	5.62	3.36	3.77	5.79		
35	NT2RP2005442	24.92	24.92	40.66	34.62	25.56	41.66		
	NT2RP2005444	10.72	10.72	19.24	21.92	21.07	25.56	*	+
	NT2RP2005453	2.79	2.79	7.44	2.63	4.09	3.15		
	NT2RP2005457	15.12	15.12	23.21	28.69	37.38	31.61	*	+
	NT2RP2005458	2.47	2.47	5.27	3.55	4.16	4.95		
40	NT2RP2005463	7.73	7.73	15.23	15.65	22.11	25.05	*	+
	NT2RP2005464	5.96	5.96	11.91	9.22	4.67	10.35		
	NT2RP2005465	1.81	1.81	6.69	3.86	3.75	3.74		
	NT2RP2005472	10.98	10.98	32.59	28.21	27.9	25.85		
	NT2RP2005476	5.01	5.01	8.99	7.01	6.98	6.08		
45	NT2RP2005490	7.51	7.51	21.09	18.18	25.55	23.45		
	NT2RP2005491	4.99	4.99	12.47	8.63	10.12	8.78		
	NT2RP2005495	3.56	3.56	5.77	3.38	4.55	4.3		
	NT2RP2005496	4.84	4.84	18.25	11.3	13.16	11.28		
	NT2RP2005498	2.92	2.92	7.45	5.18	5.03	4.98		
50	NT2RP2005501	2.04	2.04	5.54	3.12	4.34	2.46		
	NT2RP2005506	124.3	124.3	217.82	139.27	121.83	104.81		
	NT2RP2005509	6.97	6.97	10.45	11.4	9.61	15.73		
	NT2RP2005514	3.93	3.93	6	4.06	7.05	4.39		
55	NT2RP2005520	14.95	14.95	32.39	27.11	39.97	33.03		

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	NT2RP2005525	6.19	6.19	7.01	7.81	7.68	4.79	
	NT2RP2005531	2.18	2.18	3.33	1.67	2.12	1.9	
	NT2RP2005535	4.66	4.66	9.09	9.34	7.79	8.91	
5	NT2RP2005539	3.39	3.39	6.22	6.43	5.84	7.45	
	NT2RP2005540	3.2	3.2	7.15	4.79	5.58	6.59	
	NT2RP2005541	21.25	21.25	39.57	25.85	38.31	39.61	
	NT2RP2005549	2.69	2.69	7.66	6.72	4.85	7.11	
	NT2RP2005555	7.97	7.97	10.1	14.96	16.19	15.37	** +
10	NT2RP2005557	4.89	4.89	8.47	4.03	6.52	6.26	
	NT2RP2005581	3.93	3.93	9.61	6.32	7.95	6.89	
	NT2RP2005586	1.56	1.56	3.18	3.21	2.92	4.74	
	NT2RP2005597	2.77	2.77	2.93	2.98	4.1	3.84	
15	NT2RP2005600	1.81	1.81	3.71	4.03	4.29	4.44	* +
	NT2RP2005605	4.93	4.93	14.29	13.17	15.14	15.75	
	NT2RP2005614	3.06	3.06	5.62	3.68	4.11	2.45	
	NT2RP2005620	3.47	3.47	6.26	3.6	3.92	3.11	
	NT2RP2005622	6.14	6.14	5.07	6.21	7.43	4.61	
20	NT2RP2005632	5.72	5.72	10.95	11.57	10.42	14.89	
	NT2RP2005635	2.22	2.22	19.06	18.14	23.77	18.14	
	NT2RP2005637	1.53	1.53	8	3.73	3.71	4.14	
	NT2RP2005640	1.72	1.72	7.22	7.49	8.73	6.06	
	NT2RP2005645	4.68	4.68	11.8	10.61	11.47	9.67	
25	NT2RP2005651	3.45	3.45	7.88	7.64	6.78	10.15	
	NT2RP2005654	4.08	4.08	4.14	3.02	2.52	3.8	
	NT2RP2005666	4.91	4.91	5.27	4.34	7.7	4.74	
	NT2RP2005669	7.15	7.15	7.95	7.05	11.14	8.21	
	NT2RP2005670	2.35	2.35	6.91	7.77	5.04	5.2	
30	NT2RP2005671	3.12	3.12	7.83	10.77	8.9	9.78	* +
	NT2RP2005675	7.32	7.32	37.84	34.46	40.94	40.02	
	NT2RP2005683	2.56	2.56	7.01	7.16	5.19	7.16	
	NT2RP2005690	2.84	2.84	4.48	2.82	3.74	3.4	
	NT2RP2005694	4.07	4.07	5.49	3.77	6.26	3.54	
35	NT2RP2005701	5.97	5.97	8.82	10.39	10.35	9.52	* +
	NT2RP2005712	5.67	5.67	5.28	4.83	7.94	6.33	
	NT2RP2005719	1.86	1.86	3.26	4.42	3.8	3.76	* +
	NT2RP2005722	4.16	4.16	11.13	13.39	15.7	15.94	* +
	NT2RP2005723	2.71	2.71	4.2	3.65	4.58	3.67	
40	NT2RP2005726	2.55	2.55	4.13	2.86	4.01	3.22	
	NT2RP2005729	4.64	4.64	9.94	10.21	10.7	10.62	
	NT2RP2005731	3.05	3.05	3.39	2.51	2.16	1.27	* -
	NT2RP2005732	9.41	9.41	57.73	48.37	75.21	41.64	
45	NT2RP2005737	10.75	10.75	22.28	27.16	25.02	17.59	
	NT2RP2005741	3.03	3.03	5.35	3.68	3.31	3.37	
	NT2RP2005748	1.86	1.86	5.94	3.8	3.72	2.95	
	NT2RP2005752	2.46	2.46	5.55	3.27	4.37	3.8	
	NT2RP2005753	8.45	8.45	14.76	11.12	11.69	14.45	
50	NT2RP2005763	3	3	8.03	4.22	4.77	5	
	NT2RP2005767	3.72	3.72	7.79	5.55	6.75	6.29	
	NT2RP2005773	8.11	8.11	10.02	10.6	11.59	13.37	* +
	NT2RP2005774	4.25	4.25	12.72	6.86	12.24	14.61	
	NT2RP2005775	3.75	3.75	7.2	3.35	4.83	5.63	
55	NT2RP2005781	5.11	5.11	9.88	9.82	7.19	12.94	

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	NT2RP2005784	5.41	5.41	11.51	7.68	12.12	14.06		
	NT2RP2005789	3.98	3.98	11.24	7.89	9.52	8.86		
5	NT2RP2005799	2.45	2.45	6.35	2.64	4.67	3.7		
	NT2RP2005804	9.01	9.01	25	27.85	27.32	30.57		
	NT2RP2005812	2.63	2.63	4.83	2.9	3.89	5.21		
	NT2RP2005815	2.48	2.48	3.15	2.38	3.21	5.2		
	NT2RP2005835	5.99	5.99	11.26	7.13	13.74	11.69		
10	NT2RP2005841	2.32	2.32	10.04	4.89	7.43	11.23		
	NT2RP2005853	1.29	1.29	4.44	2.71	4.6	4.96		
	NT2RP2005857	7.37	7.37	9.87	13.46	7.93	20.27		
	NT2RP2005859	2.76	2.76	5	2.91	6.14	4.78		
	NT2RP2005860	1.41	1.41	3.54	1.45	1.89	2.22		
15	NT2RP2005863	3.03	3.03	6.55	10.76	18.29	15.94	*	+
	NT2RP2005868	3.86	3.86	5.85	5.1	6.3	7.77		
	NT2RP2005876	5.7	5.7	12.31	7.84	8.29	8.2		
	NT2RP2005878	2.26	2.26	8.44	5.25	4.95	6.32		
	NT2RP2005883	13.54	13.54	21.06	23.75	9.57	28.09		
20	NT2RP2005886	7.18	7.18	50.05	51.13	62.09	50.14		
	NT2RP2005887	3.76	3.76	6.51	4.74	8.05	4.81		
	NT2RP2005890	4.17	4.17	9.77	11.87	17.13	12.15	*	+
	NT2RP2005901	3.19	3.19	5.69	3.91	6.18	5.14		
	NT2RP2005902	3.17	3.17	4.33	4.78	4.77	6.25		
25	NT2RP2005908	3.09	3.09	7.86	4.89	3.7	6.34		
	NT2RP2005927	1.77	1.77	2.66	2.25	4.36	3.07		
	NT2RP2005933	2.5	2.5	5.59	6.4	4.77	6.42		
	NT2RP2005941	2.09	2.09	5.2	3.31	4.41	3.9		
	NT2RP2005942	4	4	6.86	3.08	4.59	4.64		
30	NT2RP2005946	4.63	4.63	9.49	5.33	7.06	6.24		
	NT2RP2005970	5.44	5.44	14	16.16	22.05	18.9	*	+
	NT2RP2005980	3.71	3.71	5.25	2.69	3.46	2.37		
	NT2RP2005994	2.99	2.99	6.76	4.28	3.28	5.14		
35	NT2RP2006004	1.31	1.31	2.89	2.07	6.09	2.58		
	NT2RP2006013	1.38	1.38	4.91	3.1	5.07	4.92		
	NT2RP2006023	8.37	8.37	17.77	20	21.43	21.14	*	+
	NT2RP2006028	5.03	5.03	10.23	7.47	9.89	9.71		
	NT2RP2006038	4.67	4.67	5.86	2.79	5.4	1.09		
40	NT2RP2006042	8.3	8.3	7.22	6.63	5.89	6.3	*	-
	NT2RP2006043	5.65	5.65	7.59	7.6	10.99	8.29		
	NT2RP2006052	1.48	1.48	4.48	4.13	3.12	4.54		
	NT2RP2006057	3.73	3.73	6.23	5.69	3.83	4.95		
	NT2RP2006064	4.16	4.16	7.73	5.86	6.81	9.08		
45	NT2RP2006068	2.76	2.76	6.75	6.8	7.81	5.81		
	NT2RP2006069	1.46	1.46	4.94	3.56	3.95	3.3		
	NT2RP2006071	8.37	8.37	7.8	9.28	10.48	9.11	*	+
	NT2RP2006090	6.62	6.62	5.78	3.27	3.55	3.64	**	-
	NT2RP2006092	3.78	3.78	8.3	6.18	8.04	7.07		
50	NT2RP2006097	14.05	14.05	40.38	31.2	25.81	40.02		
	NT2RP2006098	1.94	1.94	4.27	4.52	4.61	7.65		
	NT2RP2006099	3.84	3.84	11.02	10.65	10.99	13.34		
	NT2RP2006100	2.87	2.87	5.78	3.63	7.31	5.19		
	NT2RP2006103	2.39	2.39	5.54	2.6	3.93	1.71		
55	NT2RP2006106	6.48	6.48	21.51	18.05	24.81	22.3		



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	NT2RP2006127	3.17	3.17	4.92	1.62	1.26	1.21	*	-
	NT2RP2006134	4.25	4.25	4.41	6.08	6.7	5.47	**	+
	NT2RP2006141	3.91	3.91	7.94	7.45	6.04	9.08		
5	NT2RP2006166	3.1	3.1	10.65	9.01	8.94	7.85		
	NT2RP2006176	2.15	2.15	4.26	3.95	5.73	4.69		
	NT2RP2006181	1.68	1.68	2.84	3.21	3.14	2.45		
	NT2RP2006184	8.85	8.85	17.16	20.8	19.95	17.1		
10	NT2RP2006186	3.01	3.01	4.57	2.77	2.29	4.33		
	NT2RP2006196	5.24	5.24	7.21	5.25	5.23	4.16		
	NT2RP2006199	5.06	5.06	4.38	3.81	3.65	3.64	**	-
	NT2RP2006200	0.87	0.87	3.43	4.37	4.52	2.17		
	NT2RP2006210	20.08	20.08	59.85	75.37	70.55	96.59	*	+
15	NT2RP2006219	2.88	2.88	6.26	5.97	5.11	7.36		
	NT2RP2006224	3.7	3.7	7.55	9	7.7	8.93		
	NT2RP2006237	1.97	1.97	4.79	3.45	2.74	4.14		
	NT2RP2006238	3.9	3.9	6.33	4.2	4.69	3.93		
	NT2RP2006258	4.5	4.5	6.73	3.07	4.27	4.39		
20	NT2RP2006261	7.32	7.32	3.98	2.04	3.19	7.69		
	NT2RP2006269	4.11	4.11	7.96	9.52	5.46	9.06		
	NT2RP2006275	3.67	3.67	30.36	23.46	35.36	25.14		
	NT2RP2006282	3.16	3.16	8.89	8.85	8.4	7.05		
	NT2RP2006302	5.69	5.69	12.68	13.12	12.4	11.87		
25	NT2RP2006312	4.88	4.88	8.22	8.47	9.13	9.8		
	NT2RP2006320	4.27	4.27	9.87	6.42	9.32	9.69		
	NT2RP2006321	3.27	3.27	4.23	2.79	4.99	4.13		
	NT2RP2006323	4.1	4.1	2.59	2.39	3.6	1.83		
	NT2RP2006333	0.67	0.67	1.82	1.7	1.04	1.17		
30	NT2RP2006334	2.24	2.24	4.02	4.57	2.72	3.54		
	NT2RP2006338	2.4	2.4	5.26	4.73	5.11	4.04		
	NT2RP2006339	2.24	2.24	2.94	2.47	1.93	2.06		
	NT2RP2006355	3.61	3.61	4.59	3.14	3.39	2.22		
35	NT2RP2006365	3.3	3.3	4.44	2.42	2.6	1.3	*	-
	NT2RP2006374	16.34	16.34	111.62	108.73	174.7	73.65		
	NT2RP2006393	4.93	4.93	7.68	7.38	8	6.95		
	NT2RP2006394	8.59	8.59	17.91	11.3	11.18	15.38		
	NT2RP2006400	2.25	2.25	4.51	2.08	3.58	1.95		
40	NT2RP2006411	27.71	27.71	42.11	23.61	17.25	37.31		
	NT2RP2006429	2.22	2.22	7.3	2.82	5.3	2.21		
	NT2RP2006435	1.46	1.46	5.29	1.76	2.65	1.98		
	NT2RP2006436	2.33	2.33	6.43	4.33	5.28	3.75		
	NT2RP2006441	4.69	4.69	8.19	7.76	8.89	8.37		
45	NT2RP2006447	2.41	2.41	4.78	3.18	2.63	3.87		
	NT2RP2006454	2.58	2.58	5.38	4.39	3.37	4.03		
	NT2RP2006455	3.79	3.79	7.14	2.91	4.62	9.23		
	NT2RP2006456	1.96	1.96	5.99	2.51	4.49	3.17		
	NT2RP2006464	5.44	5.44	8.28	4.47	8.85	7.9		
50	NT2RP2006467	4.17	4.17	10	8.56	12.47	12.58		
	NT2RP2006472	5.05	5.05	6.84	7.24	6.92	7.37		
	NT2RP2006474	4.69	4.69	16.3	18.19	32.31	21.3		
	NT2RP2006475	2.5	2.5	9.54	6.14	6.86	7.66		
	NT2RP2006476	5.34	5.34	14.94	7.62	13.82	17.24		
55	NT2RP2006501	2.44	2.44	7.28	4.6	7.45	7.74		

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	NT2RP2006512	10.25	10.25	19.79	16.72	7.89	29.01	
	NT2RP2006526	2.09	2.09	5.19	2.24	2.78	2.31	
5	NT2RP2006527	3.61	3.61	7.05	4.56	6.14	6.46	
	NT2RP2006534	2.24	2.24	4.49	2.08	2.95	2.73	
	NT2RP2006537	6.08	6.08	15.7	11.72	17.73	12.82	
	NT2RP2006543	7.83	7.83	14.8	6.52	5.4	6.88	
	NT2RP2006554	1.33	1.33	3.71	1.79	3.76	2.2	
10	NT2RP2006565	3.78	3.78	8.91	5.79	8.42	7.55	
	NT2RP2006571	1.38	1.38	3.88	2.77	4.01	2.29	
	NT2RP2006573	2.1	2.1	4.02	3.05	3.6	2.41	
	NT2RP2006598	2.25	2.25	7.04	4.34	6.56	4.78	
	NT2RP2006601	24.92	24.92	35.13	38.45	45.47	31.69	
15	NT2RP3000002	5.04	5.04	6.09	4.7	5.04	8.18	
	NT2RP3000011	1.82	1.82	5.9	2.59	1.85	2.22	
	NT2RP3000014	3.29	3.29	7.66	4.22	3.06	4.95	
	NT2RP3000016	3.42	3.42	7	5.29	6.56	6.11	
	NT2RP3000022	1.71	1.71	3.93	1.72	4.68	0.59	
20	NT2RP3000024	3.74	3.74	7.03	4.31	4.92	4.06	
	NT2RP3000031	4.66	4.66	8.66	4	6.75	4.86	
	NT2RP3000034	3.76	3.76	6.24	4.44	7.13	3.23	
	NT2RP3000037	2.76	2.76	6.5	9.41	13.44	11.06	* +
	NT2RP3000040	2.04	2.04	5.96	3.21	3.46	3.56	
25	NT2RP3000041	2.15	2.15	7.35	3.71	3.01	3.16	
	NT2RP3000046	1.95	1.95	4.42	3.67	7.11	3.84	
	NT2RP3000047	3.25	3.25	5.55	5.85	6.2	5.94	
	NT2RP3000049	2.54	2.54	6.94	5.26	7.78	3.58	
	NT2RP3000050	4.99	4.99	9.03	3.76	8.5	6.22	
30	NT2RP3000051	5.99	5.99	10.69	8.51	11.19	9.72	
	NT2RP3000054	4.31	4.31	6.5	4.38	5.35	3.22	
	NT2RP3000055	1.98	1.98	4.76	3.81	2.67	3.96	
	NT2RP3000056	2.87	2.87	7.09	5.59	3.32	3.91	
	NT2RP3000059	2.54	2.54	5.1	1.89	4.07	1.6	
35	NT2RP3000063	2.18	2.18	5.51	3.34	5.19	2.27	
	NT2RP3000068	3.76	3.76	24.22	25.83	37.88	23.13	
	NT2RP3000069	17.44	17.44	20.58	22	28.87	18.2	
	NT2RP3000072	5.9	5.9	6.18	4.96	5.39	4.19	* -
	NT2RP3000080	4.38	4.38	6.72	3.78	5.28	3.93	
40	NT2RP3000085	1.9	1.9	4.84	5.13	4.66	5.5	
	NT2RP3000087	3.77	3.77	9.1	6.22	5.61	6	
	NT2RP3000092	1.92	1.92	3.6	2.72	3.2	2.52	
	NT2RP3000109	1.74	1.74	5.05	5.63	7.94	4.24	
	NT2RP3000119	4.66	4.66	14.27	11.29	13.7	14.28	
45	NT2RP3000125	3.02	3.02	5.56	3.42	4.53	2	
	NT2RP3000131	7.84	7.84	14.37	16.23	19.96	12.93	
	NT2RP3000134	5.96	5.96	9.01	6.61	7.25	6.46	
	NT2RP3000137	3.88	3.88	6.48	5.58	6.3	6.11	
	NT2RP3000142	2.87	2.87	7.77	7.28	5.03	5.31	
50	NT2RP3000148	1.84	1.84	6.28	4.9	5.04	5.34	
	NT2RP3000149	2.51	2.51	6.97	6.14	7.77	8.24	
	NT2RP3000163	2.16	2.16	6.17	3.27	3.9	2.5	
	NT2RP3000168	5.53	5.53	14.55	12.8	11.65	11.73	
55	NT2RP3000169	3.74	3.74	6.01	6.03	8.47	5.72	

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	NT2RP3000171	10.86	10.86	16.71	28.33	38.98	25.93	*	+
	NT2RP3000172	0.86	0.86	1.53	1.66	1.2	1.46		
	NT2RP3000186	4.32	4.32	10.6	19.18	15.43	15.82	*	+
5	NT2RP3000197	1.22	1.22	3.66	4.03	4.29	3.39		
	NT2RP3000201	2.4	2.4	7.2	10.49	8.4	7.88		
	NT2RP3000204	2.16	2.16	4.44	3.88	4.1	4.25		
	NT2RP3000207	2.87	2.87	4.71	3	2.6	2.45		
	NT2RP3000216	5.38	5.38	10.1	5.87	9.5	5.73		
10	NT2RP3000220	5.14	5.14	5.66	3.68	5.69	2.92		
	NT2RP3000221	2.18	2.18	5.45	6.26	6.63	5.93		
	NT2RP3000232	2.7	2.7	8.01	7.1	5.52	5.92		
	NT2RP3000233	1.55	1.55	6.01	6.9	5.91	4.06		
15	NT2RP3000234	3.23	3.23	9.09	12.89	10.4	11.41	*	+
	NT2RP3000235	1.57	1.57	3.3	2.35	2.92	1.38		
	NT2RP3000239	4.61	4.61	11.11	9.51	9.71	14.92		
	NT2RP3000247	3.25	3.25	5.82	2.92	4.04	1.96		
	NT2RP3000251	6.11	6.11	6.52	5.22	5.82	3.25		
20	NT2RP3000252	3.73	3.73	7.99	7.61	8.53	8.4		
	NT2RP3000255	2.18	2.18	2.96	3.26	3.13	1.97		
	NT2RP3000262	6.72	6.72	9.43	11.67	7.95	9.13		
	NT2RP3000266	6.47	6.47	15.5	13.38	10.83	12.64		
	NT2RP3000267	2.71	2.71	4.04	2.9	2.64	3.03		
25	NT2RP3000271	4.38	4.38	5.57	5.11	4.84	3.72		
	NT2RP3000278	7.84	7.84	56.85	48.55	82.07	42.57		
	NT2RP3000281	4.94	4.94	10.72	3.19	8.22	7.27		
	NT2RP3000292	5.63	5.63	14.1	9.17	6.77	6.93		
	NT2RP3000299	2.31	2.31	4.92	3.73	4.89	4.98		
30	NT2RP3000304	2.15	2.15	3.48	2.85	3.36	1.64		
	NT2RP3000310	7.24	7.24	24.22	18.94	23.07	19.88		
	NT2RP3000312	2.99	2.99	8.16	3.31	5.25	3.87		
	NT2RP3000320	7.06	7.06	6.17	5.25	4.74	4.74	**	-
35	NT2RP3000322	11.05	11.05	18.76	32.59	45.13	46.95	**	+
	NT2RP3000324	6.91	6.91	46.42	36.64	43.53	39.68		
	NT2RP3000326	1.95	1.95	6.17	4.02	5.75	3.53		
	NT2RP3000329	2.5	2.5	5.96	4.97	8.84	5.9		
	NT2RP3000330	4.1	4.1	6.18	4.62	5.53	6.12		
40	NT2RP3000333	3.23	3.23	7.45	4.36	5.28	4.52		
	NT2RP3000341	8.8	8.8	12.85	14.81	18.59	14.41	*	+
	NT2RP3000344	2.73	2.73	3.75	2.69	3.54	2.29		
	NT2RP3000345	3.09	3.09	3.57	1.65	1.97	2.66	*	-
	NT2RP3000348	444.59	444.59	802.63	824.62	1016.01	909.68		
45	NT2RP3000350	4.25	4.25	10.34	4.57	9.28	6.4		
	NT2RP3000359	9.53	9.53	24.44	8.54	11.36	16.62		
	NT2RP3000361	7.5	7.5	11.12	7.89	7.81	8.95		
	NT2RP3000366	7.38	7.38	14.27	9.52	11.84	16.13		
	NT2RP3000378	2.67	2.67	5.75	3.92	4.78	2.47		
50	NT2RP3000384	5.42	5.42	10.88	9.52	13.1	9.28		
	NT2RP3000389	12.54	12.54	21.49	23.95	35.02	27.32	*	+
	NT2RP3000393	3.74	3.74	6.16	5.03	4.53	4.77		
	NT2RP3000395	110.27	110.27	212	108.33	38.18	148.45		
	NT2RP3000397	2.83	2.83	5.28	2.51	5.26	3.31		
55	NT2RP3000398	3.39	3.39	10.12	11.46	11.18	12.26		

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	NT2RP3000403	3.22	3.22	9.39	10.1	8.2	8.44		
	NT2RP3000418	3.4	3.4	10.22	7.12	11.08	13.42		
5	NT2RP3000424	2.86	2.86	9.43	6.25	9.52	6.86		
	NT2RP3000427	4.65	4.65	9.05	11.55	13.43	12.35	*	+
	NT2RP3000431	2.05	2.05	4.93	3.43	3.26	3.93		
	NT2RP3000433	2.63	2.63	8.65	5.65	7.09	6.65		
	NT2RP3000436	11.39	11.39	20.93	18.76	9.35	18.86		
10	NT2RP3000439	1.4	1.4	3.61	2.54	3.56	2		
	NT2RP3000441	3.88	3.88	7.4	7.56	7.92	6.39		
	NT2RP3000444	3.31	3.31	7.29	2.36	3.25	2.2		
	NT2RP3000448	4.45	4.45	10.15	4.05	6.54	3.93		
15	NT2RP3000449	2.84	2.84	4.59	3.1	3.94	2.93		
	NT2RP3000451	1.76	1.76	5.12	3.7	5	2.96		
	NT2RP3000456	1.69	1.69	5.48	4.23	6.67	4.21		
	NT2RP3000460	18.87	18.87	36.67	24.52	25.24	26.25		
	NT2RP3000471	3.14	3.14	6.49	2.74	4.98	5.84		
20	NT2RP3000477	19.96	19.96	23.67	28.98	17.78	32.78		
	NT2RP3000478	5.86	5.86	8.95	5.21	8.98	2.6		
	NT2RP3000481	5.48	5.48	5.76	2.76	3.61	1.52	**	-
	NT2RP3000484	3.51	3.51	4.26	2.32	2.55	1.76	*	-
	NT2RP3000487	1.77	1.77	7.4	5.07	4.03	4.97		
25	NT2RP3000512	3.29	3.29	17.7	15.17	15.9	14.52		
	NT2RP3000523	13.05	13.05	30.74	31.75	27.83	34.4		
	NT2RP3000526	3.07	3.07	7.38	5.18	6.31	4.64		
	NT2RP3000527	2.83	2.83	6.5	3.76	7.25	5.03		
	NT2RP3000531	2.9	2.9	7.71	5.11	5.51	4.69		
30	NT2RP3000532	5.74	5.74	5.6	5.75	8.39	4.26		
	NT2RP3000542	6.23	6.23	8.1	7.21	7.3	6.39		
	NT2RP3000554	8.81	8.81	15.22	13.78	10.56	14.95		
	NT2RP3000561	1.21	1.21	3.51	3.11	2.76	2.25		
	NT2RP3000562	1.84	1.84	3.5	3.7	3.87	3.23		
35	NT2RP3000578	1.56	1.56	2.54	2.54	3.37	2.36		
	NT2RP3000582	1.26	1.26	4.66	2.24	2.52	0.41		
	NT2RP3000584	2.82	2.82	6.52	3.2	2.5	2.02		
	NT2RP3000586	4.08	4.08	4.59	3.28	3.9	2.87		
	NT2RP3000590	5.69	5.69	4.61	3.78	4.35	2.57		
40	NT2RP3000592	1.8	1.8	2.99	2.97	2.75	3.15		
	NT2RP3000596	2.27	2.27	4.89	4.5	3.33	3.03		
	NT2RP3000599	1.67	1.67	3.07	3.88	4.98	3.82	*	+
	NT2RP3000603	6.09	6.09	39.25	40.43	44.88	35.89		
45	NT2RP3000605	2.84	2.84	6.66	4.56	4.23	2.56		
	NT2RP3000607	5.35	5.35	7.59	5.74	8.46	7.55		
	NT2RP3000616	3.26	3.26	5.45	2.56	2.38	1.21		
	NT2RP3000621	5.18	5.18	8.48	10.28	10.29	6.01		
	NT2RP3000622	2.36	2.36	8.76	5.85	6.21	4.72		
50	NT2RP3000624	1.53	1.53	3.19	3.97	3.06	2.78		
	NT2RP3000628	2.44	2.44	8.04	10.27	7.85	5.58		
	NT2RP3000631	4.71	4.71	14.95	22.82	16.45	14.2		
	NT2RP3000632	2.35	2.35	5.5	7.78	8.91	5.91	*	+
	NT2RP3000638	6.95	6.95	17.93	11.8	11.6	9.97		
55	NT2RP3000644	25.72	25.72	48.41	57.98	72.01	52.49	*	+
	NT2RP3000645	5.85	5.85	10.48	9.84	12.55	8.43		

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	NT2RP3000652	3.39	3.39	5.34	6.22	5.9	7.74	*	+
	NT2RP3000658	2.26	2.26	5.01	6.16	4.24	4.86		
	NT2RP3000660	2.34	2.34	6.25	6.98	6.91	5.14		
5	NT2RP3000661	1.98	1.98	4.49	4.06	3.87	3.1		
	NT2RP3000665	4.79	4.79	12.26	11.83	11.92	7		
	NT2RP3000676	4.46	4.46	7.55	6.65	7.81	5.42		
	NT2RP3000677	2.87	2.87	4.13	2.44	3.07	1.54		
10	NT2RP3000681	19.85	19.85	30.12	32.94	41.51	34.34	*	+
	NT2RP3000683	2.68	2.68	9.67	6.69	7.09	6.69		
	NT2RP3000685	1.7	1.7	2.5	3.63	2.36	3.44		
	NT2RP3000690	2.77	2.77	3.29	3.82	3.75	2.72		
	NT2RP3000698	10	10	22.49	25.66	17.08	27.43		
15	NT2RP3000708	3.45	3.45	5.5	8.17	9.22	8.56	**	+
	NT2RP3000719	2.83	2.83	2.83	1.16	1.7	1.91	**	-
	NT2RP3000721	5.63	5.63	24.61	23.43	39.76	21.55		
	NT2RP3000728	3.33	3.33	2.57	1.4	1.64	1.05	**	-
	NT2RP3000730	2.06	2.06	5.04	2.76	4.23	1.86		
20	NT2RP3000733	2.87	2.87	6.32	3.48	4.47	4.25		
	NT2RP3000735	1.74	1.74	4.22	1.81	2.22	1.26		
	NT2RP3000736	2.71	2.71	6.35	3.29	5.05	3.65		
	NT2RP3000739	13.76	13.76	12.16	18.05	9.37	20.19		
	NT2RP3000742	3.89	3.89	10.06	4.54	4.97	4.43		
25	NT2RP3000753	2.29	2.29	3.9	2.17	2.65	6.3		
	NT2RP3000759	9.07	9.07	15.99	11.11	17.14	23.05		
	NT2RP3000789	1.58	1.58	5.76	4.89	4.23	3.69		
	NT2RP3000815	1.91	1.91	5.92	4.49	5.57	3.08		
	NT2RP3000818	4.35	4.35	11.29	6.64	10.49	8.27		
30	NT2RP3000820	9.01	9.01	18.49	18.58	20.1	16.9		
	NT2RP3000821	2.13	2.13	4.83	3.28	5.19	2.02		
	NT2RP3000825	1.87	1.87	4.94	1.92	1.47	2.27		
	NT2RP3000826	4.04	4.04	13.59	10.86	13.8	12.94		
	NT2RP3000836	5.33	5.33	11.61	11.55	14.11	13.3		
35	NT2RP3000838	319.2	319.2	741.74	710.2	743.55	1049.86		
	NT2RP3000839	2.35	2.35	6.67	4.53	6.38	4.36		
	NT2RP3000841	2.17	2.17	4.32	3.79	5.55	4.72		
	NT2RP3000845	3.96	3.96	8.89	5.76	6.71	7.85		
	NT2RP3000847	3.7	3.7	7.94	4.48	5.94	5.28		
40	NT2RP3000848	2.84	2.84	8.34	5.36	6.81	6.3		
	NT2RP3000850	5.67	5.67	7.04	6.58	11.29	7.47		
	NT2RP3000852	3.27	3.27	3.17	4.02	5.23	5.8	*	+
	NT2RP3000859	2.76	2.76	7.12	4.46	7.11	8.43		
	NT2RP3000861	2.58	2.58	10.51	6.13	10.36	6.43		
45	NT2RP3000862	15.29	15.29	24.16	16.36	9.81	23.13		
	NT2RP3000865	1.58	1.58	4.26	2.54	4.21	1.83		
	NT2RP3000866	2.08	2.08	5.03	2.37	3.59	5.22		
	NT2RP3000868	2.2	2.2	7.09	3.04	3.84	2.28		
	NT2RP3000869	3.54	3.54	11.36	9.61	15.76	7.9		
50	NT2RP3000871	1.75	1.75	3.79	1.81	3.24	1.94		
	NT2RP3000875	0.99	0.99	4.25	2.57	2.71	3.64		
	NT2RP3000895	2.54	2.54	5.56	2.84	3.55	4.93		
	NT2RP3000900	6.01	6.01	11.86	11.3	7.7	14.58		
55	NT2RP3000901	3.67	3.67	7.03	4.11	6.39	5.3		

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	NT2RP3000903	3.76	3.76	7.87	3.12	5.92	3.93		
	NT2RP3000904	3.83	3.83	8.67	3.05	4.87	3.16		
	NT2RP3000907	5.66	5.66	10.03	8.94	10.67	10.14		
5	NT2RP3000913	6.04	6.04	15.01	17.87	25.57	17.37	*	+
	NT2RP3000917	7.64	7.64	16.58	7.66	6.56	13.51		
	NT2RP3000919	1.99	1.99	5.15	3.5	4.3	2.68		
	NT2RP3000921	2.26	2.26	7.67	4.88	4.07	6.51		
10	NT2RP3000942	2.66	2.66	3.89	2.68	4.12	2.63		
	NT2RP3000968	70.24	70.24	87.55	105.89	110.05	115.38	**	+
	NT2RP3000974	5.36	5.36	9.06	3.21	4.48	2.64		
	NT2RP3000980	5.77	5.77	5.77	2.09	4.14	2.26	*	-
	NT2RP3000984	3.17	3.17	7.65	6.33	6.68	4.58		
15	NT2RP3000994	2.09	2.09	4.88	2.4	3.14	3.37		
	NT2RP3001001	1.46	1.46	3.45	3.75	4.14	1.31		
	NT2RP3001004	3.37	3.37	6.52	3.51	5.63	5.01		
	NT2RP3001007	4.46	4.46	9.87	10.02	10.62	6.81		
20	NT2RP3001012	2.78	2.78	5.4	4.99	6.83	3.65		
	NT2RP3001042	4.74	4.74	5.52	2.99	5.18	1.38		
	NT2RP3001044	6.26	6.26	7.12	7.16	6.76	4.92		
	NT2RP3001048	2.52	2.52	3.01	3.5	3.93	2.42		
	NT2RP3001050	1.79	1.79	4.99	4.68	5.94	4.7		
25	NT2RP3001055	6.55	6.55	15.6	16.48	12.44	20.49		
	NT2RP3001057	2.79	2.79	10.84	5.57	6.05	5.67		
	NT2RP3001061	3.18	3.18	6.57	5.03	7.85	5.42		
	NT2RP3001069	6.03	6.03	14.95	18.49	17.53	15.08		
	NT2RP3001074	4.2	4.2	7.22	8.72	10	6.64		
30	NT2RP3001078	5.11	5.11	7.29	7.51	8.72	5.18		
	NT2RP3001081	4	4	5.72	4.65	5.19	3.52		
	NT2RP3001084	2.7	2.7	7.92	6.85	6.71	6.23		
	NT2RP3001095	1.57	1.57	3.88	3.69	3.68	3.42		
	NT2RP3001096	2.52	2.52	7.33	16.78	8.08	18.7	*	+
35	NT2RP3001097	3.65	3.65	4.28	6.42	8.11	8.5	**	+
	NT2RP3001107	3.69	3.69	4.79	3.77	4.03	2.37		
	NT2RP3001109	3.2	3.2	5.5	6.01	9.56	7.26	*	+
	NT2RP3001111	4.58	4.58	4.19	3.41	3.51	2.29	*	-
	NT2RP3001112	12.61	12.61	18.48	25.73	29.85	24.61	**	+
40	NT2RP3001113	1.21	1.21	2.59	2.47	3.24	2.19		
	NT2RP3001115	1.51	1.51	3.32	2.57	3.77	2.19		
	NT2RP3001116	1.01	1.01	2.66	2.55	4.4	2.91		
	NT2RP3001119	3.69	3.69	6.75	9.07	6.67	5.44		
	NT2RP3001120	5.02	5.02	8.24	8.85	7.87	6.71		
45	NT2RP3001126	6.16	6.16	12.34	17.84	19.66	17.49	**	+
	NT2RP3001127	6.93	6.93	6.76	4.79	7.63	6.36		
	NT2RP3001133	3.95	3.95	4.95	3.95	4.16	3.62		
	NT2RP3001140	1.46	1.46	2.43	3.21	2.38	6.71		
	NT2RP3001147	3.16	3.16	6.96	16.08	14.49	13.84	**	+
50	NT2RP3001150	1.99	1.99	4.32	4.06	5.68	3.76		
	NT2RP3001152	1.7	1.7	3.29	3.15	3.62	2.51		
	NT2RP3001155	2.95	2.95	4.35	3.68	4.35	3.58		
	NT2RP3001156	4.38	4.38	6.57	2.91	5.72	5.67		
	NT2RP3001159	5.38	5.38	10.5	7.87	10.86	7.25		
55	NT2RP3001170	7.38	7.38	5.96	6.12	8.01	4.56		

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	NT2RP3001176	3.49	3.49	10.75	6.27	8.23	9.49		
	NT2RP3001195	2.35	2.35	4.81	6.79	5.79	6.22	*	+
	NT2RP3001209	3.47	3.47	5.98	5.96	4.64	5.22		
5	NT2RP3001214	1.63	1.63	4.91	3.44	3.87	3.81		
	NT2RP3001216	3.58	3.58	6.38	6.25	4.33	3.6		
	NT2RP3001221	3.33	3.33	4.27	3.07	3.06	1.79		
	NT2RP3001226	5.96	5.96	29.04	21.93	31.45	17.76		
10	NT2RP3001230	3.17	3.17	2.41	3.09	3.14	1.56		
	NT2RP3001232	1.8	1.8	4.72	2.36	3.7	2.85		
	NT2RP3001236	1.68	1.68	4.3	1.7	3.26	1.47		
	NT2RP3001239	1.58	1.58	5.21	2.81	4.31	2.01		
	NT2RP3001240	12.83	12.83	22.18	23.01	24.3	14.46		
15	NT2RP3001245	3.53	3.53	9.88	4.08	6.36	3.39		
	NT2RP3001253	2.79	2.79	4.87	3.34	4.53	5.21		
	NT2RP3001259	6.62	6.62	11.97	12.33	15.62	11.83		
	NT2RP3001260	3.74	3.74	5.15	3.45	5.44	3.97		
	NT2RP3001264	2.2	2.2	10.29	5.99	6.92	6.38		
20	NT2RP3001268	2.25	2.25	7.18	4.93	4.72	4.35		
	NT2RP3001271	7.06	7.06	16.29	13.07	12.27	14.24		
	NT2RP3001272	3.73	3.73	12.45	9.43	11.09	10.15		
	NT2RP3001274	6.08	6.08	8.09	6.72	6.35	5.11		
	NT2RP3001275	9.78	9.78	11.58	21.56	26.84	22.59	**	+
25	NT2RP3001280	3.39	3.39	5.5	3.58	5.24	4.18		
	NT2RP3001281	3.15	3.15	3.89	3.08	4.48	5.14		
	NT2RP3001288	49.31	49.31	103.24	124.07	142.92	164.41	*	+
	NT2RP3001297	6.39	6.39	42.01	37.04	42.75	41.14		
	NT2RP3001300	5.23	5.23	15.92	16.78	17.41	17.76		
30	NT2RP3001301	2.91	2.91	6.59	3.96	4.58	3.9		
	NT2RP3001307	1.76	1.76	7.67	2.07	2.81	2.06		
	NT2RP3001310	11.55	11.55	17.04	25.54	26.07	28.13	**	+
	NT2RP3001318	2.11	2.11	3.4	2.49	3.37	2.37		
	NT2RP3001322	3.58	3.58	5.23	2.62	3.84	5.48		
35	NT2RP3001325	2.7	2.7	8.39	5.82	6.82	5.58		
	NT2RP3001338	2.67	2.67	6.19	4.1	4.21	3.5		
	NT2RP3001339	2.53	2.53	5.64	3.08	4.89	2.91		
	NT2RP3001340	2.9	2.9	8.42	6.36	7.07	5.79		
40	NT2RP3001341	2.26	2.26	6.97	5.1	5.62	4.73		
	NT2RP3001354	3.22	3.22	9.77	4.28	6.93	9.35		
	NT2RP3001355	1.9	1.9	5.41	2.65	3.82	2.74		
	NT2RP3001356	2	2	5.34	2.59	3.2	3.55		
	NT2RP3001359	1.09	1.09	4.05	1.63	2.5	1.75		
45	NT2RP3001364	2.34	2.34	5.31	3.26	6.67	2.67		
	NT2RP3001373	1.12	1.12	3.22	2.1	3.74	1.71		
	NT2RP3001374	1.9	1.9	4.17	3.18	3.92	3.1		
	NT2RP3001383	3.84	3.84	8.96	3.92	6.65	3.85		
	NT2RP3001384	4.11	4.11	9.47	3.54	4.46	2.41		
50	NT2RP3001388	3.98	3.98	8.79	9.48	10.99	9.4		
	NT2RP3001392	4.61	4.61	6.19	3.91	6.14	3.23		
	NT2RP3001396	1.7	1.7	6.39	4.04	4.66	4.53		
	NT2RP3001398	2.51	2.51	6.55	3.85	7.05	2.94		
	NT2RP3001399	4.91	4.91	20.67	15.86	16.12	12.44		
55	NT2RP3001402	6.46	6.46	36.36	33.37	41.61	39.66		

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	NT2RP3001407	6.96	6.96	19.16	13.69	17.65	12.35	
	NT2RP3001416	7.92	7.92	15.88	13.02	18.3	14.72	
5	NT2RP3001420	5.33	5.33	6.4	3.27	3.64	1.8 *	-
	NT2RP3001425	3.73	3.73	4.92	4.74	5.67	3.15	
	NT2RP3001426	2.39	2.39	6.08	5.45	4.45	5.11	
	NT2RP3001427	1.82	1.82	5.61	3.46	2.89	3.59	
	NT2RP3001428	2.42	2.42	6.29	5.69	4.81	3.77	
10	NT2RP3001429	3.08	3.08	5.91	4.15	7.37	4.73	
	NT2RP3001432	2.14	2.14	6.61	3.72	4.44	3.58	
	NT2RP3001439	4.14	4.14	6.39	5.87	7.27	4.41	
	NT2RP3001441	6.45	6.45	12.63	11.13	14.61	11.2	
	NT2RP3001446	4.99	4.99	4.99	4.64	5.22	4.39	
15	NT2RP3001447	2.72	2.72	5.21	6.64	5.14	6.33	
	NT2RP3001449	3.95	3.95	11.85	16.9	14.57	13.16 *	+
	NT2RP3001453	1.84	1.84	3.66	3.5	4.4	2.81	
	NT2RP3001457	3.86	3.86	7.71	6.06	6.93	5.5	
	NT2RP3001459	2.39	2.39	6.03	2.64	2.78	1.17	
20	NT2RP3001463	2.77	2.77	6.74	5.93	5.94	3.98	
	NT2RP3001466	2.87	2.87	3.56	1.19	1.43	0.78 **	-
	NT2RP3001472	5.74	5.74	4.02	3.7	4.85	4.32	
	NT2RP3001475	3.54	3.54	7.61	6.91	6.65	7.39	
	NT2RP3001479	2.54	2.54	6.66	4.37	5.69	5.16	
25	NT2RP3001490	3.18	3.18	9.26	4.4	6.02	5.21	
	NT2RP3001492	4.36	4.36	7.84	7.59	7.08	5.72	
	NT2RP3001495	4.14	4.14	3.85	2.75	2.92	1.76 *	-
	NT2RP3001497	5.8	5.8	6.32	7.47	9.96	6.8	
30	NT2RP3001501	5.36	5.36	5.52	3.12	4.49	3.43 *	-
	NT2RP3001527	4.89	4.89	6.71	4.9	5.14	3.52	
	NT2RP3001529	1.51	1.51	3.5	4.12	3.95	4.18 *	+
	NT2RP3001538	1.78	1.78	6.2	6.93	7.81	6.23	
	NT2RP3001539	5.81	5.81	14.5	15.19	14.15	16.47	
35	NT2RP3001542	1.52	1.52	5.26	4.23	4.38	2.13	
	NT2RP3001549	4.75	4.75	11.12	14.57	11.37	13.44	
	NT2RP3001554	3.06	3.06	6.16	6.37	7.5	5.05	
	NT2RP3001560	4.96	4.96	5.73	4.67	6.35	2.36	
	NT2RP3001561	8.85	8.85	20.77	20.38	27.2	17.15	
40	NT2RP3001564	1.54	1.54	8.24	6.43	4.53	5.96	
	NT2RP3001568	2.1	2.1	7.68	11.84	10.29	8.49 *	+
	NT2RP3001575	3.94	3.94	7.24	6.39	6.97	6.16	
	NT2RP3001580	1.78	1.78	4.49	4.35	3.8	3.11	
	NT2RP3001587	4.38	4.38	8.74	10.75	10.04	7.77	
45	NT2RP3001589	3.17	3.17	8.21	5.6	7.79	4.36	
	NT2RP3001592	4.52	4.52	21.6	19	32.62	14.54	
	NT2RP3001607	3.42	3.42	1.86	1.59	2.8	1	
	NT2RP3001608	1.05	1.05	3.59	2.41	1.73	2.31	
	NT2RP3001613	3.08	3.08	2.77	3.89	2.91	3.99	
50	NT2RP3001619	4.31	4.31	8.15	7.69	6.45	7.62	
	NT2RP3001621	1.18	1.18	2.69	2.39	2.28	2.02	
	NT2RP3001629	2.58	2.58	3.28	2.68	2.41	1.7	
	NT2RP3001630	3.39	3.39	4.56	1.67	2.02	1.17 **	-
	NT2RP3001631	9.01	9.01	14.34	18.65	21.16	15.24 *	+
55	NT2RP3001634	4	4	5.29	4.51	6.89	5.11	



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	NT2RP3001642	3.71	3.71	7.45	5.77	4.41	5.09	
	NT2RP3001646	1.56	1.56	3.7	0.89	2.79	0.95	
	NT2RP3001650	2.06	2.06	5.81	4.86	7.03	2.08	
5	NT2RP3001667	4.66	4.66	11.91	6.93	9.95	5.13	
	NT2RP3001671	2.28	2.28	7.98	7.7	4.69	5.99	
	NT2RP3001672	1.33	1.33	4.55	1.66	1.47	1.72	
	NT2RP3001676	2.18	2.18	5.02	2.35	3.14	2.24	
	NT2RP3001678	2.86	2.86	9.24	5.12	5.14	6.03	
10	NT2RP3001679	6.12	6.12	9.19	6.74	4.73	6.91	
	NT2RP3001682	1.82	1.82	5.09	4.45	6.18	3.35	
	NT2RP3001685	3.02	3.02	6.74	3.52	6.53	3.01	
	NT2RP3001688	3.01	3.01	9.42	5.46	8.21	6.43	
	NT2RP3001690	3.21	3.21	4.87	2.91	3.54	2.99	
15	NT2RP3001693	5.69	5.69	10.93	16.59	18.34	16.12	** +
	NT2RP3001696	2.28	2.28	3.63	1.77	3.68	3.39	
	NT2RP3001698	35.35	35.35	79.65	85.09	91.88	105.32	
	NT2RP3001708	4.82	4.82	8.78	6.34	6.95	9.01	
20	NT2RP3001712	8.69	8.69	16.06	10.22	14.19	13	
	NT2RP3001716	1.44	1.44	5.45	2.14	3.42	2.31	
	NT2RP3001724	2.75	2.75	6	4.08	4.54	2.63	
	NT2RP3001727	11.73	11.73	38.73	39.17	49.36	31.26	
	NT2RP3001729	3.36	3.36	4.7	5.69	6.55	3.06	
25	NT2RP3001730	12.54	12.54	26.52	12.53	19.94	16.4	
	NT2RP3001733	1.46	1.46	3.04	2.09	3.7	1.62	
	NT2RP3001737	3.02	3.02	7.12	4.62	5.49	2.78	
	NT2RP3001738	1.59	1.59	8.22	3.38	6.01	3.03	
	NT2RP3001739	3.26	3.26	5.25	5.63	6.1	2.51	
30	NT2RP3001742	2.54	2.54	5.36	3.86	4.55	4.03	
	NT2RP3001751	3.61	3.61	11.54	9.94	12.82	8.76	
	NT2RP3001752	2.58	2.58	7.01	2.1	3.59	2.76	
	NT2RP3001753	5.73	5.73	9.48	10.83	15.3	13.69	* +
	NT2RP3001754	4.63	4.63	9.08	5.86	3.73	5.33	
35	NT2RP3001756	4.66	4.66	7.36	9.37	5.75	8.03	
	NT2RP3001764	2.1	2.1	3.76	2.54	4.25	2.49	
	NT2RP3001771	2.63	2.63	3.2	1.52	4.14	1.22	
	NT2RP3001777	2.59	2.59	5.99	3.25	5.19	3.26	
	NT2RP3001782	3.52	3.52	14.68	6.47	6.63	6.47	
40	NT2RP3001792	2.27	2.27	4.35	2.91	4.09	1.35	
	NT2RP3001799	1.76	1.76	5.18	5.71	6.36	5.68	
	NT2RP3001819	1.36	1.36	4.54	1.7	1.52	2.06	
	NT2RP3001829	21.63	21.63	43.14	35.64	17.14	24.87	
45	NT2RP3001836	7.31	7.31	10.67	15.24	7.26	11.37	
	NT2RP3001839	18.86	18.86	31.77	31.97	19.23	17.53	
	NT2RP3001844	4.15	4.15	11.37	8.33	9.59	8.54	
	NT2RP3001848	9.61	9.61	52.04	44.52	74.75	43.87	
	NT2RP3001854	6.41	6.41	11.29	12.86	16.75	13.26	* +
50	NT2RP3001855	2.27	2.27	3.94	1.87	1	1.74	
	NT2RP3001857	3.1	3.1	5.22	5.13	5.6	3.33	
	NT2RP3001858	1.53	1.53	4.45	4.41	6.04	2.97	
	NT2RP3001861	7.35	7.35	16.34	11.85	14.46	10.42	
	NT2RP3001866	4.35	4.35	9.63	5.52	10.42	7.93	
55	NT2RP3001871	4.82	4.82	6.34	5.55	6.38	4.55	

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	NT2RP3001874	6.8	6.8	9.73	7.72	11.19	6.14		
	NT2RP3001878	5.98	5.98	6.35	4.59	6.89	5.02		
	NT2RP3001885	3.21	3.21	5.3	5.65	5.25	4.42		
5	NT2RP3001896	1.64	1.64	3.49	3.37	2.13	2.02		
	NT2RP3001898	9.03	9.03	17.69	14.71	8.69	11.94		
	NT2RP3001899	3.21	3.21	7.33	4.52	6.9	5.81		
	NT2RP3001901	4.58	4.58	9.18	8.19	9.44	9.21		
10	NT2RP3001915	4.84	4.84	11.12	14.09	15.67	14.04	*	+
	NT2RP3001926	2.8	2.8	4.88	2.47	2.45	1.65		
	NT2RP3001929	3.74	3.74	4.06	2.56	3.38	0.86		
	NT2RP3001931	4.63	4.63	5.26	3.9	5.62	2.98		
	NT2RP3001938	2.27	2.27	5.53	4.93	3.93	4.75		
15	NT2RP3001943	3.27	3.27	5.36	5.77	6.5	5.56		
	NT2RP3001944	1.77	1.77	3.72	4.08	5.91	4.34		
	NT2RP3001945	4.25	4.25	12.2	11.86	11.78	6.11		
	NT2RP3001947	2.94	2.94	5.89	4.06	5.41	3.4		
	NT2RP3001949	4.21	4.21	8.9	10.49	11.08	8.08		
20	NT2RP3001952	23.54	23.54	43.64	48.59	88.56	41.86		
	NT2RP3001954	5.06	5.06	3.68	4.34	4.79	1.85		
	NT2RP3001956	4.97	4.97	9.44	7.76	8.22	6.29		
	NT2RP3001967	3.78	3.78	7.74	6.7	5.37	5.66		
	NT2RP3001969	1.71	1.71	2.91	4.05	4.39	3.62	*	+
25	NT2RP3001976	2.25	2.25	4.67	6.22	6.25	4.84	*	+
	NT2RP3001986	3.55	3.55	3.88	3.43	2.82	2.19		
	NT2RP3001989	3.76	3.76	5.23	2.86	3.58	2.54		
	NT2RP3002002	6.68	6.68	9.47	6.25	8.85	3.86		
	NT2RP3002004	5.02	5.02	6.23	3.79	5.74	3.55		
30	NT2RP3002007	1.29	1.29	2.3	3.46	4.05	1.69		
	NT2RP3002014	1.38	1.38	6.23	6.04	6.24	4.21		
	NT2RP3002015	3.61	3.61	10.33	14.17	9.94	8.85		
	NT2RP3002033	1.54	1.54	5.03	7.29	5.03	3.65		
35	NT2RP3002045	1.89	1.89	5.29	4.67	4.36	2.5		
	NT2RP3002054	5.26	5.26	8.12	6.27	9.17	5.42		
	NT2RP3002056	5.67	5.67	5.52	4.24	4.24	2.7	*	-
	NT2RP3002057	4.35	4.35	3.5	2.87	2.41	0.81	*	-
	NT2RP3002061	4.71	4.71	13.94	8.64	8.9	10.74		
40	NT2RP3002062	0.8	0.8	2.42	3.58	3.26	1.11		
	NT2RP3002063	5.61	5.61	10.31	9.29	9.3	7.31		
	NT2RP3002064	2.6	2.6	3.37	2.72	3.74	2.52		
	NT2RP3002071	1.6	1.6	3.91	1.99	3.29	1.45		
	NT2RP3002073	6.47	6.47	9.55	10.45	11.13	8.64		
45	NT2RP3002074	4.2	4.2	7.25	6.33	7.82	4.24		
	NT2RP3002075	7.58	7.58	11.93	21.64	30.17	18.15	*	+
	NT2RP3002077	3.81	3.81	5.95	2.48	3.05	2.78		
	NT2RP3002081	4.25	4.25	7.55	13.22	12.62	11.13	**	+
	NT2RP3002086	3.86	3.86	9.77	5.59	8.66	6.95		
50	NT2RP3002094	7.34	7.34	10.28	13.84	14.79	11.67	*	+
	NT2RP3002096	1.98	1.98	4.53	1.28	3.12	1.73		
	NT2RP3002097	3.77	3.77	6.16	6.1	8.34	6.88		
	NT2RP3002098	1.61	1.61	4.3	1.04	1.8	1.46		
	NT2RP3002102	2	2	4.86	3.11	3.4	3.16		
55	NT2RP3002106	2.74	2.74	4.98	2.83	4.9	2.51		

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	NT2RP3002108	3.69	3.69	7.8	3.11	3.39	3.15	
	NT2RP3002109	12.49	12.49	32.04	31.61	27.15	25.12	
	NT2RP3002110	36.38	36.38	54.93	55.24	58.94	46.55	
5	NT2RP3002113	11.15	11.15	13.99	10.66	15.22	11.44	
	NT2RP3002120	2.22	2.22	4.42	2.31	4.13	2.7	
	NT2RP3002121	5.93	5.93	14.39	13.38	14.39	15.06	
	NT2RP3002126	34.03	34.03	108.96	121.18	130.55	142.49	* +
	NT2RP3002128	4.06	4.06	8.23	3.36	6.87	3.92	
10	NT2RP3002130	8.29	8.29	18.59	11.69	10.7	14.03	
	NT2RP3002133	14.24	14.24	18.31	10.06	8.3	19.51	
	NT2RP3002136	10.32	10.32	15.42	12.49	17.64	17.49	
	NT2RP3002140	3.13	3.13	6.35	6.15	3.9	4.16	
	NT2RP3002142	16.86	16.86	50.85	56.54	81.25	62.65	* +
15	NT2RP3002146	4	4	7.22	5.14	9.31	6.56	
	NT2RP3002147	3.8	3.8	10.45	6.06	7.4	6.2	
	NT2RP3002151	5.62	5.62	10.64	6.27	4.43	7.33	
	NT2RP3002155	1.62	1.62	3.27	2.01	4.98	0.8	
20	NT2RP3002156	3.15	3.15	4.82	2.55	4.08	2.42	
	NT2RP3002160	1.57	1.57	3.43	1.36	3.43	1.56	
	NT2RP3002163	20.86	20.86	55.1	35.13	44.03	32.6	
	NT2RP3002165	4.17	4.17	3.67	6.21	8.31	4.86	
	NT2RP3002166	4.04	4.04	10.53	7.76	8.79	5.58	
25	NT2RP3002173	2.24	2.24	5.75	2.95	3.34	3.53	
	NT2RP3002174	8.41	8.41	15.8	13.21	7.82	14.77	
	NT2RP3002181	1.1	1.1	3.46	1.87	3.51	1.61	
	NT2RP3002185	2.69	2.69	4.51	2.94	4.35	2.61	
	NT2RP3002193	5.51	5.51	13.38	16.39	15.35	11.36	
30	NT2RP3002204	5.66	5.66	12.49	17.04	24.14	18.95	* +
	NT2RP3002244	4.03	4.03	8.29	5.28	6.11	4.8	
	NT2RP3002248	5.42	5.42	11.1	3.19	11.78	6.52	
	NT2RP3002253	2.61	2.61	9.3	9.66	11.26	6.18	
	NT2RP3002255	11.07	11.07	26.56	22.78	11.53	20.93	
35	NT2RP3002264	3.06	3.06	5.54	5.88	7.37	4.07	
	NT2RP3002267	1.26	1.26	4.33	3.1	4.65	1.82	
	NT2RP3002273	7.51	7.51	12.98	10.15	13.8	12.11	
	NT2RP3002276	5.22	5.22	7.89	3.08	7.68	3.48	
	NT2RP3002281	6.37	6.37	6.83	7.45	8.46	3.44	
40	NT2RP3002286	3	3	4.79	3.54	4.34	3.88	
	NT2RP3002297	10.62	10.62	29.36	22.26	20.57	23.93	
	NT2RP3002301	5.73	5.73	13.24	9.47	7.55	6.21	
	NT2RP3002303	3.01	3.01	6.39	5.29	6.65	4.58	
	NT2RP3002304	2.66	2.66	7.17	6.3	7.3	4.91	
45	NT2RP3002309	2.3	2.3	7.18	9.26	13	4.39	
	NT2RP3002311	4.54	4.54	6.67	3.17	4.02	1.83	
	NT2RP3002315	15.27	15.27	20.91	25.82	33.13	21.82	
	NT2RP3002319	2.37	2.37	5.06	3.07	3.51	2.38	
50	NT2RP3002324	8.97	8.97	61.42	49.85	51.23	55.4	
	NT2RP3002330	4.74	4.74	8.33	10.31	8.24	8.15	
	NT2RP3002333	5.13	5.13	14.32	13.14	13.65	8.12	
	NT2RP3002337	2.61	2.61	5.14	4.8	5.57	4.87	
	NT2RP3002342	5.16	5.16	11.56	5.52	7.51	6.43	
55	NT2RP3002343	3.38	3.38	7.29	5.8	7.03	4.13	

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	NT2RP3002351	4.32	4.32	4.55	4.38	3.9	2.55		
	NT2RP3002352	6.3	6.3	8.01	4.4	6.76	4.31		
	NT2RP3002353	3	3	4.85	4.87	6.18	5.9		
5	NT2RP3002362	5	5	11.74	15.86	11.03	10.49		
	NT2RP3002363	2.41	2.41	3.67	5.53	6.17	2.32		
	NT2RP3002377	2.61	2.61	5.47	6.8	7.31	4.73		
	NT2RP3002377	4.47	4.47	7.73	11.4	5.31	7.09		
10	NT2RP3002394	5.58	5.58	7.35	7.82	10.17	4.46		
	NT2RP3002397	3.77	3.77	4.81	2.7	3.12	1.68	*	-
	NT2RP3002399	4.61	4.61	7.69	14.65	13.02	16.16	**	+
	NT2RP3002402	2.84	2.84	6.99	8.94	8.7	6.99		
	NT2RP3002404	2.88	2.88	5.6	3.12	3.73	1.83		
15	NT2RP3002410	4.85	4.85	15.65	17.05	14.13	10.65		
	NT2RP3002411	2.98	2.98	5.68	3.7	5.29	2.85		
	NT2RP3002414	5.62	5.62	9.35	10.28	6.81	7.92		
	NT2RP3002430	5.11	5.11	14.63	18.24	19.29	14.51		
20	NT2RP3002448	5.4	5.4	4.6	4.35	5.25	3.62		
	NT2RP3002454	7.3	7.3	15.31	12.9	12.71	9.32		
	NT2RP3002455	4.62	4.62	12.11	14.31	9.11	13.25		
	NT2RP3002456	3.21	3.21	7.75	7.09	6.57	5.9		
	NT2RP3002462	2.79	2.79	4.16	4.94	6.17	4.79	*	+
	NT2RP3002469	3.84	3.84	6.38	9.24	6.78	8.07	*	+
25	NT2RP3002470	6.7	6.7	14.71	17.86	16.99	13.48		
	NT2RP3002484	4.01	4.01	6.86	6.81	8.01	4.59		
	NT2RP3002491	3.62	3.62	4.1	2.05	2.51	1.46	**	-
	NT2RP3002494	79.24	79.24	131.02	118.47	163.2	105.2		
30	NT2RP3002497	1.07	1.07	1.57	2.37	1.39	1.37		
	NT2RP3002500	1.23	1.23	1.13	2.72	2.02	2.07	**	+
	NT2RP3002501	5.25	5.25	8.49	8.45	8.11	9.69		
	NT2RP3002512	2.85	2.85	3.97	3.3	2.74	3.57		
	NT2RP3002529	3.94	3.94	7.5	6.59	5.14	5.85		
35	NT2RP3002533	7.95	7.95	10.26	9.79	10.51	8.18		
	NT2RP3002539	4.39	4.39	4.32	5.66	6.61	2.85		
	NT2RP3002540	5.24	5.24	5.5	3.48	4.76	3.65	*	-
	NT2RP3002543	3.44	3.44	7.17	4.93	6.21	5.31		
	NT2RP3002545	7.34	7.34	7.46	5.17	5.52	6.8	*	-
40	NT2RP3002549	3.27	3.27	7.8	4.98	6.11	4.54		
	NT2RP3002552	3.05	3.05	6.04	4.17	5.81	4.06		
	NT2RP3002558	9.54	9.54	9.39	9.93	4.26	11.27		
	NT2RP3002565	1.94	1.94	4.83	1.73	2.48	1.52		
	NT2RP3002566	3.62	3.62	7.02	4.03	8.51	3.65		
45	NT2RP3002571	2.53	2.53	4.85	3.77	5.41	3.74		
	NT2RP3002572	2.98	2.98	5.28	4.75	4.74	5.21		
	NT2RP3002573	4.31	4.31	11.38	7.06	9.48	7.06		
	NT2RP3002577	1.57	1.57	4.61	2.71	2.32	1.9		
	NT2RP3002579	3.92	3.92	6.41	4.03	7.75	11.16		
50	NT2RP3002582	5.02	5.02	7.17	11.51	14.07	8.45	*	+
	NT2RP3002587	1.9	1.9	3.13	2.68	3.04	1.97		
	NT2RP3002590	3.16	3.16	5.65	9.06	10.39	8.06	**	+
	NT2RP3002602	3.02	3.02	4.24	3.95	5.85	3.77		
	NT2RP3002603	71.53	71.53	214.41	268.41	257.84	298.26	*	+
55	NT2RP3002621	1.95	1.95	3.42	2.13	5.13	1.85		

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	NT2RP3002622	2.63	2.63	7.38	3.7	7.36	4.67		
	NT2RP3002624	2.29	2.29	7.4	4.04	4.9	3.64		
	NT2RP3002628	6.36	6.36	16.17	19.57	22.15	16.21		
5	NT2RP3002629	8.96	8.96	13.58	15.4	18.26	15.57	*	+
	NT2RP3002631	1.95	1.95	1.67	0.91	1.65	1.69		
	NT2RP3002647	4.04	4.04	4.01	5.44	7.16	4.6		
	NT2RP3002649	2.99	2.99	5.99	2.15	5.84	3.23		
	NT2RP3002650	3.32	3.32	11.62	4.98	8.53	6.88		
10	NT2RP3002652	2.27	2.27	6.59	4.91	6.83	4.25		
	NT2RP3002654	3.05	3.05	7.5	5.58	5.4	4.2		
	NT2RP3002657	14.14	14.14	13.87	17.27	26.08	18.87		
	NT2RP3002659	1.92	1.92	6.01	3.91	5.78	3.47		
	NT2RP3002660	3.09	3.09	4.84	3.77	7.72	3.52		
15	NT2RP3002663	2.39	2.39	3.33	2.54	3.13	2.84		
	NT2RP3002664	2.74	2.74	7.28	3.65	2.56	2.13		
	NT2RP3002667	2.92	2.92	6.59	6.63	5.46	5.35		
	NT2RP3002671	2.37	2.37	5.02	3.91	5.52	4.11		
	NT2RP3002682	6.34	6.34	20.62	14.37	17.64	21.7		
20	NT2RP3002684	4	4	6.34	3.32	6.16	3.18		
	NT2RP3002687	3.25	3.25	6.22	2.7	3.87	6.41		
	NT2RP3002688	3.22	3.22	4.98	2.63	3.91	2.61		
	NT2RP3002698	2.2	2.2	3.99	3.07	4.28	2.38		
25	NT2RP3002701	2.93	2.93	6.73	3.45	3.07	3.6		
	NT2RP3002705	2.17	2.17	8.01	4.36	8.76	4.72		
	NT2RP3002708	3.69	3.69	9.88	5.64	7.34	4.9		
	NT2RP3002711	6.67	6.67	7.85	7.77	7.56	6.69		
	NT2RP3002712	55.99	55.99	75.28	146.74	168.42	130.64	**	+
30	NT2RP3002713	4.31	4.31	7.06	2.66	2.19	1.87	*	-
	NT2RP3002721	5.77	5.77	10.06	11.06	16.94	8.96		
	NT2RP3002722	7.11	7.11	10.08	7.8	6.45	6.62		
	NT2RP3002723	42.31	42.31	75.85	60.39	46.74	58.76		
	NT2RP3002737	8.35	8.35	18.1	10.97	11.6	9.37		
35	NT2RP3002738	1.9	1.9	6.13	3.09	5.23	3.54		
	NT2RP3002742	14.11	14.11	23.22	30.39	28.27	27.66	*	+
	NT2RP3002744	4.09	4.09	5.24	3.92	4.92	1.71		
	NT2RP3002756	5.8	5.8	5.8	3.19	2.68	1.55	**	-
	NT2RP3002757	12	12	17.79	19.76	24.24	19.75	*	+
40	NT2RP3002758	21.11	21.11	42.35	44.47	63.91	36.38		
	NT2RP3002762	5.07	5.07	8.82	7.21	7.43	7.76		
	NT2RP3002763	1.62	1.62	4.86	3.76	4.99	2.18		
	NT2RP3002770	1.78	1.78	5.14	3.46	3.7	2.93		
	NT2RP3002771	17.04	17.04	39.53	24.93	40.21	34.4		
45	NT2RP3002785	2.42	2.42	5.45	3.36	4.09	2.66		
	NT2RP3002790	4.65	4.65	4.22	3.16	3.57	2.33	*	-
	NT2RP3002799	4.73	4.73	6.33	3.42	2.7	1.43	*	-
	NT2RP3002801	4.14	4.14	3.59	3.6	3.22	2.49		
	NT2RP3002802	2.31	2.31	6.3	6.78	5.43	4.4		
50	NT2RP3002810	2.98	2.98	5.41	7.44	12.32	13.27	*	+
	NT2RP3002818	1.5	1.5	2.44	2.18	4.16	2.47		
	NT2RP3002821	12.8	12.8	33.14	26.1	35.81	23.02		
	NT2RP3002823	3.85	3.85	8.98	4.65	5.92	3.87		
55	NT2RP3002825	5.47	5.47	13.04	13.47	19.19	7.12		

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	NT2RP3002829	5.37	5.37	6.25	4.75	4.89	3.8	
	NT2RP3002831	4.01	4.01	6.13	9.07	8.77	5.19	
	NT2RP3002836	7.33	7.33	19.42	11.56	16.91	20.66	
5	NT2RP3002845	4.17	4.17	6.63	7.87	8.6	8.45	*
	NT2RP3002852	3.37	3.37	7.57	7.8	8.72	8.21	
	NT2RP3002861	3.82	3.82	6.4	7.34	7.35	4.63	
	NT2RP3002869	3.66	3.66	3.26	2.49	1.86	0.49	*
	NT2RP3002874	11.25	11.25	21.44	25.33	31.95	25.54	*
10	NT2RP3002876	6.98	6.98	11.06	12.8	14.93	14.39	*
	NT2RP3002877	4.7	4.7	5.96	3.3	5.24	2.53	
	NT2RP3002887	0.47	0.47	3.42	2.81	3.53	3.91	
	NT2RP3002900	6.46	6.46	19.64	21.86	21.54	22.3	
15	NT2RP3002902	4.01	4.01	10.25	11.72	8.52	8.06	
	NT2RP3002909	2.61	2.61	6.19	6.67	5.38	3.93	
	NT2RP3002911	3.05	3.05	3.68	3.09	3.73	2.24	
	NT2RP3002948	4.09	4.09	4.81	2.73	4.44	2.07	
	NT2RP3002953	3.85	3.85	3.6	2.27	2.52	0.84	*
20	NT2RP3002955	6.55	6.55	3.78	1.93	2.47	0.86	*
	NT2RP3002958	5.85	5.85	11.4	16.5	10.57	16.64	
	NT2RP3002969	4.28	4.28	8.27	12.91	7.49	7.33	
	NT2RP3002972	3.55	3.55	4.82	4.41	6.18	2.29	
	NT2RP3002978	1.48	1.48	2.99	2.61	3.7	1.49	
25	NT2RP3002983	2.89	2.89	4.69	4.46	6.12	4.37	
	NT2RP3002985	4.23	4.23	17.87	13.64	20.26	11.12	
	NT2RP3002988	3.97	3.97	4.6	4.12	5.64	4.13	
	NT2RP3003000	3.11	3.11	3.46	2.46	3.2	1.51	
	NT2RP3003008	3.26	3.26	5.87	3.95	4.55	2.96	
30	NT2RP3003012	3.43	3.43	6.06	3.9	4.96	2.79	
	NT2RP3003015	1.35	1.35	4.9	1.5	2.5	0.54	
	NT2RP3003018	2.15	2.15	6.09	3.45	7.24	2.59	
	NT2RP3003028	3.53	3.53	7.23	3.5	5.05	4.01	
	NT2RP3003029	111.75	111.75	149.73	175.13	159.77	181.4	*
35	NT2RP3003032	7.06	7.06	9.05	11.87	18.84	9.94	
	NT2RP3003041	2.07	2.07	1.88	1.61	1.41	0.69	
	NT2RP3003044	3.06	3.06	7.45	5.72	6.11	7.57	
	NT2RP3003047	3.09	3.09	5.16	2.4	4.67	2.06	
	NT2RP3003050	5.96	5.96	12.03	6.74	10.3	8.42	
40	NT2RP3003053	7.46	7.46	18	14.42	17.14	13.72	
	NT2RP3003059	1.93	1.93	4.76	2.88	4.41	3.06	
	NT2RP3003061	2.8	2.8	8.59	5.49	5.68	5.16	
	NT2RP3003068	5.99	5.99	11.77	9.41	8.75	10.04	
	NT2RP3003071	7.22	7.22	10.77	10.39	14.52	10.39	
45	NT2RP3003076	2.67	2.67	9.49	5.57	6.57	4.01	
	NT2RP3003078	1.5	1.5	4.12	2.09	4.52	2.43	
	NT2RP3003081	6.21	6.21	10.54	9.94	9.6	9.97	
	NT2RP3003090	1.49	1.49	5.95	3.28	3.57	3.25	
50	NT2RP3003097	2.42	2.42	7.15	2.71	3.72	2.93	
	NT2RP3003098	2.75	2.75	4.22	2.73	3.43	1.73	
	NT2RP3003101	5.56	5.56	7.24	7.73	10.35	7.18	
	NT2RP3003109	16.11	16.11	27.38	27.36	41.03	21.91	
	NT2RP3003121	3.39	3.39	11.03	4.61	8	2.44	
55	NT2RP3003133	2.09	2.09	5.78	4.93	8.58	3.96	

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	NT2RP3003137	3.42	3.42	5.74	6.32	7.59	5.29	
	NT2RP3003138	2.36	2.36	5.27	5.26	5.7	3.74	
	NT2RP3003139	2.53	2.53	7.8	3.15	5.74	2.7	
5	NT2RP3003145	5.08	5.08	32.56	25.8	29.74	19.72	
	NT2RP3003150	2.03	2.03	5.17	3.56	3.76	1.97	
	NT2RP3003157	2.52	2.52	8.34	6.4	10.1	4.94	
	NT2RP3003185	1.77	1.77	3.88	1.91	3.34	2.62	
10	NT2RP3003193	2.62	2.62	5.75	6.03	4.59	2.65	
	NT2RP3003197	2.38	2.38	3.8	3.11	4.02	2.2	
	NT2RP3003203	11.82	11.82	14.35	16.85	10.17	15.27	
	NT2RP3003204	3.76	3.76	7.93	4.04	6.17	3.79	
	NT2RP3003210	14.48	14.48	75.3	58.97	84.6	68.66	
15	NT2RP3003212	5.15	5.15	9.44	9.21	10.67	7.36	
	NT2RP3003213	4.16	4.16	5.68	5.15	7.02	5.44	
	NT2RP3003224	1.7	1.7	4.75	2.43	2.11	2.64	
	NT2RP3003226	3.25	3.25	5.68	5.57	5.94	3.63	
	NT2RP3003230	7.79	7.79	11.47	12.39	8.89	6.72	
20	NT2RP3003235	7.61	7.61	10.79	7.77	7.73	6.89	
	NT2RP3003242	12.17	12.17	23.49	26.68	32.03	19.25	
	NT2RP3003251	5.61	5.61	9.47	3.73	4.95	4.08	
	NT2RP3003252	3.95	3.95	5.95	2.19	3.7	2.42	
	NT2RP3003258	4.92	4.92	7.89	19.94	24.95	15.47	** +
25	NT2RP3003260	4.54	4.54	12.34	13.46	11.52	12.68	
	NT2RP3003264	1.64	1.64	5.99	3.18	4.32	1.86	
	NT2RP3003273	2.18	2.18	4.93	4.57	3.58	1.72	
	NT2RP3003278	1.33	1.33	4	1.31	5.12	0.63	
	NT2RP3003280	9.85	9.85	23.11	18.18	19.52	18.19	
30	NT2RP3003282	5.29	5.29	6.25	3.62	3.97	3.48	** -
	NT2RP3003290	6.64	6.64	9.09	4.8	5.38	3.78	* -
	NT2RP3003301	4.01	4.01	5.73	4.31	4.59	3.23	
	NT2RP3003302	1.45	1.45	2.31	2.91	2.64	1.91	
	NT2RP3003311	2.45	2.45	6.76	15.72	13.09	11.55	** +
35	NT2RP3003312	1.81	1.81	3.35	3.73	3.87	2.41	
	NT2RP3003313	1.61	1.61	4.2	2.91	5.4	2.87	
	NT2RP3003327	1.62	1.62	6.24	4.81	4.95	3.34	
	NT2RP3003330	5.13	5.13	8.01	15.68	16.13	12.78	** +
	NT2RP3003344	3.36	3.36	4.14	2.92	3.74	2.6	
40	NT2RP3003346	3.81	3.81	4.83	4.38	4.05	1.24	
	NT2RP3003349	4.04	4.04	6.93	9.96	9.41	9.65	** +
	NT2RP3003353	1.95	1.95	3.24	4.06	5.37	2.45	
	NT2RP3003354	5.09	5.09	13.72	16.29	12.02	13.5	
	NT2RP3003368	3.03	3.03	4.73	4.04	4.08	2.63	
45	NT2RP3003375	4.1	4.1	7.4	7.41	9.67	6.62	
	NT2RP3003377	4.16	4.16	3.98	2.57	3.58	1.65	
	NT2RP3003384	5.77	5.77	4.55	2.83	3.43	2.56	** -
	NT2RP3003385	4.55	4.55	3.12	1.9	2.36	1.47	* -
	NT2RP3003396	3.93	3.93	13.63	16.4	8.38	12.32	
50	NT2RP3003403	1.62	1.62	2.54	3.24	4.73	1.92	
	NT2RP3003409	1.18	1.18	2.97	3.3	4.48	3.03	
	NT2RP3003411	4.59	4.59	15.42	14.11	15.42	10.96	
	NT2RP3003420	3.79	3.79	4.36	3.68	2.13	1.85	
55	NT2RP3003425	3.25	3.25	6.71	5.85	7.25	5.49	

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	NT2RP3003426	9.11	9.11	16.3	10.88	11.12	17.45	
	NT2RP3003427	5.95	5.95	10.09	9.15	13.58	8.03	
5	NT2RP3003433	2.55	2.55	6.26	8.42	9.57	4.87	
	NT2RP3003437	22.12	22.12	49.85	51.81	44	38.77	
	NT2RP3003448	1.88	1.88	4.24	3.5	3.83	2.63	
	NT2RP3003455	5.23	5.23	12.16	11.8	9.96	8.44	
	NT2RP3003462	4.96	4.96	10.07	10.76	8.25	7.08	
10	NT2RP3003464	3.79	3.79	5.03	3.01	4.76	1.2	
	NT2RP3003469	4.1	4.1	7.77	6.62	7.56	5.07	
	NT2RP3003473	22.06	22.06	36.6	54.82	69.25	56.46	** +
	NT2RP3003474	8.26	8.26	23.04	13.23	12.04	13.52	
	NT2RP3003475	2.84	2.84	4.04	4.55	4.45	3.28	
15	NT2RP3003490	2.7	2.7	5.81	4.21	4.43	3.12	
	NT2RP3003491	2.26	2.26	3	2.14	2.75	1.26	
	NT2RP3003493	11.75	11.75	30.77	34.59	28.9	34.45	
	NT2RP3003500	4.93	4.93	5.26	4.99	7.46	3.65	
	NT2RP3003527	2.73	2.73	3.09	2.42	2.92	1.72	
20	NT2RP3003532	2.7	2.7	1.81	2.14	3.33	2.13	
	NT2RP3003535	3.14	3.14	4.37	1.92	3.4	2.19	
	NT2RP3003536	3.04	3.04	5.95	3.45	5.2	4.97	
	NT2RP3003543	2.61	2.61	6.24	3.21	4.81	3.83	
25	NT2RP3003549	1.43	1.43	6.66	2.18	4.07	1.55	
	NT2RP3003552	1.8	1.8	5.76	0.64	0.84	1.58	
	NT2RP3003555	4.4	4.4	14.14	12.16	17.43	16.23	
	NT2RP3003559	2.81	2.81	6.7	3.88	5.11	5.49	
	NT2RP3003564	3.11	3.11	5.9	2.24	4.6	5.25	
30	NT2RP3003572	2.1	2.1	4.21	1.88	3.02	2.32	
	NT2RP3003576	5.88	5.88	10.15	11.32	8.98	9.22	
	NT2RP3003587	7.39	7.39	12.41	10.01	12.71	12.75	
	NT2RP3003589	15.33	15.33	22.45	23.89	23.75	26.58	
	NT2RP3003592	7.77	7.77	10.4	8.42	14.48	9.74	
35	NT2RP3003593	8.16	8.16	13.62	13.47	13.84	110.49	
	NT2RP3003614	2.66	2.66	8.18	3.11	4.48	7.09	
	NT2RP3003621	1.64	1.64	3.91	2.1	3.68	2.96	
	NT2RP3003625	1.54	1.54	6.94	3.79	5.09	4.96	
	NT2RP3003627	6.73	6.73	20.05	16.23	13.97	25.71	
40	NT2RP3003636	3.3	3.3	7.74	5.99	3.79	10.4	
	NT2RP3003642	7.12	7.12	12.2	12.85	13.15	15.83	
	NT2RP3003645	2.91	2.91	6.07	2.23	2.42	3.53	
	NT2RP3003648	2.88	2.88	3.71	2.17	2.44	3.13	
45	NT2RP3003649	2.7	2.7	9.28	6.36	5.11	12.04	
	NT2RP3003650	2.65	2.65	4.25	4.38	3.16	4.09	
	NT2RP3003656	1.69	1.69	3.23	1.94	4.12	3	
	NT2RP3003659	2.76	2.76	4.56	2.14	4.8	4.88	
	NT2RP3003662	31.39	31.39	53.28	34.35	14.68	34.64	
50	NT2RP3003664	3.56	3.56	6.5	6.18	5.45	6.55	
	NT2RP3003665	1.89	1.89	4.83	2.07	2.8	4.96	
	NT2RP3003671	2.88	2.88	4.33	3.03	2.6	4.29	
	NT2RP3003672	4.78	4.78	9.8	10.69	14.73	16.35	* +
	NT2RP3003673	4.98	4.98	9.42	5.35	3.05	4.12	
55	NT2RP3003679	40.1	40.1	95.75	69.92	23.86	83.88	
	NT2RP3003680	3.13	3.13	5.38	3.96	4.58	5.88	



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	NT2RP3003686	2.22	2.22	4.43	2.84	4.85	2.25	
	NT2RP3003689	4.05	4.05	9.69	5.94	5.63	8.27	
	NT2RP3003697	13.79	13.79	120.74	108.93	77.49	68.74	
5	NT2RP3003701	2.7	2.7	5.17	2.58	3.05	2.57	
	NT2RP3003704	2.99	2.99	6.96	7.09	7.61	6.96	
	NT2RP3003714	1.39	1.39	4.25	1.68	0.89	1.14	
	NT2RP3003716	2.05	2.05	4.23	3	2.29	2.24	
10	NT2RP3003721	1.83	1.83	3.27	1.85	3.45	2.18	
	NT2RP3003722	3.45	3.45	8.18	8.08	7.79	5.45	
	NT2RP3003726	3.5	3.5	4.9	2.77	4.51	2.32	
	NT2RP3003729	4.1	4.1	8.53	4.22	5.44	4.6	
	NT2RP3003731	5.06	5.06	6.98	4.19	3.54	7.45	
15	NT2RP3003740	2.58	2.58	5.08	2.42	2.48	2.94	
	NT2RP3003746	3.63	3.63	8.14	6.7	5.94	6.59	
	NT2RP3003749	0.67	0.67	2.58	1.55	2.08	1.73	
	NT2RP3003754	3.32	3.32	7.31	4.66	5.87	5.81	
	NT2RP3003759	1.16	1.16	4.44	2.49	4.41	1.43	
20	NT2RP3003764	3.97	3.97	7.08	6.85	7.41	5.06	
	NT2RP3003766	6.93	6.93	7.84	3.3	5.87	3.79	*
	NT2RP3003767	11.19	11.19	16.8	14.83	21.08	16.97	
	NT2RP3003778	3.36	3.36	4.89	4.46	5.55	4.27	
25	NT2RP3003779	4.05	4.05	15.26	13.02	8.74	10.52	
	NT2RP3003783	9.25	9.25	21.72	22.42	13.65	18.76	
	NT2RP3003787	2.15	2.15	4.65	4.41	4.74	6.37	
	NT2RP3003789	5.12	5.12	10.16	11.63	12.19	14.96	* +
	NT2RP3003795	1.48	1.48	6.48	4.09	2.82	2.24	
30	NT2RP3003799	2.67	2.67	5.5	3.08	2.38	1.75	
	NT2RP3003800	4.36	4.36	5.92	4.14	4.57	6.91	
	NT2RP3003805	8.15	8.15	6.78	8.4	5.48	5.89	
	NT2RP3003809	1.94	1.94	7.2	5.83	5.4	4.82	
	NT2RP3003819	3.39	3.39	6.07	7.3	5.97	6.35	
35	NT2RP3003824	5.69	5.69	10.69	14.08	14.85	13.32	* +
	NT2RP3003825	9.06	9.06	16.31	12.87	16.88	16.75	
	NT2RP3003828	4.7	4.7	14.38	13.36	15.69	14.55	
	NT2RP3003831	4.01	4.01	6.38	5.77	6.54	7.23	
40	NT2RP3003833	5.12	5.12	7.5	6.44	8.88	6.96	
	NT2RP3003836	6.37	6.37	5.05	5.74	6.47	4.31	
	NT2RP3003842	2.7	2.7	9.08	6.84	6.51	7.09	
	NT2RP3003843	9.26	9.26	26.77	16.67	12.71	16.2	
	NT2RP3003844	20.38	20.38	46.56	42.84	27.94	44.32	
45	NT2RP3003846	4.04	4.04	8.45	8.94	7.18	8.05	
	NT2RP3003849	2.27	2.27	2.68	2.67	2.73	1.68	
	NT2RP3003862	28.91	28.91	45.63	32	37.58	44.88	
	NT2RP3003870	4.76	4.76	4.81	2.54	2.93	2.05	** -
	NT2RP3003874	21.46	21.46	20.88	33.11	47.25	36.44	* +
50	NT2RP3003876	1.62	1.62	8.08	5.45	7.49	6.81	
	NT2RP3003880	1.74	1.74	4.63	5.31	4.66	4.73	
	NT2RP3003889	1.69	1.69	3.04	3.41	3.53	9.53	
	NT2RP3003891	1.88	1.88	2.98	2.56	3.19	1.37	
	NT2RP3003914	3.1	3.1	7.35	6.88	5.15	7.39	
55	NT2RP3003915	5.03	5.03	8.44	9.52	11.35	8.6	
	NT2RP3003918	6.79	6.79	10.39	10.04	13.71	12.42	

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	NT2RP3003920	6.9	6.9	9.13	8.31	10.22	8.96	
	NT2RP3003924	2.25	2.25	9.57	6.49	5.34	6.91	
5	NT2RP3003932	1.41	1.41	3.85	5.17	5.26	3.85	
	NT2RP3003939	3.48	3.48	11.88	9.86	14.05	11.09	
	NT2RP3003940	11.34	11.34	27.33	23.54	20.59	23.06	
	NT2RP3003943	2.6	2.6	2.83	2.85	2.78	3.88	
	NT2RP3003959	3.52	3.52	6.96	6.54	5.93	5.49	
10	NT2RP3003963	4.83	4.83	7.59	4.01	4.61	2.52	
	NT2RP3003965	11.14	11.14	13.85	18.75	20.67	17.22	** +
	NT2RP3003972	26.1	26.1	40.32	22.13	17.98	38.48	
	NT2RP3003973	2.85	2.85	4.33	1.96	3.6	3.96	
	NT2RP3003979	5.89	5.89	12.53	6.92	8.49	8.84	
15	NT2RP3003980	3.52	3.52	9.41	9.34	8.89	7.92	
	NT2RP3003982	4.2	4.2	4.63	2.44	1.6	4.61	
	NT2RP3003989	6.24	6.24	4.69	9.61	5.62	16.05	
	NT2RP3003992	2.13	2.13	4.89	2.47	5.12	4.8	
20	NT2RP3004000	2.81	2.81	6	1.72	3.22	2.62	
	NT2RP3004001	11.38	11.38	19.94	11.62	11.37	21.11	
	NT2RP3004005	2.89	2.89	7.79	4.7	4.48	6.84	
	NT2RP3004013	2.23	2.23	7.2	2.66	4.87	3.57	
	NT2RP3004016	1.5	1.5	7.1	2.22	3.14	2.88	
25	NT2RP3004025	4.02	4.02	7.69	7.48	12.19	9.01	
	NT2RP3004030	7.05	7.05	12.64	13.97	15.8	17.66	* +
	NT2RP3004041	5.65	5.65	11.38	10.48	9.57	19.81	
	NT2RP3004042	15.22	15.22	102.33	97.27	103.6	99.67	
	NT2RP3004044	2.13	2.13	6.51	5.14	7.21	4.22	
30	NT2RP3004051	2.6	2.6	5.79	2.23	5.51	4.69	
	NT2RP3004052	7.1	7.1	11.22	5.63	4.98	9.78	
	NT2RP3004053	15.87	15.87	35.04	23.12	40.67	40.17	
	NT2RP3004055	2.38	2.38	5.33	2.98	3.3	4.47	
	NT2RP3004059	4.05	4.05	8.8	8.15	7.03	11	
35	NT2RP3004063	5.13	5.13	11.23	8.78	11.27	12.33	
	NT2RP3004067	4.24	4.24	8.4	6.62	6.42	4.47	
	NT2RP3004070	3.58	3.58	9.92	6.26	4.4	5.47	
	NT2RP3004075	4.16	4.16	11.23	12.62	11.88	13.3	
	NT2RP3004078	2.6	2.6	5.25	4.94	4.19	2.79	
40	NT2RP3004083	2.93	2.93	6.23	4.57	6.8	11.37	
	NT2RP3004084	4.65	4.65	20.29	6.18	8.56	5.32	
	NT2RP3004087	4.2	4.2	7.86	7.14	10.81	9.03	
	NT2RP3004090	4.11	4.11	6.42	9	8.19	8.61	** +
45	NT2RP3004093	2.38	2.38	7.49	4.07	3.51	4.47	
	NT2RP3004095	5.02	5.02	13.11	11.57	10.17	18.55	
	NT2RP3004102	3.32	3.32	5.59	5.25	4.27	3.21	
	NT2RP3004110	12.74	12.74	18.66	22.12	14.31	19.97	
	NT2RP3004119	3.3	3.3	7.71	3.91	4.08	3.73	
50	NT2RP3004125	5.55	5.55	12.05	8.13	10.88	8.38	
	NT2RP3004129	4.62	4.62	7.38	3.36	2.95	6.08	
	NT2RP3004130	11.81	11.81	28.12	21.92	31.13	21.05	
	NT2RP3004133	4.51	4.51	12.95	14.62	8.94	16.81	
	NT2RP3004145	1.43	1.43	4.17	2.62	4.87	3.59	
55	NT2RP3004148	2.67	2.67	7.07	5.26	6.24	4.5	
	NT2RP3004155	2.37	2.37	4.82	4.7	4.57	6.59	

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	NT2RP3004165	17.94	17.94	29.96	29.58	31.82	39.18		
	NT2RP3004179	7.34	7.34	6.72	2.71	5.41	3.3	*	-
	NT2RP3004185	5.2	5.2	5.53	2.76	2.76	1.95	**	-
5	NT2RP3004188	4.77	4.77	10.82	7.74	11.35	7		
	NT2RP3004189	4.23	4.23	5.91	4.97	4.82	6.28		
	NT2RP3004190	2.6	2.6	5.57	5.84	4.36	5.26		
	NT2RP3004191	14.09	14.09	23.4	31.41	29.45	30.09	*	+
10	NT2RP3004202	2.04	2.04	4.56	4.16	4.42	2.3		
	NT2RP3004205	8.75	8.75	21.54	21.27	25.35	20.28		
	NT2RP3004206	4.5	4.5	9.74	5.14	6.37	9		
	NT2RP3004207	5.19	5.19	4.99	3.09	3.25	1.77	**	-
	NT2RP3004209	4.74	4.74	7.74	8.2	11.23	9.08	*	+
15	NT2RP3004215	1.86	1.86	6.7	3.96	2.41	4.55		
	NT2RP3004219	5.15	5.15	11.25	10.04	8.81	13.65		
	NT2RP3004242	4.65	4.65	10.36	9.8	10.19	14.56		
	NT2RP3004246	4.5	4.5	9.39	9.18	10.95	3.8		
20	NT2RP3004253	1.89	1.89	4.85	3.64	4.99	2.8		
	NT2RP3004258	5.45	5.45	10.89	12.77	11.07	11.39		
	NT2RP3004262	4.26	4.26	5.71	2.63	2.99	2.01	*	-
	NT2RP3004275	5.59	5.59	3.43	1.4	2.97	2.34	*	-
	NT2RP3004282	5.45	5.45	68.08	51.29	52.72	53.57		
25	NT2RP3004289	1.79	1.79	2.95	1.9	2.18	3.99		
	NT2RP3004294	2.74	2.74	6.02	6.95	6.93	7.24	*	+
	NT2RP3004298	8.76	8.76	48.63	46.33	60.89	50.83		
	NT2RP3004309	3.3	3.3	6.46	5.2	5.22	5.31		
	NT2RP3004321	3.71	3.71	6.11	3.29	3.74	3.34		
30	NT2RP3004322	5.61	5.61	6.86	6.06	6.43	6.56		
	NT2RP3004332	11.69	11.69	100.11	78.54	102.41	76.72		
	NT2RP3004334	1.49	1.49	6.97	8.56	6.06	9.06		
	NT2RP3004336	2.11	2.11	6.24	6.02	4.44	5.63		
	NT2RP3004338	3.09	3.09	8.41	10.22	9.52	16.47		
35	NT2RP3004341	1.81	1.81	4.56	6.13	5.17	9.13		
	NT2RP3004345	4.1	4.1	8.68	9.3	9.63	8.48		
	NT2RP3004348	5.06	5.06	11.25	13.04	10.79	12.54		
	NT2RP3004349	5	5	7.5	4.89	7.75	5.76		
40	NT2RP3004355	5.57	5.57	7.09	7.55	7.07	7.18		
	NT2RP3004356	5.76	5.76	21.51	11.29	15.14	15.56		
	NT2RP3004360	3.4	3.4	5.26	6.01	5.32	7.85		
	NT2RP3004361	2.6	2.6	6.26	7.67	7.3	8.87	*	+
	NT2RP3004374	3.06	3.06	10.09	8.8	6.6	5.75		
45	NT2RP3004378	10.48	10.48	18.57	28.26	24.09	34.81	*	+
	NT2RP3004399	3.88	3.88	5.77	3.53	3.17	9.06		
	NT2RP3004405	4.07	4.07	6.77	3.03	5.52	3.93		
	NT2RP3004406	5.36	5.36	6.23	5.19	6.03	6.12		
	NT2RP3004411	5.93	5.93	13.28	8.08	6.39	9.51		
50	NT2RP3004424	1.53	1.53	2.43	3.27	1.81	2.83		
	NT2RP3004428	3.03	3.03	5.36	5.07	3.82	4.09		
	NT2RP3004432	3.3	3.3	3.52	3.61	3.11	4.38		
	NT2RP3004434	3.42	3.42	8.41	7.28	9.09	7.99		
	NT2RP3004446	3.29	3.29	4.6	3.29	4.1	2.63		
55	NT2RP3004451	3.2	3.2	6.01	3.89	3.38	2.48		
	NT2RP3004454	2.96	2.96	4.16	2.69	3.5	2.5		

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	NT2RP3004466	3.5	3.5	7.89	5.25	3.85	5.61	
	NT2RP3004470	7.42	7.42	24.53	18.4	16.35	24.72	
5	NT2RP3004472	2.49	2.49	4.4	3.97	3.84	3.88	
	NT2RP3004475	1.71	1.71	5.52	2.72	5.93	3.9	
	NT2RP3004480	14.12	14.12	17.04	18.94	10.5	18.82	
	NT2RP3004481	5.42	5.42	11.37	5.04	7.37	12.39	
	NT2RP3004490	2.66	2.66	8.45	3.92	7.03	8.25	
10	NT2RP3004496	4.8	4.8	14.38	7.22	9.3	11.08	
	NT2RP3004498	6.39	6.39	21.39	16.86	15.11	18.92	
	NT2RP3004503	2.78	2.78	9.34	4.85	6.23	5.88	
	NT2RP3004504	3.91	3.91	11.09	6.05	10.67	11.52	
	NT2RP3004505	17.38	17.38	28.56	37.35	26.72	37.82	
15	NT2RP3004507	1.57	1.57	6.6	2.52	5.52	1.68	
	NT2RP3004519	4.9	4.9	7.73	4.93	8.36	8.75	
	NT2RP3004524	10.04	10.04	29.21	26.88	26.43	29.62	
	NT2RP3004527	3.03	3.03	3.22	1.29	2.23	2.08	*
	NT2RP3004534	3.08	3.08	10.44	5.58	12	7.38	
20	NT2RP3004539	4.45	4.45	12.17	9.8	8.97	12	
	NT2RP3004541	2.65	2.65	11.06	5.48	9.44	8.25	
	NT2RP3004544	3.54	3.54	8.89	6.62	5.24	9.48	
	NT2RP3004551	3.46	3.46	6.75	6.6	6.6	6.98	
	NT2RP3004552	2.76	2.76	4.33	2.84	3.22	4.98	
25	NT2RP3004557	5.68	5.68	8.73	9.74	15.44	13.16	* +
	NT2RP3004561	1.96	1.96	3.77	2.55	4.46	4.1	
	NT2RP3004566	3.09	3.09	11.55	7.2	10.05	8.79	
	NT2RP3004569	2.21	2.21	7.09	4.63	5.36	6.91	
30	NT2RP3004572	4.37	4.37	6.83	7.08	5.55	7.07	
	NT2RP3004578	2.35	2.35	5.38	4.15	4.27	3.24	
	NT2RP3004584	4.76	4.76	28.36	34.99	37.13	30.29	
	NT2RP3004588	2.38	2.38	4.89	1.6	3.7	3.28	
	NT2RP3004594	2.25	2.25	5.9	5.67	6.49	8.94	
35	NT2RP3004603	34.16	34.16	99.64	80.2	102.6	97.27	
	NT2RP3004612	4.71	4.71	12.17	5.3	3.36	5.34	
	NT2RP3004617	1.09	1.09	2.32	2.49	3.3	2.39	
	NT2RP3004618	4.61	4.61	5.9	2.49	5.21	5.9	
	NT2RP3004625	3.97	3.97	8.17	4.55	6.92	7.1	
40	NT2RP3004635	4.76	4.76	7.83	1.52	2.86	3.47	
	NT2RP3004640	10.61	10.61	62.15	59.33	67.97	48.32	
	NT2RP3004642	8.04	8.04	29.31	22.82	26.12	25.12	
	NT2RP3004647	3.5	3.5	5.65	5.89	7.35	6.88	* +
	NT2RP3004652	1.76	1.76	10.37	4.2	3.71	4.34	
45	NT2RP3004669	2.01	2.01	5.36	4.01	5.33	3.46	
	NT2RP3004670	5.04	5.04	10.58	12.4	9.19	14.23	
	NT2RP4000008	45.17	45.17	71.24	49.77	32.43	48.77	
	NT2RP4000018	11.64	11.64	14.61	11.69	14.8	14.87	
50	NT2RP4000023	6.96	6.96	8.91	4.86	7.38	5.98	
	NT2RP4000025	16.2	16.2	22.16	26.22	29.89	24.7	* +
	NT2RP4000035	6.3	6.3	12.01	11.28	15.33	11.01	
	NT2RP4000041	14.46	14.46	34.8	22.01	17.41	23.68	
	NT2RP4000049	2.64	2.64	6.34	6.59	6.88	5.3	
55	NT2RP4000050	2.24	2.24	6.87	3.54	4.48	4.05	
	NT2RP4000051	4.66	4.66	10.5	10.58	10.02	8.96	

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	NT2RP4000063	20.51	20.51	33.5	26.77	31	18.33		
	NT2RP4000065	7.54	7.54	9.24	11.85	15.01	11.47	*	+
	NT2RP4000070	6.63	6.63	5.29	3.79	4.54	3.84	*	-
5	NT2RP4000074	6.55	6.55	13.63	10.29	15.39	9.52		
	NT2RP4000078	3.41	3.41	9.55	12.2	11.66	12.56	*	+
	NT2RP4000080	3.52	3.52	7.01	5.06	6.84	6.81		
	NT2RP4000099	128.86	128.86	236.22	149.44	161.1	211.56		
10	NT2RP4000102	3.55	3.55	6.48	5.27	4.97	5.54		
	NT2RP4000103	2	2	5.47	2.57	2.85	3.96		
	NT2RP4000108	4.66	4.66	7.91	9.33	10.73	10.61	*	+
	NT2RP4000109	18.89	18.89	22.84	19.87	24.15	16.14		
	NT2RP4000111	4.56	4.56	6.38	4.87	5.27	4.85		
15	NT2RP4000112	5.62	5.62	10.14	12.45	8.7	11.81		
	NT2RP4000115	2.94	2.94	3.62	4.95	7.82	10.93		
	NT2RP4000129	2.18	2.18	4.58	3.02	5.04	5.03		
	NT2RP4000137	3.36	3.36	10.05	5.34	8.72	11.4		
	NT2RP4000138	7.21	7.21	10.91	17.75	20.19	19.17	**	+
20	NT2RP4000141	3.25	3.25	6.1	5.22	4.9	3.57		
	NT2RP4000147	6.21	6.21	4.49	4.27	5.2	3.47		
	NT2RP4000150	5.96	5.96	6.93	7.33	10.41	7.06		
	NT2RP4000151	2.82	2.82	7.82	5.69	6.24	5.05		
	NT2RP4000157	73.27	73.27	222.87	169.53	97.5	173.8		
25	NT2RP4000159	2.02	2.02	5.03	3.38	5.03	2.92		
	NT2RP4000163	5.21	5.21	8.74	10.89	9.18	6.63		
	NT2RP4000167	3.26	3.26	4.35	4.32	3.22	3.69		
	NT2RP4000171	5.72	5.72	7	5.72	7.45	5.03		
	NT2RP4000175	62.48	62.48	94.56	144.06	214.73	147.88	*	+
30	NT2RP4000180	17.17	17.17	106.15	88.61	123.6	81.8		
	NT2RP4000185	7.64	7.64	31.76	31.82	23.23	34.01		
	NT2RP4000192	1.04	1.04	4.78	4.19	3.6	3.05		
	NT2RP4000194	3.13	3.13	7.53	7.58	4.98	6.36		
35	NT2RP4000196	6.81	6.81	43.94	35.57	46.56	41.91		
	NT2RP4000210	5.63	5.63	9.71	9.96	8.35	9.27		
	NT2RP4000212	5.59	5.59	8.88	8.57	8.41	9.08		
	NT2RP4000214	5.53	5.53	10.21	5.72	6.68	11.29		
	NT2RP4000216	8.89	8.89	7.36	7	12.63	10.08		
40	NT2RP4000218	3.45	3.45	9.78	7.25	6.07	5.77		
	NT2RP4000223	21.18	21.18	177.28	121.8	125.75	125.3		
	NT2RP4000243	16.52	16.52	54.51	42.94	41.61	51.74		
	NT2RP4000246	17.75	17.75	37.97	26.43	11.42	27.5		
	NT2RP4000250	16.86	16.86	31.23	24.92	23.85	26.39		
45	NT2RP4000256	4.38	4.38	8.45	4.99	6.44	4.67		
	NT2RP4000257	32.45	32.45	44.22	48.67	57.52	39.19		
	NT2RP4000259	7.07	7.07	6.96	8.48	13.07	9.08		
	NT2RP4000261	4.18	4.18	8.13	4.07	4.55	6.48		
	NT2RP4000262	8.36	8.36	11.02	7.11	10.05	7.64		
50	NT2RP4000263	2.6	2.6	5.14	3.47	3.67	3.78		
	NT2RP4000280	5.84	5.84	11.62	9.05	11.58	14.23		
	NT2RP4000286	4.73	4.73	10.16	4.38	6.77	11.94		
	NT2RP4000290	5.77	5.77	5.42	3.18	3.19	5.5		
	NT2RP4000291	42.53	42.53	73.59	62.12	70.23	70.61		
55	NT2RP4000301	3.31	3.31	20.59	22.93	34.62	26.63	*	+

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	NT2RP4000312	7.76	7.76	45.27	39.01	43.59	45.92	
	NT2RP4000321	3.73	3.73	8.16	7.88	7.14	9.75	
5	NT2RP4000323	1.44	1.44	4.26	2.27	2.55	2.12	
	NT2RP4000324	7.77	7.77	16.76	8.33	10.2	11.08	
	NT2RP4000334	20.97	20.97	77.78	63.81	71.76	68.24	
	NT2RP4000343	2.48	2.48	5.54	1.57	3.16	2.38	
	NT2RP4000348	3.4	3.4	10.81	8.38	6.75	13.2	
10	NT2RP4000349	1.78	1.78	0.83	0.37	0.72	2.48	
	NT2RP4000355	3.98	3.98	14.84	7.18	9.13	9.04	
	NT2RP4000356	8.3	8.3	22.64	9.22	11.44	21.13	
	NT2RP4000360	3.04	3.04	6.98	5.06	5.43	4.73	
	NT2RP4000367	2.18	2.18	3.72	2.04	2.58	2.83	
15	NT2RP4000370	4.21	4.21	7.51	3.62	7.12	5.99	
	NT2RP4000373	3.33	3.33	5.18	3.19	5.23	2.95	
	NT2RP4000376	4.2	4.2	5.5	4.85	5.53	6.5	
	NT2RP4000381	1.97	1.97	6.46	4.31	7.01	5.59	
20	NT2RP4000388	85.82	85.82	204.63	128.93	93.38	116.03	
	NT2RP4000390	12.16	12.16	94.1	78.97	76.6	82.02	
	NT2RP4000393	8.66	8.66	9.77	9.09	5.99	10.79	
	NT2RP4000398	5.51	5.51	26.52	22.08	28.3	26.61	
	NT2RP4000406	6.68	6.68	15.61	12.95	15.02	10.08	
25	NT2RP4000407	6.17	6.17	11.52	9.41	14.74	9.13	
	NT2RP4000413	1.79	1.79	3.63	1.15	2.35	2.12	
	NT2RP4000415	7.59	7.59	26.11	18.6	21.68	21.68	
	NT2RP4000417	7.76	7.76	26.64	14.47	12.79	19.19	
	NT2RP4000423	3.52	3.52	7.56	7	6.98	6.46	
30	NT2RP4000424	2.51	2.51	7.2	3.07	5.03	3.27	
	NT2RP4000447	10.3	10.3	64.21	64.91	71.82	68.48	
	NT2RP4000448	5.59	5.59	6.67	4.32	3.56	6.27	
	NT2RP4000449	5.67	5.67	20.48	14.2	19.45	14.67	
	NT2RP4000453	3.53	3.53	6.32	9.02	10.32	10.12	** +
35	NT2RP4000455	2.64	2.64	3.98	1.81	1.75	2.4	
	NT2RP4000456	12.57	12.57	21.7	14.7	9.86	13.58	
	NT2RP4000457	1.54	1.54	7.12	3.9	7.55	2.98	
	NT2RP4000461	5.7	5.7	9.84	7.65	6.41	4.6	
40	NT2RP4000462	11.76	11.76	15.32	11.86	11.53	17.37	
	NT2RP4000463	10.2	10.2	52.59	50.66	69.3	48.36	
	NT2RP4000471	6.36	6.36	10.74	5.74	6.23	4.98	
	NT2RP4000472	3.97	3.97	4.41	1.27	1.27	1.66	** -
	NT2RP4000476	27.14	27.14	52.56	74.95	94.93	65.35	* +
45	NT2RP4000480	11.56	11.56	29.27	19.08	9.95	26.66	
	NT2RP4000481	2.29	2.29	4.76	3.73	4.16	4.33	
	NT2RP4000483	1.38	1.38	7.59	7.58	7.85	6.26	
	NT2RP4000487	1.54	1.54	4.9	2.26	3.17	0.91	
	NT2RP4000496	2.16	2.16	4.98	2.95	4.07	3.65	
50	NT2RP4000497	17.15	17.15	22.33	34.9	44.46	29.9	* +
	NT2RP4000498	10.46	10.46	21.39	20.15	30.33	24.49	
	NT2RP4000500	2.43	2.43	3.21	2.03	1.49	1.39	* -
	NT2RP4000507	5.63	5.63	9.02	12.49	10.62	17.51	* +
	NT2RP4000515	12.85	12.85	88.89	90.3	101.29	96.12	
55	NT2RP4000516	8.77	8.77	26.09	19.63	21.76	21.82	
	NT2RP4000517	3.22	3.22	5.73	4.69	5.89	4.79	

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	NT2RP4000518	3.42	3.42	7.4	4.47	6.05	3.82	
	NT2RP4000519	2.9	2.9	5.76	2.18	2.22	1.77	
5	NT2RP4000524	4.2	4.2	3.44	2.05	1.72	1.3 **	-
	NT2RP4000528	3.67	3.67	3.06	3.01	3.27	8.01	
	NT2RP4000537	35.4	35.4	62.6	36.23	30.93	44.52	
	NT2RP4000541	2.04	2.04	2.45	3.34	4.33	3.09 *	+
	NT2RP4000543	2.93	2.93	8.94	7.96	9.72	8.75	
10	NT2RP4000545	4.03	4.03	6.38	4.99	6.43	4.78	
	NT2RP4000546	3.34	3.34	5.93	5.53	4.9	6.03	
	NT2RP4000549	23.81	23.81	56.43	41.6	51.57	38.82	
	NT2RP4000556	7.36	7.36	13.04	14.69	15.54	12.07	
	NT2RP4000557	6.1	6.1	4.53	1.82	3.97	6.27	
15	NT2RP4000558	30.12	30.12	94.23	68.16	57.01	73.2	
	NT2RP4000560	14.8	14.8	52.31	49.75	58.69	56.12	
	NT2RP4000568	1.72	1.72	3.83	5.6	6.08	4.46 *	+
	NT2RP4000583	11.61	11.61	20.2	23.65	14.97	20.56	
20	NT2RP4000585	3.04	3.04	4.14	3.12	2.55	3.24	
	NT2RP4000588	8.65	8.65	12.77	14.58	16.96	13.55 *	+
	NT2RP4000590	24.89	24.89	41.97	41.86	50.81	32.65	
	NT2RP4000599	4.29	4.29	3.24	2.44	2.23	3.59	
	NT2RP4000603	14.08	14.08	33.32	31.06	21.01	29.12	
25	NT2RP4000607	2.41	2.41	10.04	4.45	7.87	15.35	
	NT2RP4000614	6.14	6.14	15.21	15.57	12.53	15.19	
	NT2RP4000634	6.61	6.61	11	7.78	9.84	10.31	
	NT2RP4000638	3.59	3.59	7.77	8.45	5.8	4.73	
	NT2RP4000648	3.13	3.13	4.26	2.54	2.69	2.19	
30	NT2RP4000657	9.94	9.94	15.38	15.95	18.93	14.49	
	NT2RP4000691	5.76	5.76	5.82	4.92	7.47	7.73	
	NT2RP4000697	3.74	3.74	8.5	5.55	6.56	6.12	
	NT2RP4000704	8.91	8.91	47.2	44.17	54.81	38.14	
	NT2RP4000710	40.22	40.22	98.85	90.4	59.28	83.71	
35	NT2RP4000713	4.35	4.35	19.92	16.67	20.85	15.52	
	NT2RP4000724	6.29	6.29	12.5	8.19	9.81	7.83	
	NT2RP4000725	3.61	3.61	4	1.88	1.74	2.33 **	-
	NT2RP4000728	10.13	10.13	41.12	43.53	66.46	39.83	
40	NT2RP4000737	4.07	4.07	2.15	3.63	3.09	3.28	
	NT2RP4000739	5.07	5.07	7.71	4.61	3.63	5.84	
	NT2RP4000749	2.4	2.4	5.29	2.59	3.97	1.68	
	NT2RP4000769	4.93	4.93	10.12	4.67	6.27	6.2	
	NT2RP4000774	3.34	3.34	8.87	5.12	6.63	4.27	
45	NT2RP4000781	2.15	2.15	5.12	2.06	2.26	1.55	
	NT2RP4000783	6.81	6.81	15.16	13.48	15.44	12.67	
	NT2RP4000787	1.45	1.45	2.27	0.31	0.51	0.54 *	-
	NT2RP4000788	3.58	3.58	23.26	16	18.3	18.73	
	NT2RP4000792	3.68	3.68	5.64	5.5	5.8	9.45	
50	NT2RP4000809	43.7	43.7	56.09	46.75	50.47	81.62	
	NT2RP4000817	3.65	3.65	7.83	7.92	7.25	5.82	
	NT2RP4000821	31.34	31.34	38.66	28.32	33.11	25.22	
	NT2RP4000822	2.46	2.46	5.91	4.29	6.19	2.6	
	NT2RP4000823	697.74	697.74	1127.48	923.16	1026.8	947.85	
55	NT2RP4000831	9.98	9.98	61.97	44.37	68.47	50.69	
	NT2RP4000833	3.19	3.19	11.26	6.73	7.19	11.91	

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	NT2RP4000837	1.41	1.41	4.03	1.56	3.65	2.29		
	NT2RP4000839	12.23	12.23	97.13	79.71	85.74	86.06		
5	NT2RP4000846	3.8	3.8	10.13	4.65	3.46	6.65		
	NT2RP4000848	4.63	4.63	10.74	8.65	8.58	6.07		
	NT2RP4000855	2.91	2.91	4.7	4	3.85	3.43		
	NT2RP4000863	3.08	3.08	4.33	3.11	5.3	3.78		
	NT2RP4000865	6.43	6.43	25.36	20.09	39.64	21.24		
10	NT2RP4000873	9.64	9.64	88.25	63.22	69.65	71.33		
	NT2RP4000874	1.76	1.76	3.98	2.37	3.67	2.03		
	NT2RP4000875	3.31	3.31	9.24	6.88	6.52	7.19		
	NT2RP4000878	24.17	24.17	42.53	28.01	16.35	29.04		
	NT2RP4000879	2.56	2.56	5.1	2.95	5.29	2.62		
15	NT2RP4000880	5.17	5.17	21.59	20.97	27.22	16.8		
	NT2RP4000891	81.07	81.07	192.57	252.29	351.53	221.08	*	+
	NT2RP4000894	5.16	5.16	9.81	8.53	4.8	6.97		
	NT2RP4000898	0.86	0.86	2.74	1.88	2.14	1.64		
	NT2RP4000899	9.63	9.63	29.48	24.01	20.85	23.95		
20	NT2RP4000907	2.14	2.14	3.58	1.74	4.04	0.81		
	NT2RP4000908	4.62	4.62	9.67	7.51	5.9	5.87		
	NT2RP4000910	14.4	14.4	104.68	124.04	197.74	160.9	*	+
	NT2RP4000918	2.85	2.85	4.76	4.73	4.26	5.35		
25	NT2RP4000925	3.9	3.9	5.53	2.81	3.15	1.86		
	NT2RP4000927	1.99	1.99	2.5	0.46	1.08	0.6	**	-
	NT2RP4000928	3.11	3.11	6.8	4.48	4.22	5.18		
	NT2RP4000929	1.44	1.44	3.68	1.94	2.86	0.84		
	NT2RP4000946	0.92	0.92	3.41	1.78	3.22	1.47		
30	NT2RP4000947	1.71	1.71	3.51	1.94	3.31	1.79		
	NT2RP4000949	4.94	4.94	7.84	3.88	5.48	2.38		
	NT2RP4000955	4.17	4.17	6.34	2.07	2.86	0.54	*	-
	NT2RP4000959	20.55	20.55	28.14	36.21	42.82	36.14	*	+
35	NT2RP4000962	3.4	3.4	4.24	8.33	10.09	4.53		
	NT2RP4000973	8.6	8.6	16.04	10.31	8.92	9.03		
	NT2RP4000975	2.18	2.18	5.84	3.29	3.05	2.62		
	NT2RP4000979	3.83	3.83	8.67	5.55	8.13	7.1		
	NT2RP4000984	1.61	1.61	4.31	3.15	3.93	1.85		
	NT2RP4000986	7.32	7.32	13.27	12.66	12.35	2.52		
40	NT2RP4000988	5.74	5.74	8.37	4	5.2	2.63		
	NT2RP4000989	6.24	6.24	6.55	4.05	3.48	2.89	**	-
	NT2RP4000990	3.16	3.16	4	1.92	1.69	2.16	**	-
	NT2RP4000994	4.04	4.04	7.67	16.48	10.13	15.95	*	+
	NT2RP4000996	3.54	3.54	7.49	6.77	6.52	7.38		
45	NT2RP4000997	21.59	21.59	36.81	28.52	15.18	34.38		
	NT2RP4001001	5.53	5.53	9.17	16.66	18.38	15.09	**	+
	NT2RP4001004	1.71	1.71	4.88	2.84	3.09	1.37		
	NT2RP4001006	3.46	3.46	8.12	6.85	6.52	6.13		
50	NT2RP4001009	9.3	9.3	10.45	15.44	20.46	8.25		
	NT2RP4001010	7.33	7.33	9.13	7.38	9.75	6.68		
	NT2RP4001013	23.29	23.29	50.16	30.87	28.1	30.91		
	NT2RP4001029	2.49	2.49	5.95	4.05	2.84	3.63		
	NT2RP4001036	7.55	7.55	13.55	9.11	11.51	13.16		
55	NT2RP4001041	6.57	6.57	14.4	9.89	12.3	6.35		
	NT2RP4001042	4.34	4.34	8.11	9.44	12.5	8.79		



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	NT2RP4001046	6.98	6.98	9.95	13.24	16.28	15.36	**	+
	NT2RP4001050	5.28	5.28	4.81	3.79	4.64	3.35	*	-
	NT2RP4001051	6.48	6.48	8.44	5.43	6.82	5.26		
5	NT2RP4001057	0.76	0.76	2.19	2.34	2.43	1.87		
	NT2RP4001063	1.48	1.48	4.39	3.34	3.53	1.8		
	NT2RP4001064	3.51	3.51	9.18	12.02	9.13	11.57		
	NT2RP4001067	4.42	4.42	9.77	10.96	9.63	6.6		
10	NT2RP4001078	2.12	2.12	3.43	2.67	2.53	1.82		
	NT2RP4001079	5.3	5.3	9.35	8.51	8.02	8.98		
	NT2RP4001080	4.1	4.1	5.27	3.52	4.52	2.3		
	NT2RP4001086	5.08	5.08	4.19	3.93	6.64	2.85		
	NT2RP4001095	2.49	2.49	7.25	7.96	6.49	6.85		
15	NT2RP4001098	0.92	0.92	3.38	3.87	2.95	3.41		
	NT2RP4001100	6.47	6.47	24.34	20.89	20.64	16.99		
	NT2RP4001105	3.13	3.13	7.23	6.51	5.58	4.61		
	NT2RP4001110	1.75	1.75	3.5	7.07	8.35	5.29	*	+
	NT2RP4001115	9.95	9.95	17.68	20.6	18.48	15.31		
20	NT2RP4001117	19.81	19.81	30.49	35.35	42.53	27.5		
	NT2RP4001122	6.06	6.06	6.09	5.17	6.25	3.27		
	NT2RP4001123	3.62	3.62	7.76	7.95	5.96	6.27		
	NT2RP4001126	4.36	4.36	11.28	10.87	9.09	8.04		
25	NT2RP4001127	3.25	3.25	4.59	3.39	3.08	2.17		
	NT2RP4001138	2.46	2.46	5.8	3.41	2.56	1.62		
	NT2RP4001143	2.73	2.73	5.98	6.44	6.54	5.66		
	NT2RP4001148	3.72	3.72	6.76	3.77	3.03	2.05		
	NT2RP4001149	5.07	5.07	7.28	6.76	9.03	6.37		
30	NT2RP4001150	3.8	3.8	3.17	3.15	3.7	2.88		
	NT2RP4001159	7.08	7.08	11.61	7.69	5.58	10.46		
	NT2RP4001162	3.77	3.77	6.14	4.07	6.06	3.41		
	NT2RP4001170	1.15	1.15	4.53	1.28	3.2	2.15		
	NT2RP4001174	4.16	4.16	12.27	7.91	11.95	5.02		
35	NT2RP4001175	9.65	9.65	19.14	15.72	21.29	13.28		
	NT2RP4001176	99.19	99.19	161.51	174.03	241.92	194	*	+
	NT2RP4001184	4.83	4.83	27.1	25.76	32.51	22.85		
	NT2RP4001198	21.66	21.66	48.22	29.54	29.17	38.54		
	NT2RP4001199	2.52	2.52	6.45	2.59	4.74	3.71		
40	NT2RP4001206	8.25	8.25	33.2	25.92	32.07	25.48		
	NT2RP4001207	2.38	2.38	5.15	2.21	3.11	4.01		
	NT2RP4001210	2.73	2.73	5.2	3.62	4.26	2.64		
	NT2RP4001213	3.42	3.42	5.11	3.99	4.23	3.63		
	NT2RP4001214	3.34	3.34	4.3	3.51	3.76	2.16		
45	NT2RP4001219	7.4	7.4	12.05	14.35	19.28	13.39	*	+
	NT2RP4001228	5.26	5.26	9.63	12.15	15.74	20.07	*	+
	NT2RP4001235	2.42	2.42	7.45	3.46	6.02	4.48		
	NT2RP4001256	2.11	2.11	4.24	1.66	3.41	2.66		
	NT2RP4001257	2.48	2.48	7.27	4.05	4.35	4.05		
50	NT2RP4001260	3.16	3.16	5.79	2.52	3.86	2.92		
	NT2RP4001261	3.84	3.84	6.63	8.42	6.47	5		
	NT2RP4001274	22.92	22.92	38.08	25.02	31.56	21.25		
	NT2RP4001276	5.24	5.24	10.03	11.38	15.97	11.63	*	+
	NT2RP4001283	20.72	20.72	122.55	87.44	93.43	86.47		
55	NT2RP4001299	9.62	9.62	15.14	14.95	10.52	15.18		

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	NT2RP4001313	1.45	1.45	3.26	1.72	2.96	0.97	
	NT2RP4001315	6.06	6.06	11.14	7.45	9.92	7.74	
5	NT2RP4001320	14.6	14.6	42.74	32.02	38.13	29.24	
	NT2RP4001325	32.53	32.53	146.14	142.88	178.36	128.89	
	NT2RP4001336	6.69	6.69	40.75	38.55	46.66	32.11	
	NT2RP4001339	4.12	4.12	5.6	3.35	5.56	2.76	
	NT2RP4001343	10.46	10.46	83.37	54.71	61.01	60.06	
10	NT2RP4001344	6.7	6.7	60.08	49.79	55.21	42.62	
	NT2RP4001345	1.65	1.65	6.68	5.64	5.7	3.87	
	NT2RP4001351	4.1	4.1	15.97	10.01	20.05	11.42	
	NT2RP4001353	2.8	2.8	5.91	1.63	2.94	1.86	
	NT2RP4001355	2.57	2.57	8.67	1.83	3.12	2.08	
15	NT2RP4001367	10.64	10.64	17.66	11.92	17.06	13.16	
	NT2RP4001372	2.26	2.26	3.82	2.1	2.06	2.07	
	NT2RP4001373	8.86	8.86	16.4	10.99	8.59	11.48	
	NT2RP4001375	2.71	2.71	6.06	4.91	7.42	2.94	
	NT2RP4001379	1.74	1.74	3.52	2.34	4.67	1.38	
20	NT2RP4001381	5.6	5.6	12.51	12.8	12.66	8.27	
	NT2RP4001386	6.39	6.39	14.52	14.77	20.11	12.32	
	NT2RP4001389	7.28	7.28	8.66	5.43	9.25	4.09	
	NT2RP4001396	5.76	5.76	6.42	2.83	4.61	2.12	*
25	NT2RP4001407	2.92	2.92	2.98	3.07	2.04	1.76	
	NT2RP4001409	13.6	13.6	28.28	8.87	5.85	8.84	
	NT2RP4001410	33.56	33.56	61.26	40.57	18.92	37.8	
	NT2RP4001414	16.59	16.59	37.89	14.29	21.3	16.8	
	NT2RP4001424	3.55	3.55	8.85	7.99	10.45	7.41	
30	NT2RP4001433	3.85	3.85	6	8.39	9.79	3.38	
	NT2RP4001438	9.95	9.95	27.94	46.22	53.63	30.76	* +
	NT2RP4001442	4.33	4.33	4.97	3.3	3.41	2.64	* -
	NT2RP4001447	4.42	4.42	4.69	5.08	5.51	3.41	
	NT2RP4001466	3.74	3.74	5.45	7.38	3.23	5.57	
35	NT2RP4001467	21.67	21.67	58.89	54.18	44.07	55.8	
	NT2RP4001472	8.05	8.05	12.19	11.7	11.76	11.97	
	NT2RP4001474	2.83	2.83	4.81	3.2	5.73	1.98	
	NT2RP4001483	1.48	1.48	4.33	2.61	3.7	1.19	
	NT2RP4001488	21.03	21.03	32.41	39.07	46.9	33.42	
40	NT2RP4001492	4.18	4.18	6.73	3.21	3.81	1.91	
	NT2RP4001498	4.3	4.3	2.43	2.95	3.52	2.13	
	NT2RP4001502	28.2	28.2	57.38	27.65	34.81	41.83	
	NT2RP4001503	3.83	3.83	6.74	5.51	4.1	3.37	
	NT2RP4001507	2.39	2.39	3.69	5.03	5.95	5.18	** +
45	NT2RP4001510	1.74	1.74	4.63	5.64	5.05	3.02	
	NT2RP4001516	3.54	3.54	4.16	2.52	1.9	1.27	* -
	NT2RP4001520	25.33	25.33	70.64	73.93	107.21	85.05	
	NT2RP4001523	5.57	5.57	9.99	8.4	7.79	6.19	
	NT2RP4001524	6.1	6.1	10.17	8.92	11.45	5.98	
50	NT2RP4001529	29.8	29.8	74.89	59.39	60.69	55.29	
	NT2RP4001531	2.88	2.88	10.96	8.63	11.05	7.81	
	NT2RP4001546	143.48	143.48	388.31	316.63	215.6	309.45	
	NT2RP4001547	9.05	9.05	26.31	28.76	23.06	18.81	
55	NT2RP4001551	2.27	2.27	3.93	3.87	4.08	2.02	
	NT2RP4001555	2.95	2.95	5.8	4.14	3.58	1.74	

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	NT2RP4001567	6.54	6.54	6.88	5.82	7.12	5.68	
	NT2RP4001568	7.58	7.58	11.65	10.02	19.33	12.97	
	NT2RP4001569	15.49	15.49	41.42	32.56	40.11	27.18	
5	NT2RP4001571	5.75	5.75	13.28	9.06	7.43	8.13	
	NT2RP4001574	8.5	8.5	19.03	15.54	17.52	15.29	
	NT2RP4001575	2.46	2.46	5.86	5.71	5.53	4.24	
	NT2RP4001578	17.21	17.21	45.64	52.76	53.63	40.92	
10	NT2RP4001592	9.76	9.76	13.68	14.13	19.64	11.68	
	NT2RP4001593	9.4	9.4	18.11	22.12	27.3	18.04	
	NT2RP4001605	5.97	5.97	4.78	4.1	7.77	4.66	
	NT2RP4001606	2.9	2.9	8.34	6.01	3.51	6.75	
	NT2RP4001607	2.04	2.04	5.24	4.57	3.26	3.78	
15	NT2RP4001610	1.74	1.74	2.42	2.6	2.48	1.7	
	NT2RP4001614	2.17	2.17	7.19	5.38	4.34	6.86	
	NT2RP4001623	2.38	2.38	5.26	2.43	2.65	2.02	
	NT2RP4001626	9.48	9.48	11.67	18.67	23.9	19.44	** +
	NT2RP4001634	2.74	2.74	4.93	3.67	5.24	4.26	
20	NT2RP4001638	3.41	3.41	3.03	2.36	2.11	1.87	** -
	NT2RP4001644	7.86	7.86	33.73	24.36	26.04	24.99	
	NT2RP4001646	11.61	11.61	15.02	7.42	10.74	11.21	
	NT2RP4001656	3.75	3.75	5.23	2.89	4.51	2.07	
	NT2RP4001666	1.99	1.99	4.68	3.26	6.25	2.02	
25	NT2RP4001670	11.74	11.74	15.51	12.45	7.09	8.31	
	NT2RP4001677	28.27	28.27	42.75	42.01	45.48	47.53	
	NT2RP4001679	8.82	8.82	33.83	33.23	51.5	29.78	
	NT2RP4001695	7.71	7.71	12.76	15.66	20.35	12.87	
30	NT2RP4001696	2.64	2.64	5.45	3.13	3.92	3.72	
	NT2RP4001699	3.58	3.58	8.03	3.18	4.12	4.42	
	NT2RP4001717	2.79	2.79	7.03	3.29	5.84	4.15	
	NT2RP4001719	3.59	3.59	9.11	7.6	9.27	6.28	
	NT2RP4001725	2.27	2.27	4.79	2.28	5.07	1.43	
35	NT2RP4001726	7.07	7.07	11.18	5.85	6.91	4.98	
	NT2RP4001730	3.11	3.11	12.82	11.96	19.81	16.3	
	NT2RP4001739	2.83	2.83	5.83	5.79	6.55	4.98	
	NT2RP4001741	7.25	7.25	15.93	9.28	12.42	10.97	
	NT2RP4001753	3.04	3.04	8.4	4.39	4.64	6.64	
40	NT2RP4001760	4.32	4.32	6.6	7.79	7.73	12.96	
	NT2RP4001787	67.61	67.61	173.05	169.17	187.1	193.22	
	NT2RP4001790	2	2	5.29	3.42	2.97	2.58	
	NT2RP4001795	9.31	9.31	12.31	14.38	19.76	12.34	
	NT2RP4001803	3.35	3.35	3.6	3.94	4.78	3.67	
45	NT2RP4001805	2.64	2.64	3.57	3.64	2.47	2.95	
	NT2RP4001809	4.84	4.84	26.35	18.18	23.17	11.33	
	NT2RP4001817	11.55	11.55	19.09	9.5	10.78	12.71	
	NT2RP4001822	2.09	2.09	5.36	3.73	5.11	3.33	
	NT2RP4001823	1.91	1.91	3.95	1.14	3.34	1.24	
50	NT2RP4001827	14.88	14.88	25.96	35.78	40.37	29.5	* +
	NT2RP4001828	9.76	9.76	34.37	27.78	34.21	26.3	
	NT2RP4001836	7.74	7.74	33.26	27.19	39.14	26.78	
	NT2RP4001838	1.59	1.59	7.49	2.09	4.5	2.71	
	NT2RP4001841	8.75	8.75	80.37	61.67	50.27	56.46	
55	NT2RP4001849	1.9	1.9	4.55	2.51	5.08	1.58	

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	NT2RP4001861	7.27	7.27	34.6	36.09	41.9	34.39		
	NT2RP4001877	6.59	6.59	8.44	12.87	9.04	14.1	*	+
5	NT2RP4001879	9.64	9.64	15.47	11.58	14.24	10.73		
	NT2RP4001889	5.09	5.09	10.66	6.68	11.25	8.91		
	NT2RP4001893	3.97	3.97	7.34	3.19	6.11	2.72		
	NT2RP4001896	3.18	3.18	6.86	5.38	7.87	4.92		
	NT2RP4001898	7.83	7.83	26.41	22.98	20.13	20.15		
10	NT2RP4001901	1.73	1.73	4.69	4.08	5.87	2.69		
	NT2RP4001910	39.51	39.51	58.21	53.45	33.59	45.93		
	NT2RP4001925	4.1	4.1	10.21	6.69	6.32	6.12		
	NT2RP4001926	6.41	6.41	7.22	7.1	9.54	5.52		
	NT2RP4001927	6.26	6.26	9.97	5.83	8.13	2.82		
15	NT2RP4001931	8.64	8.64	14.16	15.49	17.54	11.89		
	NT2RP4001933	38.49	38.49	87.13	96.81	133.51	91.22		
	NT2RP4001938	2.93	2.93	4.53	4.27	3.31	3.55		
	NT2RP4001942	13.44	13.44	27.12	31.34	24.8	18.71		
	NT2RP4001945	1.41	1.41	4	1.55	3.67	1.77		
20	NT2RP4001946	1.97	1.97	5.67	3.04	3.96	1.66		
	NT2RP4001947	4.42	4.42	8.93	5.92	9.81	5.16		
	NT2RP4001950	4.13	4.13	5	2.25	2.84	1.34	*	-
	NT2RP4001953	10.44	10.44	14.15	13.81	19.4	14.36		
25	NT2RP4001966	2.44	2.44	2.41	2.51	4.26	1.52		
	NT2RP4001970	2.26	2.26	5.32	3.91	3.4	2.88		
	NT2RP4001975	8.56	8.56	20.03	18.32	13.05	12.02		
	NT2RP4001988	6.72	6.72	18.78	22.92	24.78	29.44	*	+
	NT2RP4001996	5.27	5.27	12.83	10.65	16.35	12.42		
30	NT2RP4002014	3.4	3.4	8.14	43.19	37.87	33.17	**	+
	NT2RP4002018	6.19	6.19	13.71	10.47	11.39	10.36		
	NT2RP4002035	5.35	5.35	5.95	5.4	4.17	2.54		
	NT2RP4002043	7.1	7.1	10.8	9.64	12.2	6.5		
	NT2RP4002046	9.74	9.74	20.08	21.94	15.28	17.11		
35	NT2RP4002047	8.37	8.37	19.18	22.28	24.07	28.83	*	+
	NT2RP4002052	5.78	5.78	10.36	9.02	9.36	9.37		
	NT2RP4002056	32.58	32.58	71.49	58.09	76.58	49.75		
	NT2RP4002057	6.37	6.37	11.06	12.13	13.58	7.41		
	NT2RP4002058	3.85	3.85	6.6	4.1	4.2	3.22		
40	NT2RP4002064	5.93	5.93	4.39	2.6	4.16	2.07	*	-
	NT2RP4002071	6.67	6.67	7.07	6.95	10.06	6.27		
	NT2RP4002075	1.16	1.16	2.11	2.27	2.35	1.27		
	NT2RP4002078	2.25	2.25	8.63	6.86	8.24	4.97		
	NT2RP4002081	8.11	8.11	26.15	18.73	18.78	19.42		
45	NT2RP4002083	1.39	1.39	5.25	3.36	3.16	1.88		
	NT2RP4002099	3.26	3.26	4.73	2.84	3.56	2.51		
	NT2RP4002106	10.35	10.35	20.34	22.36	25.93	20.55		
	NT2RP4002111	11.7	11.7	12.37	19.77	30.44	17.72		
	NT2RP4002112	6.15	6.15	10.97	8.9	8.34	3.22		
50	NT2RP4002116	12.6	12.6	47.19	37.43	41.25	28.65		
	NT2RP4002122	5.34	5.34	9.29	14.84	14.86	12.67	**	+
	NT2RP4002126	6.42	6.42	14.44	16.82	14.35	10.42		
	NT2RP4002133	7.56	7.56	20.82	29.17	26.14	21		
	NT2RP4002136	3.63	3.63	5.74	4.89	5.38	2.69		
55	NT2RP4002139	26.89	26.89	31.12	60.65	61.92	32.88		

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	NT2RP4002174	139.27	139.27	232.64	240.71	275.01	193.19
	NT2RP4002185	7.77	7.77	13.2	12.36	19.06	11.58
	NT2RP4002186	4.5	4.5	9.83	7.82	4.72	6.78
5	NT2RP4002187	15.42	15.42	32.13	26.94	19.84	21.17
	NT2RP4002188	3.01	3.01	8.34	8.3	7.75	6.41
	NT2RP4002199	1.85	1.85	3.73	2.6	2.91	3.78
	NT2RP4002206	2.08	2.08	3.39	2.48	2.34	1.29
10	NT2RP4002210	3.13	3.13	4.75	2.02	2.86	0.98
	NT2RP4002222	4.2	4.2	6.63	5.56	6.28	4.16
	NT2RP4002241	7.97	7.97	8.24	10.82	11.75	7.19
	NT2RP4002248	5.08	5.08	16.69	10.74	8.9	8.13
	NT2RP4002250	1.54	1.54	3.22	0.73	1.69	0.56
15	NT2RP4002259	4.86	4.86	9.82	3.21	4.85	1.75
	NT2RP4002268	16.62	16.62	29.54	28.9	28.18	25.68
	NT2RP4002288	6.42	6.42	12.57	13.29	14.36	11.97
	NT2RP4002290	7.55	7.55	7.61	7.96	7.67	5.87
	NT2RP4002298	3.92	3.92	4.18	5.54	5.03	4.18
20	NT2RP4002306	2.38	2.38	5.79	2.97	5.77	2.64
	NT2RP4002308	2.04	2.04	6.03	5.31	5.23	4.1
	NT2RP4002336	2.71	2.71	6.33	3.71	4.19	4.63
	NT2RP4002340	1.09	1.09	3.96	1.28	2.75	0.49
	NT2RP4002361	2.77	2.77	5.78	3.73	4.03	2.48
25	NT2RP4002367	2.27	2.27	5.84	3.23	2.48	2.77
	NT2RP4002368	9.87	9.87	17.2	18.26	19.27	16
	NT2RP4002377	3.3	3.3	23.8	25.46	30.75	23.93
	NT2RP4002408	2.22	2.22	3.87	3.75	6.37	4.11
	NT2RP4002425	2.84	2.84	5.81	8.24	7.98	5.23
30	NT2RP4002432	12.33	12.33	85.4	61.06	72.53	67.82
	NT2RP4002447	2.97	2.97	7.68	3.96	5.4	4.59
	NT2RP4002451	5.48	5.48	6.2	5.84	5.85	6.83
	NT2RP4002461	9.8	9.8	32.09	32.76	38.91	29.04
	NT2RP4002486	3.5	3.5	6.71	2.47	4.15	2.87
35	NT2RP4002517	3.65	3.65	9.11	7.02	8.53	7.18
	NT2RP4002556	4.29	4.29	3.91	5.68	10.03	6.41
	NT2RP4002569	3.36	3.36	7.36	4.93	5.29	3.42
	NT2RP4002587	2.26	2.26	4.19	2.8	3.4	2.02
40	NT2RP4002591	2.21	2.21	4.89	2.89	4.5	3.08
	NT2RP4002607	1.43	1.43	3.34	2.87	4.63	1.58
	NT2RP4002627	17.83	17.83	61.9	55.9	76.17	65.3
	NT2RP4002628	7.28	7.28	15.48	14.53	23.95	12.54
	NT2RP4002630	4.19	4.19	5.25	6.72	9.4	7.16 * +
45	NT2RP4002639	9.43	9.43	70.25	52.38	77.24	57.28
	NT2RP4002641	1.58	1.58	9.03	3.94	4.07	4.1
	NT2RP4002658	114.62	114.62	166.93	76.49	34.96	109.83
	NT2RP4002669	3.5	3.5	5.67	5.4	5.33	4.68
	NT2RP4002677	6.24	6.24	9.41	10.14	7.99	13.62
50	NT2RP4002715	8.42	8.42	34.92	40.1	48.46	32.3
	NT2RP4002750	2.6	2.6	8.29	1.68	2.04	1.33
	NT2RP4002784	3.71	3.71	9.51	9.44	11.22	7.06
	NT2RP4002791	4.91	4.91	9.44	4.88	9.76	5.33
	NT2RP4002811	1.63	1.63	6.38	3.17	2.95	3.43
55	NT2RP4002830	4.26	4.26	7.45	3.9	5.9	5.46

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	NT2RP4002832	2.12	2.12	3.13	2.38	5.59	2.54		
	NT2RP4002850	5.07	5.07	12.04	14.36	12.63	8.06		
5	NT2RP4002874	5.17	5.17	6.67	3.41	5.14	1.96		
	NT2RP4002884	28.81	28.81	49.75	43.57	74.75	52.87		
	NT2RP4002888	5.55	5.55	4.83	3.67	4.32	3.08	*	-
	NT2RP4002891	5.48	5.48	15.79	13.16	19.42	11.91		
	NT2RP4002894	12.04	12.04	24.47	18.44	12.76	16.4		
10	NT2RP4002896	5.54	5.54	12.2	8.96	6.18	7.78		
	NT2RP4002905	1.71	1.71	4.27	2.32	3.58	1.28		
	NT2RP4002907	5.11	5.11	7.62	6.94	10.72	1.41		
	NT2RP5003459	68.11	68.11	133.25	154.61	146.15	164.37	*	+
	NT2RP5003461	7.34	7.34	10.14	10.85	14.36	8		
15	NT2RP5003471	106.6	106.6	168.71	124.4	148.85	112.14		
	NT2RP5003477	2.71	2.71	2.62	2.59	2.33	1.9		
	NT2RP5003487	157.44	157.44	424.89	292.71	256.56	354.93		
	NT2RP5003492	3.1	3.1	4.91	5.25	6.17	5.91	*	+
20	NT2RP5003500	1.5	1.5	3.28	2.38	2.54	2.59		
	NT2RP5003506	4.96	4.96	9.3	7.83	10.37	9.04		
	NT2RP5003512	2.21	2.21	4.35	2.63	3.46	2.15		
	NT2RP5003522	4.1	4.1	5.97	4.62	4.19	2.34		
	NT2RP5003524	4.38	4.38	3.86	1.61	1.54	0.84	**	-
25	NT2RP5003527	24.72	24.72	71.27	76.81	87.24	60.59		
	NT2RP5003531	7.16	7.16	17.2	15.58	14.06	14.11		
	NT2RP5003534	2.68	2.68	5.49	5.54	6.82	4.55		
	NT2RP6000020	8.69	8.69	19.96	14.65	15.13	16.29		
	NT2RP6000022	3.19	3.19	4.05	4.06	3.96	2.44		
30	NT2RP6000050	3.95	3.95	3.99	4.98	5.82	2.88		
	NT2RP6000063	3.91	3.91	6.04	3.61	2.52	2.56		
	NT2RP6000074	5.38	5.38	4.88	3.41	3.27	2.17	**	-
	NT2RP6000083	7.76	7.76	11.18	11.49	16	9.91		
	NT2RP6000100	2.49	2.49	4.58	4.04	4.71	3.3		
35	NT2RP6000123	1.94	1.94	3.29	5.1	4.26	4.22	*	+
	NT2RP6000129	1.9	1.9	4.47	4.06	4.27	2.74		
	NT2RP6000147	3.75	3.75	11.74	10.8	11.03	7.48		
	NT2RP6000163	2.62	2.62	4.23	2.28	1.95	1.71		
40	NT2RP6000181	8.03	8.03	12.4	9.44	13.25	9.01		
	NT2RP6000182	5.44	5.44	6.42	4.82	5.56	3.88		
	OVARC1000001	4.97	4.97	5.24	6.04	7.48	2.35		
	OVARC1000003	3.21	3.21	8.31	8.51	7.66	7.05		
	OVARC1000004	9.87	9.87	116.19	88.04	109.99	85.44		
45	OVARC1000006	3.57	3.57	6.58	9.04	7.88	4.73		
	OVARC1000013	6.51	6.51	9.19	7.32	8.36	8.33		
	OVARC1000014	3.39	3.39	5.02	4.23	5.02	4.17		
	OVARC1000017	3.11	3.11	6.81	4.2	4.45	2.72		
	OVARC1000026	24.79	24.79	32.1	56.82	69.34	44.53	*	+
50	OVARC1000035	11.11	11.11	20.26	20.41	23.65	15.36		
	OVARC1000037	8.73	8.73	19.12	15.64	9.13	15.9		
	OVARC1000058	6.06	6.06	11.69	13.84	7.56	10.6		
	OVARC1000060	1.89	1.89	6.28	5.98	5.24	5.13		
	OVARC1000068	2.38	2.38	5.33	5.31	3.56	2.42		
55	OVARC1000069	74.66	74.66	101.53	75.95	84.36	86.42		
	OVARC1000071	4.4	4.4	4.77	6.47	5.35	4.04		

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	OVARC1000075	55.43	55.43	125.63	120.89	150.97	117.03		
	OVARC1000083	9.58	9.58	9.24	13.12	12.7	10.64	*	+
	OVARC1000085	106.6	90.9	156.14	214.2	177.05	273.14	*	+
5	OVARC1000086	3.98	6.82	9.23	11.98	11.3	14.09	*	+
	OVARC1000087	1.51	2.83	1.79	4.03	3.57	3.35	*	+
	OVARC1000090	1.48	4.1	6.14	10.88	9.58	8.79	*	+
	OVARC1000091	4.88	8.33	8.01	7.99	7.76	6.82		
10	OVARC1000092	2.83	6.81	4.18	4.68	6.25	4.85		
	OVARC1000105	9.73	14.86	17.21	26.29	25.62	22.88	*	+
	OVARC1000106	26.02	23.03	46.38	66.36	50.1	53.01	*	+
	OVARC1000109	9.12	13.08	18.04	16.72	12.91	17.46		
	OVARC1000113	4.12	6.25	6.53	6.83	8.19	7.65		
15	OVARC1000114	2.14	3.44	5.77	5.94	5.86	4.98		
	OVARC1000133	2.53	4.96	6.36	4.05	4.97	2.95		
	OVARC1000137	6.14	10.05	13.51	13.3	18.59	14.39		
	OVARC1000139	14.75	20.77	83.44	71.14	98.1	69.29		
	OVARC1000145	0.72	6.64	2.89	1.78	2.42	2		
20	OVARC1000148	5.09	4.98	7.88	4.91	5.32	7.91		
	OVARC1000151	1.41	2.11	2.4	3.58	4.08	3.58	**	+
	OVARC1000157	10.99	14.16	17.51	21.21	25.06	22.76	*	+
	OVARC1000162	1.22	4.4	2.5	2.93	2.49	2.59		
	OVARC1000168	1.98	8.46	6.2	8.01	9.61	9.96		
25	OVARC1000169	32.03	45.07	49.48	70.63	69.6	89.08	*	+
	OVARC1000178	0.84	5.08	2.53	3.37	3.18	2.78		
	OVARC1000182	0.8	3.3	1.42	2.02	1.95	1.78		
	OVARC1000186	2.51	3.72	3.23	5.95	3.27	4.77		
30	OVARC1000188	1.04	2.67	2.33	2.48	2.87	1.9		
	OVARC1000191	1.01	3.8	2.63	3.12	2.85	2.54		
	OVARC1000198	2.09	3.59	4.32	5.62	5.12	5.06	*	+
	OVARC1000208	6.49	10.37	22.5	17.79	24.54	22.02		
	OVARC1000209	7.99	13.69	22.32	23.42	27.81	29.16		
35	OVARC1000212	2.47	5.63	3.59	4.76	5.03	4.88		
	OVARC1000216	1.72	4.96	4.35	15.43	11.3	12.54	**	+
	OVARC1000240	2.98	3.53	8.13	5.39	5.46	4.87		
	OVARC1000241	1.29	2.47	3.18	2.65	3.17	1.4		
	OVARC1000249	4.14	5.43	8.17	5.46	5	6.13		
40	OVARC1000254	33.15	39.39	100.99	100.41	131.42	100.89		
	OVARC1000255	0.85	4.83	2.51	2.98	2.45	1.95		
	OVARC1000267	2.37	6.41	6.71	6.66	7.16	7.31		
	OVARC1000275	79.02	93.7	161.08	199.43	240.76	175.96	*	+
	OVARC1000287	226.67	224.66	236.08	433.91	512.76	470.31	**	+
45	OVARC1000288	3.2	4.25	7.38	6.23	5.32	4.47		
	OVARC1000298	8.96	10.09	19.62	13.37	7.19	9.6		
	OVARC1000302	1.12	2.14	2.13	2.47	1.85	2		
	OVARC1000304	1.09	2.68	3.23	5.02	3.41	6		
	OVARC1000307	2.95	6.19	4.74	7.59	4.7	6.29		
50	OVARC1000309	1.18	7.16	3.22	3.24	2.85	2.4		
	OVARC1000312	2.83	11.64	6.03	4.17	5.4	2.46		
	OVARC1000313	10.48	19.25	14.81	9.39	17.54	22.17		
	OVARC1000321	31.6	24.05	47.79	30.5	31.37	15.43		
	OVARC1000326	1.52	2.3	3.9	3.84	3.17	2.79		
55	OVARC1000327	1.52	3.28	4.24	3.13	1.49	2.46		

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	OVARC1000331	2.22	4.72	2.41	4.33	4.45	4.58		
	OVARC1000335	2.3	5.84	4.02	2.72	5.16	4.75		
5	OVARC1000347	1.83	8.18	6.24	7.35	9.24	8.44		
	OVARC1000348	1.61	10.62	3.73	2.84	4.59	3.05		
	OVARC1000363	3.7	9.61	6.51	7.31	11.52	6.83		
	OVARC1000377	1.07	2.09	2.43	2.28	2.51	2.45		
	OVARC1000382	3.34	3.39	4.33	5.07	2.52	1.03		
10	OVARC1000384	4.2	5.42	8.35	5.32	4.4	6.04		
	OVARC1000401	0.62	3.63	2.09	3.35	4.08	3.64		
	OVARC1000406	18.98	23.3	49.12	57.09	74.48	54.63	*	+
	OVARC1000407	1.99	6.28	3.99	4.11	6.42	3.16		
	OVARC1000408	27.5	38.45	70.39	74.84	111.17	71.25		
15	OVARC1000410	6.83	12.72	10.41	4.78	6.65	5.01		
	OVARC1000411	0.91	1.5	2.6	3.49	3	2.22		
	OVARC1000414	1.31	2.22	3.7	4.5	3.78	3.71		
	OVARC1000420	1.44	2.76	3.29	3.3	2.59	2.1		
	OVARC1000421	1.42	2.65	3.33	3.96	4.21	4.99	*	+
20	OVARC1000427	25.78	27.02	130.06	156.9	215.67	142.19		
	OVARC1000431	10.51	17.6	19.12	33.66	31.78	25.78	*	+
	OVARC1000437	3.14	6.37	7.31	5.97	7.63	6.36		
	OVARC1000439	5.81	10.95	13.82	21.81	23.01	21.52	**	+
	OVARC1000440	2.56	3.74	5.01	7.47	9.31	7.08	*	+
25	OVARC1000442	2.34	2.38	6.81	6.66	9.5	8.12		
	OVARC1000443	2.09	2.2	2.88	3.29	3.41	2.62		
	OVARC1000461	1.11	2.84	2.2	2.55	1.12	2.14		
	OVARC1000465	3.27	5.01	3.51	3.94	4.62	3.95		
30	OVARC1000466	1.94	5.47	5.9	6.54	10.13	6.76		
	OVARC1000467	1.01	5.08	2.41	3.65	2.98	3.78		
	OVARC1000470	1.13	5.81	3.03	3.18	4.02	3.78		
	OVARC1000473	1.81	1.95	2.65	2.44	4.16	1.39		
	OVARC1000479	5.67	5.88	9.88	10.35	14.26	6.88		
35	OVARC1000484	3.99	5.74	6.54	8.66	9.93	6.87		
	OVARC1000486	3.17	4.71	4.49	5.74	4.93	4.28		
	OVARC1000496	0.93	3.55	0.66	0.31	1.07	0.62		
	OVARC1000520	0.84	5.89	1.18	1.32	2.27	2		
	OVARC1000522	4.1	7.19	12	13.85	14.03	10.34		
40	OVARC1000526	1.96	7.04	3.75	5.93	5.48	4.69		
	OVARC1000529	2.38	2.57	4.44	3.66	4.16	3.08		
	OVARC1000533	3.3	4.66	7.95	8.89	12.29	7.83		
	OVARC1000543	0.84	2.44	2.06	2.57	3.08	2.72		
	OVARC1000550	0.75	3.68	2.32	2.82	4.04	2.34		
45	OVARC1000553	2.1	5.63	7.02	7.72	7.69	6.95		
	OVARC1000556	5.77	15.21	11.77	8.95	13.91	8.96		
	OVARC1000557	0.83	5.12	1.4	1.61	2.29	1.88		
	OVARC1000561	3.48	7.38	9.26	13	17.66	15.09	*	+
	OVARC1000564	8.89	9.02	10.44	17.84	11.31	16.69	*	+
50	OVARC1000573	1.87	3.68	4.86	5.75	5.32	3.83		
	OVARC1000576	24.12	29.23	124.94	83.09	93.83	98.58		
	OVARC1000578	2.43	4.6	5.53	8.64	4.46	3.93		
	OVARC1000581	0.34	3.28	1.15	1.75	1.27	1.23		
	OVARC1000586	22.54	28.9	41.17	34.58	43.39	40.93		
55	OVARC1000588	0.74	5.23	2.03	2.75	3.72	2.05		



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	OVARC1000605	1.98	2.62	2.88	4.47	4.23	3.87	**	+
	OVARC1000622	3.86	4.59	11.57	12.7	11.13	11.6		
	OVARC1000636	1.64	3.79	4.58	4.19	4.03	5.09		
5	OVARC1000640	1.97	4.72	3.93	4.21	3.67	3.09		
	OVARC1000649	9.69	14.8	53.54	53.32	64.51	52.67		
	OVARC1000661	1.14	9.33	2.99	5.34	5.24	5.24		
	OVARC1000677	8.53	10.16	14.87	11.77	10.98	15.47		
10	OVARC1000678	1.21	4.49	2.71	3.28	4.17	3.26		
	OVARC1000679	2.86	3.25	4.09	5.29	5.16	6.25	*	+
	OVARC1000681	1.47	1.55	3.2	2.41	2.22	1.71		
	OVARC1000682	10.09	11.33	50.91	33.79	47.49	44.31		
	OVARC1000689	3.81	7.1	19.94	20.18	22.12	21.83		
15	OVARC1000700	1.8	10.37	3.18	4.98	4.37	5.14		
	OVARC1000703	1.74	7.18	5.35	6.4	6.64	7.77		
	OVARC1000722	10.59	11.92	47.93	43.41	60.06	39.34		
	OVARC1000726	1.44	3.48	4.62	4.88	5.89	3.58		
	OVARC1000727	1.93	2.09	4.13	3.78	3.79	3.89		
20	OVARC1000730	5.95	5.86	9.01	4.07	4.16	5.62		
	OVARC1000741	4.85	6.13	8.74	15.19	10.58	13.71	*	+
	OVARC1000746	0.89	3.61	2.43	2.06	2.9	2.84		
	OVARC1000764	1.76	4.93	4.77	5.35	7.01	5.44		
	OVARC1000769	1.13	4.3	3.6	3.76	4.42	5.2		
25	OVARC1000771	2.42	6.28	2.3	4.02	4.81	3.71		
	OVARC1000773	19.09	24.7	31.93	44.69	56.24	46.24	*	+
	OVARC1000775	11.67	8.94	16.44	12.16	8.7	4.26		
	OVARC1000778	2.37	3.89	5.69	4.59	6.23	4.92		
	OVARC1000779	0.8	2.02	1.85	2.23	2.45	1.46		
30	OVARC1000781	1.67	5.05	4.16	6.37	3.45	5.07		
	OVARC1000787	1.64	4.79	4.22	2.97	5.44	3.25		
	OVARC1000789	7.62	14.23	16.39	24.95	29.69	25.94	**	+
	OVARC1000800	2.91	10.72	5.72	6.41	10.65	6.2		
35	OVARC1000802	1.55	8.77	2.97	2.99	5.34	2.76		
	OVARC1000810	3.37	3.54	8.29	6.66	7.99	7.21		
	OVARC1000811	2.41	2.73	7.5	4.88	3.67	4.95		
	OVARC1000814	3.44	4.55	9.03	7.92	11.3	9.05		
	OVARC1000816	7.64	10.41	12.41	10.99	10.58	14.11		
40	OVARC1000817	1.18	3.38	1.27	1.71	2.14	1.55		
	OVARC1000834	2.46	8.3	3.39	4.84	5.81	4.01		
	OVARC1000846	2.23	10.02	5.35	7.38	9.66	7.72		
	OVARC1000850	1.74	8.37	3.38	3.39	2.51	3.1		
	OVARC1000853	23.21	24.23	43.4	30.67	37.81	18.39		
45	OVARC1000862	2.28	2.66	4.91	3.05	1.61	1.49		
	OVARC1000873	2.56	2.98	4.14	4.4	3.79	3.85		
	OVARC1000875	1.47	3.07	1.79	2.35	3.09	1.87		
	OVARC1000876	3.71	5.67	4.46	5.11	6.06	5.45		
	OVARC1000883	6.06	9.53	9.18	12.43	15.42	13.05	*	+
50	OVARC1000885	2.84	9.95	3.38	3.74	5.66	4.11		
	OVARC1000886	4.31	8.19	4.29	3.74	5.15	4.39		
	OVARC1000890	17.47	18.3	91.22	70.97	78.71	51.68		
	OVARC1000891	1.28	1.44	3.03	2.85	2.19	3.22		
	OVARC1000897	0.48	1.74	1.29	1.21	1.33	0.5		
55	OVARC1000912	2.06	3.22	4.33	5.21	6.1	5.86	*	+

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	OVARC1000914	1.48	6.18	1.61	3.68	3.02	2.18	
	OVARC1000915	1.71	6.64	4.14	4.87	3.54	4.76	
	OVARC1000916	1.91	5.19	2.56	4.05	4.32	3.88	
5	OVARC1000924	1.45	5.5	3.09	3.28	3.85	3.48	
	OVARC1000928	6.05	5.46	8.78	4.22	5.83	5.35	
	OVARC1000936	1.37	1.39	2.17	2.04	3.25	2.49	
	OVARC1000937	1.69	3.01	1.94	4.17	3.26	3.24	
10	OVARC1000945	1.55	3.67	3.62	3.83	3.22	2.28	
	OVARC1000948	1.57	3.85	2.66	3.15	3.68	1.99	
	OVARC1000956	1.41	5.08	4.36	7.56	7.26	5.51	
	OVARC1000959	1.8	4.87	3.39	4.88	3.02	3.9	
	OVARC1000960	2.64	7.53	9.55	11.64	13.89	12.86	* +
15	OVARC1000964	19.89	17.19	103.98	118.41	165.46	96.14	
	OVARC1000971	0.42	1.58	1.4	2.53	2.27	2.28	* +
	OVARC1000975	5.93	8.3	36.1	31.27	51.54	30.22	
	OVARC1000976	0.65	2.12	1.27	2.17	1.46	1.5	
	OVARC1000981	4.06	7.18	4.94	7.97	12.1	8.53	
20	OVARC1000982	2.83	5.41	2.23	3.13	3.02	3.54	
	OVARC1000984	1.78	5.43	3.32	3.01	3.08	2.16	
	OVARC1000995	2.94	6.59	4.5	5.98	6.19	6.72	
	OVARC1000996	1.68	1.87	4.29	3.58	4.15	4.56	
	OVARC1000999	6.02	5.65	15.29	15.61	13.18	13.29	
25	OVARC1001000	1.96	4.5	6.2	6.26	7.09	6.86	
	OVARC1001004	0.51	3.4	1.45	2.05	3.3	1.47	
	OVARC1001010	1.35	3.99	1.66	3.04	1.4	1.54	
	OVARC1001011	1.46	5.57	1.13	2.39	3.27	2.45	
30	OVARC1001030	96.19	101.41	143.98	119.24	154.26	133	
	OVARC1001032	1.42	5.34	1.89	1.83	2.82	1.92	
	OVARC1001034	4.44	5.58	6.51	3.29	5.21	3.77	
	OVARC1001038	3.62	5.03	7.4	10.3	10.88	8.61	* +
	OVARC1001040	2.63	3.77	6.93	5.25	6.51	4.25	
	OVARC1001041	4.54	8.03	12.87	8.57	12.25	9.4	
35	OVARC1001044	1.05	2.92	1.83	1.96	2.43	1.84	
	OVARC1001049	3.78	8.78	10.67	10.65	11.87	10.26	
	OVARC1001051	40.95	55.97	80.66	66.89	109.71	87.49	
	OVARC1001054	1.22	4.06	3.22	2.86	4.19	1.93	
40	OVARC1001055	2.13	3.38	3.82	4.32	5.61	5.22	* +
	OVARC1001062	5.8	6.15	12.54	8.04	9.94	9.57	
	OVARC1001065	8.85	13.63	51.33	51.41	60.3	56.97	
	OVARC1001068	2.82	5.62	4.76	4.72	4.02	5.52	
	OVARC1001072	0.73	4.18	4.41	3.2	3.71	3.07	
45	OVARC1001073	0.92	5.7	2.65	2.91	2.54	1.79	
	OVARC1001074	0.81	4.66	3.31	1.87	2.95	2.04	
	OVARC1001078	2	5.12	2.79	3.57	3.08	2.83	
	OVARC1001085	2.41	2.83	3.66	5.54	5.02	6.36	** +
	OVARC1001086	1.97	3.17	2.85	3.98	2.83	4.13	
50	OVARC1001091	16.24	19.32	92.73	76.48	96.74	77.99	
	OVARC1001092	4.62	5.35	7.22	9.69	7.84	6.05	
	OVARC1001104	1.05	4.37	2.66	3.16	2.58	2.03	
	OVARC1001107	11.59	15.6	40.28	31.21	49.49	42.22	
	OVARC1001113	1.04	5.81	1.59	2.46	3.05	2.39	
55	OVARC1001117	2.71	6.63	4.31	4.67	5.74	2.67	

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	OVARC1001118	2.38	3.69	7.08	7.36	6.91	8.28		
	OVARC1001125	2.02	2.9	3	5.92	4.97	5.9	**	+
	OVARC1001129	2.61	4.58	3.19	8.46	9.43	11	**	+
5	OVARC1001132	1.7	6.48	2.66	3.69	4.26	4.66		
	OVARC1001138	9.52	15.82	23.8	48.95	45.16	44.97	**	+
	OVARC1001141	1.68	4.97	3.48	3.77	3.68	3.84		
	OVARC1001154	18.31	29.49	68.39	60.43	83.49	65.64		
	OVARC1001161	2.49	5.55	6.15	7.03	6.69	5.89		
10	OVARC1001162	2.2	3.13	5.34	5.09	4.86	5.26		
	OVARC1001163	0.69	3.59	2.77	2.2	3.98	2.54		
	OVARC1001167	3.03	4.57	7.69	10.19	12.95	9.3	*	+
	OVARC1001169	0.74	4.87	2.68	2.47	1.91	2.06		
	OVARC1001170	7.81	15.04	17.59	14.61	19.45	14.99		
15	OVARC1001171	15.57	17.71	24.31	16.12	23.34	22.51		
	OVARC1001173	2.09	5.08	5.1	4.32	6.75	5.49		
	OVARC1001176	22.57	21.48	89.96	76.74	102.3	70.7		
	OVARC1001180	3.01	4.58	12.7	11.81	10.77	9.56		
20	OVARC1001188	2.66	3.7	3.95	3.62	3.44	4.16		
	OVARC1001200	1.52	4.56	3.62	3.47	2.9	2.96		
	OVARC1001202	3.75	6.65	6.53	9.26	7.79	10.23	*	+
	OVARC1001206	1.52	5.52	1.15	1.59	1.13	1.9		
	OVARC1001209	4.89	8.92	27.46	24.69	30.38	24.27		
25	OVARC1001219	1.81	6.36	4.71	5.33	3.95	3.62		
	OVARC1001222	2.5	8.36	5.01	3.2	4.34	5.63		
	OVARC1001232	2.91	4.18	7.74	6.75	6.02	5.65		
	OVARC1001240	2.05	3.27	6.84	5.55	5.06	5.4		
	OVARC1001243	0.94	2.59	1.76	3.64	2.64	1.86		
30	OVARC1001244	9.07	12.05	18	21.61	18.57	26.62		
	OVARC1001246	30.48	50.95	48.51	80.54	100.83	101.88	**	+
	OVARC1001247	3.64	9.86	7.7	6.57	7.02	4.49		
	OVARC1001260	1.05	9.07	1.85	2.62	2.65	1.85		
	OVARC1001261	4.23	10.5	6.99	3.46	2.08	2.94		
35	OVARC1001268	24.4	19.69	52.37	32.58	35.32	14.16		
	OVARC1001270	14.46	15.1	20.83	9.69	9.8	8.65	*	-
	OVARC1001271	2.62	3.62	3.88	3.95	7.02	4.26		
	OVARC1001282	0.88	3.02	3.09	1.37	1.59	2		
	OVARC1001296	3.02	8.06	2.3	3.04	4.11	5.41		
40	OVARC1001306	1.48	8.27	2.4	2.04	2.29	3.82		
	OVARC1001314	0.49	8.47	1.57	1.06	1.79	1.32		
	OVARC1001316	2.77	7.17	4.81	5.48	8.11	5.36		
	OVARC1001329	6.12	6.18	21.11	17.09	19.29	16.22		
45	OVARC1001330	0.2	1.89	1.38	1.22	1.35	1.42		
	OVARC1001336	1.92	3.7	3.59	5.67	4.09	4.02		
	OVARC1001338	0.26	2.87	0.86	2.49	1.71	1.07		
	OVARC1001339	12.07	18.29	22.73	33.65	32.72	37.29	**	+
	OVARC1001340	0.72	4.83	1.23	1.33	2.44	1.3		
50	OVARC1001341	4.35	9.25	6.77	7.94	11.38	9.69		
	OVARC1001342	90.37	98.53	136.12	129.68	163.22	127.78		
	OVARC1001344	2.1	2.51	6.27	6.52	6.89	6.2		
	OVARC1001357	5.61	8.93	16.02	15.52	11.34	11.69		
	OVARC1001359	8.96	12.4	16.15	21.66	13.84	10.6		
55	OVARC1001360	0.44	2.52	0.99	1.97	2.6	1.62		

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	OVARC1001369	1.56	5.66	1.89	3.41	1.88	3.1		
	OVARC1001372	0.96	4.23	3.33	1.52	2.77	1.95		
	OVARC1001376	1.82	5.1	3.62	5.79	5.79	4.18		
5	OVARC1001381	4.51	6.44	9.94	10.95	12.91	11.21		
	OVARC1001391	0.5	1.62	1.44	1.88	1.27	1.26		
	OVARC1001392	2.12	4.69	6.14	11.96	12.7	7.79	*	+
	OVARC1001399	0.98	3.59	2.16	1.77	2.54	1.1		
10	OVARC1001417	1.01	3.07	1.76	2.39	3.61	2.81		
	OVARC1001419	2.47	5.4	3.06	4.39	4.03	3.16		
	OVARC1001425	2.29	5.58	5.15	8.76	8.5	8.07	*	+
	OVARC1001436	1.37	5.85	2.54	2.9	3.57	3.18		
	OVARC1001442	0.64	4.84	1.39	2.27	1.52	0.69		
15	OVARC1001451	3.09	2	3.89	5.18	5.98	4.75	*	+
	OVARC1001452	1.35	2.41	2.87	2.96	4.69	3.13		
	OVARC1001453	1.21	2.84	1.88	2.3	1.82	1.57		
	OVARC1001476	10.67	14.38	16.52	17.22	12.9	13.09		
	OVARC1001480	0.93	4.73	1.5	3.1	2.98	2.21		
20	OVARC1001489	0.97	6.89	2.51	3.01	2.83	2.09		
	OVARC1001493	2.09	6.59	3.75	7.38	8.78	10.48	*	+
	OVARC1001496	4.65	9.58	8.63	10.74	7.37	11.03		
	OVARC1001499	1.24	1.18	2.6	3.47	2.68	2.84		
	OVARC1001506	2.9	2.7	5.31	5.33	6.73	5.48		
25	OVARC1001509	1.73	3.89	3.69	4.07	4.59	3.07		
	OVARC1001510	0.16	3.69	1.42	1.94	1.73	0.86		
	OVARC1001516	2.57	5.78	3.85	6.04	4.97	4.39		
	OVARC1001525	0.53	4.76	2.12	1.94	2.01	1.81		
30	OVARC1001542	8.8	12.86	13.01	15.91	13.63	17.23		
	OVARC1001544	2.14	6.6	6.72	7.54	8.33	6.22		
	OVARC1001546	4.08	4.32	4.6	6.12	5.31	7.23	*	+
	OVARC1001547	1.29	2.53	1.68	2.44	1.85	2.22		
	OVARC1001555	10.39	16.51	68.77	48.66	65.39	56.39		
35	OVARC1001560	3.35	4.91	5.52	5.36	4.93	5.34		
	OVARC1001569	1.63	4.75	4.79	5.92	5.19	5.1		
	OVARC1001570	3.96	7.9	6.93	7.72	10.7	8.55		
	OVARC1001577	1.68	5.89	5.41	8.61	6.9	10.2		
	OVARC1001578	0.25	3.47	-0.19	-0.47	0.24	0.15		
40	OVARC1001596	12.13	11.65	14.23	13.51	14.82	27.15		
	OVARC1001600	1.13	2.9	1.48	2.81	2.67	3.67		
	OVARC1001607	6.22	7.72	10.91	13.42	14.01	13.45	*	+
	OVARC1001610	1.81	5.25	2.84	4.25	2.66	2.7		
	OVARC1001611	0.13	5.11	1.24	1.48	2.89	1.79		
45	OVARC1001615	0.58	5.42	1.93	1.54	2.56	1.74		
	OVARC1001636	1.09	3.75	1.05	2.39	2.05	2.15		
	OVARC1001668	3.77	6.75	10.04	10.5	11.4	10.48		
	OVARC1001702	1.18	2.21	2.42	3.86	2.07	2.25		
	OVARC1001703	2.82	3.18	2.97	2.64	4.71	4.65		
50	OVARC1001710	3.58	7.03	8.67	8.01	6.28	9.55		
	OVARC1001711	1.96	7.3	3.36	5.01	4.15	5.4		
	OVARC1001713	9.17	11.54	44.65	36.47	51.48	43.79		
	OVARC1001725	1.01	5.45	6.11	2.56	3.77	4.01		
	OVARC1001726	1.64	4.48	3.23	4.97	5.6	5.18		
55	OVARC1001727	1.4	2.41	1.52	1.43	2.35	1.14		

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	OVARC1001731	120.62	110.86	255.43	140.73	139.03	74.2		
	OVARC1001735	1.29	3.44	3.54	3.75	3.25	2.89		
	OVARC1001741	3.3	4.73	15.28	13.09	12.93	13.17		
5	OVARC1001745	2.72	5.39	6.83	9.17	10.23	8.89	*	+
	OVARC1001759	3.31	9.01	6.31	7.61	7.61	11.95		
	OVARC1001762	3.96	7.78	6.38	10.3	11.01	13.4	*	+
	OVARC1001766	5.33	7.8	11.99	15.56	16.86	15.33	*	+
10	OVARC1001767	0.94	3.76	1.18	1.97	1.96	2.41		
	OVARC1001768	3.31	3.86	3.76	5.35	4.59	3.54		
	OVARC1001770	3.04	6.58	9.98	11.46	9.08	9.46		
	OVARC1001776	2.11	4.7	3.5	4.72	3.64	2.92		
	OVARC1001791	1.13	4.77	3.54	3.07	3.12	3.42		
15	OVARC1001795	0.89	6.19	1.24	2.31	2.87	2.11		
	OVARC1001798	2.81	12.11	7.57	9.72	11.93	9.04		
	OVARC1001802	1.73	11.64	4.9	5.6	5.93	4.01		
	OVARC1001805	1.92	6.96	2.58	3.62	4.59	3.51		
	OVARC1001807	1.9	2.53	4.18	3.06	3.12	2.46		
20	OVARC1001809	12.38	14.06	76.32	55.87	81.41	52.83		
	OVARC1001812	1.44	3.39	3.15	3.23	4.63	3.71		
	OVARC1001813	1.61	4.29	2.33	2.93	3.98	2.51		
	OVARC1001820	1.67	7.15	3.21	3.47	3.76	3.22		
	OVARC1001828	0.78	6.85	2.36	1.91	3.23	2.2		
25	OVARC1001833	1.07	8.12	2.02	2.4	2.1	1.92		
	OVARC1001839	1.56	8.43	2.98	2.91	3.59	1.15		
	OVARC1001846	1.91	1.38	2.9	2.15	2.11	1.8		
	OVARC1001849	1.21	2.52	2.42	5.79	3.69	4.03	*	+
30	OVARC1001861	1.46	3.56	2.73	2.78	2.5	2.09		
	OVARC1001873	3.09	3.78	4.68	5.47	4.42	4.73		
	OVARC1001879	1.44	6.08	3.48	2.35	2.93	2.22		
	OVARC1001880	0.91	7.84	2.94	3.63	5.78	3.8		
	OVARC1001883	0.99	7.61	3.12	2.61	3.42	2.52		
35	OVARC1001900	1.11	7.07	4.03	2.57	3.61	2.89		
	OVARC1001901	0.54	1.84	1.21	2.42	1.37	2.43		
	OVARC1001911	0.59	1.57	1.66	1.51	1.39	1.55		
	OVARC1001916	1.86	3.13	3.35	4.16	4.61	3.51		
	OVARC1001928	1.45	3.53	1.55	1.58	1.62	1.72		
40	OVARC1001937	5.12	11.69	8.13	17.41	11.63	15.16		
	OVARC1001940	1.1	4.51	3.13	3.72	3.14	2.78		
	OVARC1001942	3.85	7.4	8.03	11.47	13.91	12.77	*	+
	OVARC1001943	7.16	10.07	11.08	9.62	13.85	11.87		
	OVARC1001949	1.69	3.34	4.15	5.35	4.01	5.55		
45	OVARC1001950	1.53	2.41	3.79	6.3	4.35	3.98		
	OVARC1001952	11.3	11.38	53.57	52.33	78.84	38.05		
	OVARC1001954	1.12	2.99	2.2	3.09	2.67	2.05		
	OVARC1001963	1	4.91	2.89	4.5	3.39	3.21		
50	OVARC1001983	3.62	14.16	14.25	20.96	19.21	21.67		
	OVARC1001987	3.12	6.54	5.94	6.08	8.39	8.02		
	OVARC1001989	1.41	5.2	4.96	4.54	5.59	5.26		
	OVARC1001991	1.74	3.27	4.08	4.57	3.86	3.27		
	OVARC1002005	4.14	3.55	7.66	10.01	9.06	8.2	*	+
	OVARC1002044	3.73	3.94	6.17	6.57	8.32	6.99	*	+
55	OVARC1002046	10.28	16.21	20.07	29.4	37.78	37.02	**	+

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	OVARC1002050	1.7	5.6	2.43	3.96	3.82	2.53		
	OVARC1002058	4.23	6.11	4.02	4.69	5.55	5.43		
5	OVARC1002066	11.47	13.5	25.49	26.02	28.69	22.63		
	OVARC1002082	3.6	8.55	8.81	9.6	8.89	6.49		
	OVARC1002091	3.17	5.67	8.37	9.49	5.49	7.64		
	OVARC1002092	1.38	2.72	2.2	4	3.97	1.88		
	OVARC1002093	1.79	3.1	4.51	5.01	4.44	3.88		
10	OVARC1002094	1.55	6.24	4.17	36.42	27.25	28.35	**	+
	OVARC1002107	1.42	4.63	2.69	4.86	5.48	3.6		
	OVARC1002112	6.17	11.59	8.5	13.47	17.48	11.92		
	OVARC1002126	2.66	6.35	6.68	7.95	6.44	8.79		
	OVARC1002127	0.73	5.04	1.86	1.92	2.61	1.52		
15	OVARC1002138	1.4	1.79	1.86	3.16	4.82	2.75	*	+
	OVARC1002143	0.73	1.51	1.55	1.29	3.03	2.09		
	OVARC1002156	2.42	3.87	4.19	4.43	3.9	3.65		
	OVARC1002158	0.88	2.63	1.6	2.36	1.57	1.51		
20	OVARC1002165	4.85	6.3	9.83	10.73	14.03	10.87		
	OVARC1002176	0.86	5.08	3.59	2.01	3.46	2.64		
	OVARC1002178	0.83	5.35	3.12	3.8	5.02	4.25		
	OVARC1002182	1.29	2.89	3.77	2.45	4.64	3.12		
	OVARC1002185	11.45	13.19	62.79	43.91	53.43	55.56		
25	PLACE1000004	1.42	3.23	2.35	3.87	4.25	4.05	*	+
	PLACE1000005	1.18	3.06	3.3	5.27	5.31	4.83	*	+
	PLACE1000006	2.01	8.33	3.23	4.2	5.44	4.67		
	PLACE1000007	0.97	5.13	2.89	3.03	2.47	2.56		
	PLACE1000014	2.9	8.06	6.26	6.67	8.18	6.55		
30	PLACE1000031	0.88	4.81	0.45	2.61	2.71	2.79		
	PLACE1000033	1.23	2.15	2.75	2.42	3.17	2.56		
	PLACE1000040	3.08	4.43	6.18	7.11	5.54	7.37		
	PLACE1000048	1.83	3.24	2.14	3.32	3.96	3.74		
	PLACE1000050	2.12	5.36	9.1	9	6.55	8.25		
35	PLACE1000061	138.29	147.36	249.77	165.55	233.98	230.37		
	PLACE1000066	14.23	15	19.46	15.86	15.62	18.52		
	PLACE1000075	3.03	6.24	9.08	4.98	6.93	7.11		
	PLACE1000078	2.1	5.75	5	6.07	6.93	5.19		
	PLACE1000081	1.08	1.88	1.52	1.13	1.89	1.27		
40	PLACE1000086	4.97	6.55	11.25	8.1	9.16	7.75		
	PLACE1000094	0.7	4.18	1.72	1	3.44	2.96		
	PLACE1000101	4.67	8.44	7.7	11.69	10.38	13.65	*	+
	PLACE1000121	0.87	6.29	2.02	1.95	2.85	2.39		
45	PLACE1000133	6.65	11.93	17.66	15.19	17.59	21.71		
	PLACE1000142	1.79	6.03	5.66	2.64	4.77	4.24		
	PLACE1000146	1.95	4.51	2.89	3.71	5.02	2.82		
	PLACE1000163	4.52	5.99	10.71	16.27	10.95	13.78		
	PLACE1000172	1.12	2.63	1.48	1.81	3.21	2.29		
50	PLACE1000181	1.06	3	2.98	2.63	3.75	2.86		
	PLACE1000184	1.17	3.08	1.48	1.87	3.28	2.27		
	PLACE1000185	2.99	6.52	8.47	9.53	9.99	12.03		
	PLACE1000198	0.78	4.09	2.49	2.19	2.17	1.93		
	PLACE1000213	3.3	5.87	7.36	4.35	5.38	8.09		
55	PLACE1000214	1.37	4.29	4.54	5.22	6.72	4.22		
	PLACE1000220	9.61	7.84	16.78	7.48	5.77	4.1		

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	PLACE1000231	2.48	4.1	4.92	4.57	4.65	3.91		
	PLACE1000236	0.66	3.33	2.43	2.8	3.63	2.37		
5	PLACE1000245	2.92	5.88	6.34	9.34	11.24	10.55	*	+
	PLACE1000246	5.15	8.27	9.95	3.29	2.55	2.86	*	-
	PLACE1000258	5.4	12.61	13.52	14.88	16.7	14.95		
	PLACE1000288	1.68	7.22	2.96	2.83	4.02	2.48		
	PLACE1000292	3.72	9.02	8.85	10.23	20.58	9.21		
10	PLACE1000302	0.56	1.01	1.39	1.07	0.92	0.62		
	PLACE1000304	1.13	3.26	3.17	3.75	2.32	3.05		
	PLACE1000308	2.54	4.35	4.17	4.42	3.87	1.34		
	PLACE1000309	2.29	4.02	4	6.72	5.23	7.88	*	+
	PLACE1000312	1.33	3.44	2.48	2.74	3.99	2.5		
15	PLACE1000330	0.46	5.76	3.02	1.32	1.93	1.35		
	PLACE1000332	1.02	8.82	2.01	3.01	3.78	1.68		
	PLACE1000347	2.3	9.48	3.89	2.59	5.81	3.22		
	PLACE1000351	1.2	1.5	2.87	2.2	2.4	2		
	PLACE1000374	2.01	3.03	7.02	8.89	6.55	6.85		
20	PLACE1000380	2.39	4.27	3.95	4.9	2.12	2.38		
	PLACE1000383	1.03	2.62	1.9	2.53	3.64	2.4		
	PLACE1000397	0.63	4.06	1.89	2.82	3.34	3.47		
	PLACE1000401	1.22	6.39	2.24	2.23	3.05	2.36		
	PLACE1000406	1.08	8.76	3.4	3.72	4.08	3.64		
25	PLACE1000412	1.61	6.38	1.56	1.62	3.45	1.46		
	PLACE1000420	2.59	3.51	4.6	8.95	7.28	5.6	*	+
	PLACE1000421	0.99	1.3	2.32	2.97	2	1.7		
	PLACE1000423	16.6	23.29	32.85	10.67	8.02	8.09	*	-
30	PLACE1000424	1.36	3.09	2.12	3.35	2.65	1.97		
	PLACE1000430	0.77	4.36	1.95	3.51	2.94	3.77		
	PLACE1000433	1.06	5.9	1.65	1.89	2.6	1.8		
	PLACE1000435	1.39	7.21	4.77	6.22	6.29	4.22		
	PLACE1000437	6.06	10.65	10.14	17.29	20.07	18.79	**	+
35	PLACE1000442	3.75	3.85	6.27	7.81	5.7	6.7		
	PLACE1000444	2.14	3.94	8.96	11.14	11.55	9.8		
	PLACE1000453	5.57	11.03	14.16	10.42	7.4	2.99		
	PLACE1000456	1.25	2.21	1.97	1.33	2.18	1.07		
	PLACE1000465	2.09	5.63	6.62	12.97	11.8	10.69	**	+
40	PLACE1000481	2.32	8.1	3.73	6.89	6.64	6.45		
	PLACE1000492	1.15	4.45	2.95	3.27	3.06	2.81		
	PLACE1000508	1.36	4.64	4	3.91	4.24	3.71		
	PLACE1000512	4.91	4.29	6.39	8.12	7.8	4.6		
	PLACE1000540	5.18	3.93	7.84	5.44	6.9	5.57		
45	PLACE1000541	13.59	15.07	48.84	60.62	81.24	41.96		
	PLACE1000546	0.86	3.61	2.82	4.72	4.63	2.5		
	PLACE1000547	2.16	4.61	3.83	6.31	5.64	5.92	*	+
	PLACE1000560	2.08	5.97	2.1	1.62	2.8	1.72		
	PLACE1000562	2.8	6.23	6.04	8.86	11.26	8.61	*	+
50	PLACE1000564	1.54	6.4	3.07	3.16	4.41	3.43		
	PLACE1000583	3.75	3.28	6.32	6.78	11.53	6.8		
	PLACE1000587	8.52	9.32	12.99	13.64	14.69	9.43		
	PLACE1000588	1.92	4.36	3.99	8.79	8.15	4.48		
	PLACE1000596	1.99	5.34	4.39	7.8	6.74	4.51		
55	PLACE1000599	2.39	5.51	7.05	7.92	7.79	6.46		

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	PLACE1000605	5.12	11.43	7.06	14.2	15.1	12.67	*	+
	PLACE1000610	2.01	6.08	3.54	5.26	4.48	2.94		
	PLACE1000611	13.18	19.13	24.68	16.45	20.37	22.79		
5	PLACE1000626	3.19	4.04	8.04	5.71	9.93	8.12		
	PLACE1000633	1.32	2.12	3.95	4.8	6.06	3.59		
	PLACE1000636	1.15	2.54	1.43	2.72	4.25	2.94		
	PLACE1000653	5.07	8.56	9.29	11.07	11.87	14.08	*	+
10	PLACE1000656	4.2	12.9	25.22	16.66	16.71	12.92		
	PLACE1000663	2	6.43	3.59	2.39	6.61	4.03		
	PLACE1000706	2	6.3	5.04	5.37	7.27	6.26		
	PLACE1000712	3.9	9.52	10.82	10.49	10.07	9.11		
	PLACE1000716	0.98	2.75	3.44	2.44	3.2	2.82		
15	PLACE1000740	2.74	5.28	6.24	8.83	8.13	9.69	*	+
	PLACE1000748	3.35	3.51	6.81	3.12	5.02	4.23		
	PLACE1000749	3.49	6.35	5.94	4.61	4.65	6.02		
	PLACE1000751	2.71	5.34	4.07	7.81	8.32	8.36	**	+
	PLACE1000755	1.39	6.14	1.93	2.55	5.1	2.96		
20	PLACE1000769	2.29	6.8	3.45	3.33	4.58	2.6		
	PLACE1000778	0.87	1.48	1.99	2.05	2.94	2.38		
	PLACE1000785	9.56	12.21	27.18	28	24.34	29.54		
	PLACE1000786	2.68	4.22	3.63	3.09	3.77	3.7		
	PLACE1000793	4.05	7.21	6.7	6.06	7.6	9.1		
25	PLACE1000795	2.15	5.5	3.99	4.44	5.29	4.31		
	PLACE1000798	0.88	8.44	3.24	3.13	3.8	3.72		
	PLACE1000812	2.13	5.08	4.46	5.06	5.16	6.03		
	PLACE1000823	1.71	5.2	4.89	5.67	7.28	4.84		
	PLACE1000825	1.6	2.86	2.02	3.77	3.96	3.76	*	+
30	PLACE1000838	16	15.77	23.73	13.88	15.6	15.65		
	PLACE1000841	1.22	3.78	3.31	3.97	10.65	3.77		
	PLACE1000843	2.14	6.2	5.68	5.79	7.7	5.38		
	PLACE1000849	2.79	8.82	6.72	7.24	6.78	10.02		
35	PLACE1000856	2.01	5.3	3.59	3.42	4.79	4.19		
	PLACE1000863	5.2	7.58	9.56	8.97	12.34	11.53		
	PLACE1000876	3.65	7.6	6.02	6.7	9.95	9.06		
	PLACE1000899	1.36	2.24	3.12	4.12	5.14	4.22	*	+
	PLACE1000907	4.82	5.53	9.59	6.77	8.44	5.83		
40	PLACE1000909	1.18	3.31	2.45	3.65	3.88	3.44		
	PLACE1000912	0.42	4.55	1.77	1.76	2.72	1.46		
	PLACE1000914	1.05	4.41	3.5	3	6.09	4.22		
	PLACE1000918	0.54	4.49	1.61	1.82	3.13	1.98		
	PLACE1000927	10.48	12.41	16.9	20.91	23.21	25.47	*	+
45	PLACE1000931	0.69	3.44	2.12	2.44	3.94	3.3		
	PLACE1000944	2.55	2.24	4.78	3.84	3.32	2.09		
	PLACE1000948	0.52	2.31	2.96	2.21	2.72	1.72		
	PLACE1000958	0.12	2.2	1.73	1.11	1.77	2.27		
	PLACE1000972	1.01	3.43	2.89	4.49	5.33	3.75		
50	PLACE1000977	2.33	5.67	4.42	2.71	5.33	5.25		
	PLACE1000979	1.63	8.01	3.93	4.24	5.92	4.57		
	PLACE1000986	3.37	16.51	6.63	6.97	8.75	7.69		
	PLACE1000987	1.76	10.13	4.79	4.17	4.74	5.11		
	PLACE1001000	4.85	4.62	7.76	6.02	4.25	3.02		
55	PLACE1001007	7	6.94	14.66	5.39	3.76	3.47		



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	PLACE1001010	0.61	2.04	2.45	2.56	2.73	2.84		
	PLACE1001015	0.88	2.55	1.84	2.36	1.72	2.42		
5	PLACE1001016	1.79	4.54	4.29	6.37	9	6.57	*	+
	PLACE1001022	0.68	6.5	2.45	1.9	2.39	1.29		
	PLACE1001024	1.05	8.89	1.83	1.34	2.49	2.35		
	PLACE1001036	2.63	10.55	5.42	3.62	5.49	5.43		
	PLACE1001038	50.16	49.81	118.83	82.67	64.83	52.8		
10	PLACE1001048	1.07	1.82	0.92	2.39	2.09	1.21		
	PLACE1001054	9.95	10.74	63.88	62.96	79.44	66.71		
	PLACE1001062	1.45	4.19	3.71	3.12	4.17	3.05		
	PLACE1001063	1.35	3.74	2.2	4.06	3.65	2.74		
	PLACE1001076	0.46	6.48	1	1.86	2.18	1.62		
15	PLACE1001081	1.53	7.95	3.33	3.65	5.24	4.8		
	PLACE1001088	1.32	5.24	1.22	1.42	2.81	1.37		
	PLACE1001092	2.31	2.47	4.68	5.8	4.18	3.9		
	PLACE1001098	0.93	2.62	4.53	5.49	4.05	3.17		
20	PLACE1001100	1.31	2.58	2.48	4.27	4.17	3.37	*	+
	PLACE1001104	1.95	4.09	4.54	3.39	3.42	4.47		
	PLACE1001114	1.56	6.54	4.33	5.17	3.78	3.27		
	PLACE1001118	2.52	5.77	6.12	6.21	6.14	5.1		
	PLACE1001123	2.86	5.3	7.53	7.08	8.51	7.63		
25	PLACE1001136	1.58	4.39	5.13	5.29	5.95	5.85		
	PLACE1001144	6.27	5.67	13.43	10.34	11	10.08		
	PLACE1001147	2.11	2.98	6.03	6.13	5.15	4.83		
	PLACE1001148	1.72	1.31	1.89	1.76	2.39	2.31		
	PLACE1001159	0.86	2.37	2.05	2.27	3.73	1.43		
30	PLACE1001168	8.87	14.52	15.09	25.46	23.18	30.79	*	+
	PLACE1001171	0.69	3.89	1.23	2.53	1.42	1.53		
	PLACE1001183	0.24	3.61	1.81	1.57	2.78	1.38		
	PLACE1001185	3.13	7.43	3.76	5	6.4	5.64		
	PLACE1001201	1.77	2.8	3.29	6.32	6.94	6.32	**	+
35	PLACE1001229	7.51	8.56	12.64	15.24	11.45	10.42		
	PLACE1001231	1.83	2.73	3.07	4.09	5.1	2.3		
	PLACE1001238	1.52	4.35	3.74	3.65	4.52	4.57		
	PLACE1001241	1.63	5.58	2.92	5.73	8.13	7.04		
	PLACE1001242	22.28	29.54	30.28	46.43	48.89	62.65	*	+
40	PLACE1001247	2.43	7.02	4.07	5.03	5.91	4.52		
	PLACE1001250	1.01	5.36	3.61	4.68	4.39	4.81		
	PLACE1001257	2.99	3.06	7.06	7.89	9.21	7.69		
	PLACE1001272	3.19	4.27	5.68	7.13	6.43	5.14		
45	PLACE1001279	0.96	3.12	2.74	3.08	3.81	3.29		
	PLACE1001280	1.08	4.75	2.68	4.98	4.45	2.86		
	PLACE1001294	1.91	7.23	6.91	4.88	5.57	6.18		
	PLACE1001295	4.16	9.94	7.53	8.55	11.85	8.43		
	PLACE1001300	2.46	7.9	4.31	4.65	14.73	4.95		
	PLACE1001304	3	8.27	10.47	8.57	10.81	10.64		
50	PLACE1001311	3.95	3.34	5.67	6.85	9.14	7.6	*	+
	PLACE1001323	2.17	2.95	5.12	5.66	8.43	5.5		
	PLACE1001325	0.88	1.95	3.71	2.84	3.56	3.27		
	PLACE1001340	5.18	6.99	9.8	8.69	12.02	10.48		
55	PLACE1001344	1.52	3.49	1.77	2.34	2.06	1.75		
	PLACE1001351	3.23	6.39	8.39	6.4	8.62	6.1		

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	PLACE1001366	1	4.49	4.02	4.19	4.6	3.72		
	PLACE1001377	3.02	4.97	5.1	7.91	7.28	5.83	*	+
5	PLACE1001383	2.31	4.13	3.53	2.62	5.5	5.72		
	PLACE1001384	1.81	3.23	2.89	2.05	3.43	3.15		
	PLACE1001387	1.65	3.64	3.7	3.03	4.83	3		
	PLACE1001395	3.72	6.64	6.54	7.01	7.61	7.73		
	PLACE1001399	3.71	6.58	9.31	7.37	8.61	9.22		
10	PLACE1001401	0.83	5.25	2.33	1.55	1.76	0.87		
	PLACE1001407	11.65	21.8	24.47	22.63	18.09	26.24		
	PLACE1001412	1.6	4.98	4.53	4.08	4.42	3.83		
	PLACE1001414	2.3	3.02	5.86	7.57	5.13	6.83		
	PLACE1001416	2.99	4.71	3.29	5.62	4.04	7.08		
15	PLACE1001433	33.62	33.05	51.64	49.1	58.33	55.88		
	PLACE1001440	1.95	3.99	3.96	3.6	3.53	2.1		
	PLACE1001456	1.64	5.5	4.26	4.15	4.87	4.49		
	PLACE1001464	32.76	28.05	47.41	53.22	68.42	61.32	*	+
20	PLACE1001468	0.85	5.04	1.17	1.56	2.55	2.27		
	PLACE1001484	1.31	4.85	2.96	4.25	5.8	3.04		
	PLACE1001500	0.92	2.22	2.14	2.72	3.34	3.26	*	+
	PLACE1001502	1.36	3.6	3.9	3.54	5.9	4.54		
	PLACE1001503	1.7	4.58	6.72	7.47	8.2	8.05		
25	PLACE1001505	6.34	14.13	16.16	39.97	27.14	46.65	*	+
	PLACE1001513	4.09	10.82	8.17	5.87	8.53	14.61		
	PLACE1001516	0.61	4.33	1.33	1.71	3.49	1.99		
	PLACE1001517	5.56	8.58	14.77	14.14	14.96	14.28		
	PLACE1001523	12.83	14.09	20.42	22.79	19.74	32.9		
30	PLACE1001526	5.12	4.89	8.42	9.51	9.11	6.89		
	PLACE1001534	2.12	5.12	3.58	3.62	5.55	3.99		
	PLACE1001536	0.61	2.5	1.52	2.11	3.2	1.9		
	PLACE1001545	17.97	23.9	38.46	33.78	45.13	66.08		
35	PLACE1001551	2.55	6.26	6.15	4.72	6.59	6.71		
	PLACE1001564	1.37	4.87	2.88	4.01	3.57	3.7		
	PLACE1001570	2.62	5.95	4.18	2.19	3.82	4.32		
	PLACE1001571	2.04	4.51	6.07	5.69	6.27	5.81		
	PLACE1001595	4.73	4.64	10.04	11.6	8.27	5.28		
40	PLACE1001602	7.23	8.39	18.65	20.38	18.68	19.71		
	PLACE1001603	2.01	3.83	5.37	6.86	5.86	4.56		
	PLACE1001608	3.44	7.22	5.9	5.82	7.73	8.7		
	PLACE1001610	3.77	8.4	8.22	9.26	9.49	9.85		
	PLACE1001611	1.94	7.34	3.65	2.28	3.85	1.88		
45	PLACE1001629	0.78	6.77	2.24	3.62	3.36	3.52		
	PLACE1001632	1.66	8.26	4.04	4.3	4.14	4.37		
	PLACE1001634	7.4	9.92	39.12	23.85	32.41	18.38		
	PLACE1001637	0.84	2.16	1.25	1.41	2.4	1.1		
	PLACE1001640	1.33	3.27	4.66	2.68	4.85	4.49		
50	PLACE1001655	0.83	2.93	2.06	2.82	2.14	2.02		
	PLACE1001672	1.84	7.04	4.01	3.3	4.41	4.09		
	PLACE1001676	1.38	8.49	3.54	4.63	4.77	3.85		
	PLACE1001683	12.79	23.62	24.61	25.33	30.22	27.13		
	PLACE1001691	3.41	12.29	6.72	9.03	8.96	9.83		
55	PLACE1001692	1.47	2.96	5.25	5.87	5.6	5.13		
	PLACE1001705	3.02	3.75	9.88	10.06	9.21	8.32		

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	PLACE1001716	1.68	3	2.61	2.24	3.79	3.58		
	PLACE1001720	1.49	2.62	2.21	1.56	2.45	1.71		
	PLACE1001728	1.43	6.19	4.24	1.96	2.04	2.51		
5	PLACE1001729	2.12	8.13	4.44	3.8	4.52	4.36		
	PLACE1001739	2.61	9.55	4.04	4.95	7.24	6.16		
	PLACE1001740	0.92	5.36	2.09	1.92	2.1	1.69		
	PLACE1001745	1.15	0.98	3.22	1.87	2.48	2.31		
10	PLACE1001746	1.04	2.25	2.55	4.64	3.4	2.82		
	PLACE1001748	4.74	7.01	8.18	8.19	6.58	5.96		
	PLACE1001753	2.06	3.54	3.29	7.44	5.57	5.82	*	+
	PLACE1001756	5.6	11.31	38.07	31.78	44.99	35.99		
	PLACE1001760	6.54	12.23	12.85	16.36	16.96	16.66	*	+
15	PLACE1001767	11.26	14.98	59.72	45.37	61.46	45.39		
	PLACE1001771	1.96	6.64	4.03	4.32	5.22	4.54		
	PLACE1001775	2.23	2.81	6.72	5.1	3.11	4.79		
	PLACE1001777	83.34	145.9	190.82	142.92	71.27	59.69		
20	PLACE1001781	1.9	3.86	4.91	8.72	3.39	2.3		
	PLACE1001783	0.76	3.21	2.06	4.84	2.09	1.54		
	PLACE1001786	1.77	6.61	2.72	3.7	3.32	2.6		
	PLACE1001788	5.16	9.07	7.14	10.52	8.74	9.32		
	PLACE1001795	1.92	4.4	4.82	5.42	4.61	5.42		
25	PLACE1001799	0.69	3.62	2.11	1.86	2.83	1.97		
	PLACE1001810	0.89	1.52	1.76	2.73	3.91	1.73		
	PLACE1001817	5.53	6.12	10.88	10.56	9.4	6.38		
	PLACE1001821	4.68	6.07	7.11	8.37	9.92	4.99		
	PLACE1001836	0.91	3.12	2.38	2.69	4.12	2.63		
30	PLACE1001844	1.55	5.1	3.48	4.42	4.36	4.09		
	PLACE1001845	3.62	8.38	7.39	7.88	7.55	9.93		
	PLACE1001858	2.56	6.58	3.52	5.26	7.48	6.05		
	PLACE1001869	3.13	7.15	4.85	6.09	6.46	5.66		
	PLACE1001890	11.74	11.92	21.45	173.44	255.31	125.13	*	+
35	PLACE1001897	9.19	13.85	16.44	22.22	23.13	12.95		
	PLACE1001902	10.13	12.6	21.53	22.74	27.67	12.77		
	PLACE1001904	1.38	3.72	1.51	2.45	2.53	2.35		
	PLACE1001907	3.36	6.76	5.71	7.67	5.67	5.59		
	PLACE1001910	83.6	82.16	135.34	301.29	325.42	244.59	**	+
40	PLACE1001912	1.53	6.6	3.36	5.54	5.48	4.85		
	PLACE1001918	17.31	22.95	30.16	31.14	40.44	40.02	*	+
	PLACE1001920	2.07	3.51	5.43	11.97	13.8	11.4	**	+
	PLACE1001928	3.06	2.96	4.67	5.29	9.7	5.31		
45	PLACE1001930	1.17	3.92	2.2	2.9	4.73	3.22		
	PLACE1001949	1.16	3.67	1.78	3.84	4.24	3.18		
	PLACE1001959	1.36	4.7	3.16	2.63	3.17	2.26		
	PLACE1001969	2.09	7.83	7.21	6.56	10.73	6.57		
	PLACE1001974	7.39	11.98	11.87	11.43	16.09	16.06		
50	PLACE1001981	0.77	4.38	3.22	1.77	3.88	2.36		
	PLACE1001983	3.81	4.12	5.32	5.92	6.16	5.72	*	+
	PLACE1001989	2.34	4.15	5.02	4.37	5.91	3.72		
	PLACE1002004	3.07	4.06	8.05	9.22	9.69	7.18		
	PLACE1002008	8.4	11.76	17	23.36	22.19	22.42	*	+
55	PLACE1002015	26.96	30.92	67.62	105.75	88.42	94.15	*	+
	PLACE1002044	3.79	8.07	5.86	4.64	6.39	6.4		

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	PLACE1002046	1.78	5.68	1.9	4.3	5.79	4.97		
	PLACE1002052	1.09	4.98	2.26	1.38	2.41	2.32		
5	PLACE1002066	4.79	6.3	8.29	10.24	10.77	9.93	*	+
	PLACE1002072	2.55	3.91	4.86	6	5.48	6	*	+
	PLACE1002073	0.51	2.83	2.29	2.35	4.06	2.91		
	PLACE1002080	1.81	6.49	6.13	4.76	6.82	5.72		
	PLACE1002081	1.66	6.13	4.06	3.74	4.86	4.3		
10	PLACE1002090	7.74	16.55	13.87	12.53	14.4	19.41		
	PLACE1002095	2.97	6.22	8.45	10.01	10.18	11.32	*	+
	PLACE1002102	4.26	8.56	8.81	9.47	9.56	10.67		
	PLACE1002109	2.57	5.08	3.81	4.66	6.17	6.32		
	PLACE1002115	1.75	3.57	2.48	2.78	4.26	2.59		
15	PLACE1002119	15.65	15.3	35.78	37.28	32.59	38.23		
	PLACE1002140	5.25	8.45	14.05	19.93	17.14	17.19	*	+
	PLACE1002150	1.54	8.26	4.25	3.23	5.36	4.12		
	PLACE1002153	1.6	5.75	2.58	3.47	5.76	4.48		
	PLACE1002157	0.87	2.96	1.72	1.76	3.28	3.73		
20	PLACE1002163	2.13	4.67	4.55	6.21	8.81	6.03		
	PLACE1002168	2.39	4.04	4.42	4.68	6.28	3.22		
	PLACE1002170	2.73	3.53	7.35	4.89	5.33	3.74		
	PLACE1002171	3.09	6.11	10.02	18.44	14.63	13.93	*	+
	PLACE1002180	3.16	6.23	6.77	4.63	8.54	8.39		
25	PLACE1002184	9.2	15.58	18.42	124.63	250.27	333.14	*	+
	PLACE1002200	1.35	5.67	2.38	2.97	2.89	2.26		
	PLACE1002205	3.3	6.47	18.07	17.08	18.38	14.61		
	PLACE1002213	2.2	4.16	4.93	5.52	8.03	6.03		
30	PLACE1002219	1.05	1.91	2.23	3.33	3.53	1.96		
	PLACE1002227	0.68	2.65	1.7	1.5	3.03	1.67		
	PLACE1002253	0.32	2.67	1.28	1.47	0.76	0.43		
	PLACE1002256	1.16	4.78	3.31	3.54	3.01	4.79		
	PLACE1002259	1.46	5.69	4.48	3.22	2.98	2.31		
35	PLACE1002285	1.16	10.74	2.29	1.55	2.38	1.24		
	PLACE1002301	9.42	17.5	14.68	12.7	10.48	11.7		
	PLACE1002310	4.28	10.16	9.86	8.82	7.87	9.94		
	PLACE1002311	1.84	2.94	3.87	2.96	2.87	2.03		
	PLACE1002319	2.31	2.64	2.94	3.21	3.23	3.92	*	+
40	PLACE1002329	0.56	2.54	2.5	4.07	3.58	3.07		
	PLACE1002333	1.34	3.1	1.96	1.22	2.44	2		
	PLACE1002342	4.19	9.04	9.44	5.06	8.52	8.17		
	PLACE1002343	0.49	6.98	2.94	2.08	1.9	2.52		
	PLACE1002355	1.31	9.39	2.36	3.33	4.35	2.63		
45	PLACE1002358	1.15	7.94	3.3	2.6	2.65	2.13		
	PLACE1002359	1.91	2.17	3.47	4.7	3.91	3.42		
	PLACE1002374	29.69	28.18	54.19	53.9	34.73	36.14		
	PLACE1002376	3.58	5.91	7.86	6.23	6.82	6.56		
	PLACE1002379	6.24	7.66	6.63	10.13	9.68	10.9	**	+
50	PLACE1002386	0.86	5.32	1.35	1.87	2.05	1.51		
	PLACE1002395	3.69	9.97	17.13	16.43	20.62	16.16		
	PLACE1002399	2.38	11.09	3.42	5.31	10.38	7.39		
	PLACE1002407	1.09	5.22	2.31	2.3	4.01	3.66		
	PLACE1002433	1.63	2.17	2.97	2.96	4.35	3.66		
55	PLACE1002437	0.79	1.4	1.47	1.41	3.28	1.35		

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	PLACE1002438	0.74	2.38	1.96	1.8	2.43	3.38		
	PLACE1002446	4.64	8.42	5.95	10.27	8.88	11.99	*	+
	PLACE1002447	1.26	6.06	2.05	3.92	3.14	4.32		
5	PLACE1002450	1.19	5.92	3.24	4.32	4.21	5.05		
	PLACE1002462	0.81	4.02	2.94	3.51	2.99	3.13		
	PLACE1002465	0.96	4.69	2.2	2.69	4.31	2.24		
	PLACE1002474	1.61	2.26	3.23	3.85	4.41	3.6	*	+
	PLACE1002477	11.11	14.51	32.39	44.06	41.42	26.68		
10	PLACE1002493	3.39	4.1	10.1	14.39	16.66	9.49		
	PLACE1002497	0.68	2.81	0.67	1.45	0.93	0.99		
	PLACE1002499	2.12	4.73	3	5.98	6.44	5.28	*	+
	PLACE1002500	2.61	6.52	7.36	7.58	10.45	7.25		
15	PLACE1002514	0.3	4.49	1.84	1.74	2.47	1.75		
	PLACE1002518	2.86	7.65	6.9	5.62	7.55	4.67		
	PLACE1002529	1.14	1.56	2.21	3.19	3.4	1.44		
	PLACE1002532	1.31	1.82	3.18	5.75	4.94	5.59	**	+
	PLACE1002536	3.59	3.75	3.44	5.84	6.07	3.85		
20	PLACE1002537	1.63	4.06	2.7	2.69	4.07	3.08		
	PLACE1002539	1.86	5.68	2.75	4.53	5.29	4.78		
	PLACE1002547	6.09	8.06	7.3	12.32	11.02	11.26	**	+
	PLACE1002571	2.84	6.85	5.19	6.84	8.65	6.23		
	PLACE1002578	3.57	8.34	8.35	11.11	12.19	8.11		
25	PLACE1002583	1.33	1.61	2.32	3.18	4.02	2.46		
	PLACE1002591	0.82	1.62	2.34	3.25	4.43	1.92		
	PLACE1002598	6.56	10.95	12.39	11.93	9.04	7.74		
	PLACE1002604	1.73	3.57	2.69	3.75	5.38	3.51		
	PLACE1002612	2.89	8.47	5.95	11.25	10.88	8.06		
30	PLACE1002625	1.25	4.79	3.18	2.7	3.25	1.82		
	PLACE1002638	2.94	8.01	6.66	7.78	6.81	7.29		
	PLACE1002655	1.39	6.51	5.57	7.19	7.62	6.46		
	PLACE1002665	4.57	3.88	5.4	7.47	12.16	10.75	*	+
	PLACE1002685	0.58	1.12	1.3	0.67	2.43	0.98		
35	PLACE1002692	7.42	8.56	16.7	19.27	22.67	16.29		
	PLACE1002714	1.8	3	2.11	2.43	3.14	2.24		
	PLACE1002721	2.94	4.37	3.88	5.88	7.1	4.28		
	PLACE1002722	0.92	5.42	1.97	1.37	3.28	1.85		
40	PLACE1002726	1.6	6.24	3.66	4.6	5.7	5.26		
	PLACE1002756	1.57	4.5	7.04	5.92	9.63	7.78		
	PLACE1002768	1.05	3.72	2.16	2.1	2.34	1.71		
	PLACE1002772	0.54	2.15	1.32	2.49	2.86	2.3		
	PLACE1002775	4.33	4.71	9.15	7.05	7.08	8.67		
45	PLACE1002780	185.63	218.72	325.36	272.21	244.38	305.38		
	PLACE1002782	0.4	3.76	1.1	1.62	1.69	1.14		
	PLACE1002794	1.5	6.71	3.27	2.26	4.59	4.36		
	PLACE1002795	1.92	6.45	0.81	2.37	3.63	2.77		
	PLACE1002811	0.6	1.57	1.34	1.9	1.46	1.16		
50	PLACE1002815	6.39	7	10.49	7.24	3.16	9.21		
	PLACE1002816	8.5	9.72	9.05	7.22	8.2	7.97	*	-
	PLACE1002822	0.58	2.51	2.06	2.2	2.87	1.94		
	PLACE1002833	9.98	15.11	16.78	15.42	15.99	16.56		
	PLACE1002834	3.2	8.08	6.57	6.23	6.79	8.41		
55	PLACE1002835	0.62	4.14	1.72	0.85	1.83	1.79		

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	PLACE1002839	1.13	5.75	2.72	2.89	4.72	2.81		
	PLACE1002851	1.52	1.87	1.41	1.98	2.15	2.7		
	PLACE1002853	4.18	6.23	9.15	6.26	5.6	7		
5	PLACE1002881	3.42	5.2	11.04	8.35	11.57	10.26		
	PLACE1002901	9.66	12.66	20.09	24.14	25.51	30.67	*	+
	PLACE1002904	0.89	7.35	1.41	1.98	1.95	3.09		
	PLACE1002905	1.36	5.46	3.26	4.04	4.46	3.4		
10	PLACE1002908	1.6	5.19	3.18	3.84	5.27	3.81		
	PLACE1002911	3.91	6.96	6.9	4.66	7.89	6.75		
	PLACE1002941	1.57	2.2	2.48	3.94	2.02	2.31		
	PLACE1002950	9.59	9.15	14.74	5.31	8.02	14.51		
	PLACE1002955	47.83	40.69	72.7	82.17	62.5	84.64		
15	PLACE1002958	19.36	26.92	35.27	35.6	35.35	59.02		
	PLACE1002962	1.03	4.03	2.2	1.41	2.63	1.67		
	PLACE1002967	1.34	4.83	3.19	4.37	3.52	2.81		
	PLACE1002968	1.2	5.14	2.7	2.55	3.05	1.81		
	PLACE1002976	8.94	12.08	24.23	24.5	36.89	30.05		
20	PLACE1002991	2.68	3.05	6.66	3.49	4.56	3.6		
	PLACE1002993	2.72	3.86	5.52	8.21	6.92	5.56		
	PLACE1002996	2.02	3.03	3.43	5.54	3.52	3.01		
	PLACE1003010	1.91	3.69	4.27	4.31	3.86	3.32		
25	PLACE1003025	2.85	7.01	6.1	8.57	11.37	10.11	*	+
	PLACE1003027	5.02	13.08	9.31	8.55	12.45	12.76		
	PLACE1003044	1.95	8.24	2.61	3.64	4.16	2.74		
	PLACE1003045	1.41	7.75	1.77	1.88	2.64	1.01		
	PLACE1003052	2.19	3.16	5.74	4.44	3.6	1.99		
30	PLACE1003083	1.59	3.04	3.23	3.06	1.61	2.25		
	PLACE1003085	3.91	6.19	5.6	9.46	5.89	3.33		
	PLACE1003092	3.94	4.87	6.25	7	5.6	6.17		
	PLACE1003097	0.37	3.06	1.44	2.12	1.88	1.63		
	PLACE1003100	1.65	7.1	4.2	3.88	4.74	4.29		
35	PLACE1003108	1.26	10.37	2.91	3.32	4.44	2.39		
	PLACE1003115	11.39	18.3	58.59	73.64	99.24	69.1	*	+
	PLACE1003120	3.1	3.08	9.71	11.34	8.32	10.19		
	PLACE1003135	0.72	2.04	1.09	1.56	2.89	1.08		
	PLACE1003136	3.95	5.82	6.05	9.03	6.55	7.34		
40	PLACE1003141	2.04	2.97	2.1	1.97	2.49	1.8		
	PLACE1003145	1.21	4.17	2.52	6.24	6.88	7.67	*	+
	PLACE1003147	2.87	7.85	5.71	5.02	5.25	6.28		
	PLACE1003153	0.54	7.63	2.14	1.66	3.2	1.82		
	PLACE1003163	6.09	13.55	8.19	8.39	14.09	12.26		
45	PLACE1003172	23.21	21.74	44.19	47.78	43.17	39.52		
	PLACE1003174	2.31	2.49	3.75	4.3	3.55	1.68		
	PLACE1003176	0.47	2	1.89	2.88	1.27	1.46		
	PLACE1003181	1.72	4.19	2.72	2.5	2.76	2.36		
	PLACE1003184	0.76	3.92	1.53	1.91	1.49	2.06		
50	PLACE1003190	2.39	9.81	8.67	10.73	7.98	10.34		
	PLACE1003200	0.29	4.48	1.84	0.72	1.92	1.16		
	PLACE1003205	3.94	7.07	9.68	6.82	10.38	7.2		
	PLACE1003209	1.43	2.18	2.62	2.28	1.82	2.89		
55	PLACE1003214	0.83	1.3	2	2.15	2.44	1.81		
	PLACE1003229	2.08	2.78	2.9	2.78	3.35	3.48		

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	PLACE1003238	0.46	2.34	1.24	1.35	2	0.75		
	PLACE1003249	1.87	5.04	4.7	7.33	7.56	5.89		
	PLACE1003256	3.47	7.69	7.94	8.82	7.68	6.08		
5	PLACE1003258	1.03	3.81	3.48	2.42	2.19	0.87		
	PLACE1003279	3.09	7.19	9.02	11.15	13.56	11.58	*	+
	PLACE1003294	0.95	1.54	1.59	1.57	1.25	2.64		
	PLACE1003296	1.49	2.6	2.45	2.59	3.11	2.4		
10	PLACE1003297	7.52	10.15	31.88	23.01	23.49	19.3		
	PLACE1003302	3.92	5.16	6.99	5.8	4.72	5.47		
	PLACE1003334	1.51	4.41	1.91	2.4	3.59	3.09		
	PLACE1003337	13.69	16.3	29.83	28.53	34.27	25.76		
	PLACE1003342	1.05	4.07	1.89	2.15	2.35	1.97		
15	PLACE1003343	1.07	4.98	1.61	2.02	2.75	2.12		
	PLACE1003344	6.25	5.33	12.83	11.18	11.35	11.98		
	PLACE1003353	19.67	16.04	40.09	37.78	42.55	40.26		
	PLACE1003361	1.82	3.64	3.72	5.85	5.31	4.6	*	+
	PLACE1003366	1.45	4.35	3.63	3.22	3.33	2.97		
20	PLACE1003369	2.75	4.51	3.49	3.29	3.25	4.62		
	PLACE1003372	2.08	5.73	2.68	5.45	4.72	3.39		
	PLACE1003373	2.85	7.37	6.62	8.8	11.81	9.89		
	PLACE1003375	1.42	4.91	1.92	2.59	2.95	3.21		
	PLACE1003378	0.94	0.94	0.98	0.7	1.66	1.08		
25	PLACE1003383	0.87	1.55	2.33	1.59	3.15	1.57		
	PLACE1003394	10.55	12.49	24.08	11.75	22.99	17.27		
	PLACE1003401	0.79	3.91	1.34	1.03	2.13	1.04		
	PLACE1003405	1.5	3.97	2.22	2.54	2.46	2.04		
30	PLACE1003407	2.39	6.06	5.16	3.96	6.3	4.02		
	PLACE1003420	3.26	7.69	6.19	6.8	10.92	8.7		
	PLACE1003428	0.63	3.3	2.62	2.07	2.94	1.96		
	PLACE1003432	6.14	5.81	8.2	6.64	7.05	5.42		
	PLACE1003438	0.45	2.66	0.93	2.41	2.34	1.99		
35	PLACE1003452	1.87	5.02	5.08	4.53	3.43	3.84		
	PLACE1003454	2.49	5.59	7.34	7.31	6.95	5.61		
	PLACE1003455	2.58	4.26	2.35	2.97	3.01	3.17		
	PLACE1003456	3.22	7.74	8.62	6.9	7.2	7.79		
	PLACE1003460	6.39	13.35	14.87	13.02	16.76	12.86		
40	PLACE1003478	1.15	1.71	0.86	2.33	2.07	1.24		
	PLACE1003484	12.06	12.21	45.33	28.12	31.5	34.2		
	PLACE1003493	1.61	4.72	4.9	3.84	5.96	5.08		
	PLACE1003503	85.45	87.35	107.79	115.17	111.85	172.81		
	PLACE1003505	1.99	6.77	4.78	7.44	6.63	8.87		
45	PLACE1003516	0.86	6.78	2.7	2.8	3.95	2.39		
	PLACE1003519	17.58	26.29	50.41	45.77	36.97	58.75		
	PLACE1003520	14.18	25.48	35.96	25.73	31.4	32.19		
	PLACE1003521	2.71	3.64	4.93	5.97	4.71	7.4		
	PLACE1003525	8.45	11.81	45.05	33.94	43.71	36.88		
50	PLACE1003528	39.18	44.68	136.4	106.04	122.76	127.22		
	PLACE1003529	1.46	4.26	3.29	2.4	3.94	3.83		
	PLACE1003537	4.41	9.05	11.05	11.36	13.77	13.3		
	PLACE1003549	1.1	5.02	4.59	5.61	6.01	5.93		
	PLACE1003553	1.6	5.89	3.88	4.02	4.17	4.23		
55	PLACE1003566	5.93	9.8	17.51	13.03	19.09	14.58		

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	PLACE1003568	3.01	2.71	5.76	5.69	4.43	4.04		
	PLACE1003573	0.98	2.43	1.19	2.16	1.87	1.48		
5	PLACE1003575	2.16	3.09	3.44	3.34	3.5	4.15		
	PLACE1003583	0.97	3.45	3.34	2.29	4.16	2.23		
	PLACE1003584	1.23	4.46	4.01	3.56	3.8	2.65		
	PLACE1003592	4.4	8.48	9.48	7.11	10.48	9.53		
	PLACE1003593	0.84	5.55	2.4	2.23	3.02	1.55		
10	PLACE1003594	4.24	6.76	6.01	5.78	6.68	7.36		
	PLACE1003596	13.77	11.31	22.53	15.68	17.69	8.25		
	PLACE1003598	2.83	3.63	5.02	4.89	3.7	2.95		
	PLACE1003602	1.8	4.24	6.36	4.37	3.54	2.68		
	PLACE1003605	17.43	21.72	45.86	94.65	95.6	91.55	**	+
15	PLACE1003611	2.34	5.18	6.07	5.65	7.14	6		
	PLACE1003618	0.67	7.39	2.09	1.58	2.4	1.32		
	PLACE1003625	1.78	10.41	2.75	3.33	5.48	2.8		
	PLACE1003626	8.77	15.99	17.14	10.87	14.46	13.19		
20	PLACE1003630	1.8	2.57	5.8	7.05	4.67	5.86		
	PLACE1003635	2.15	1.83	3.19	2.96	2.82	2.44		
	PLACE1003638	1.3	2.58	3	5.21	4.19	3.13		
	PLACE1003644	4.01	5.7	7.25	7.81	9.13	8.76	*	+
	PLACE1003654	2.56	6.14	4.04	3.54	6.96	6.4		
25	PLACE1003656	2.69	7.79	6.12	6.54	5.63	4.77		
	PLACE1003660	0.26	9.54	3.5	3.08	4.92	4.11		
	PLACE1003669	2.43	9.05	3.67	2.59	4.26	3.08		
	PLACE1003670	5.37	5.7	9.44	11.01	8.26	8.76		
	PLACE1003671	1.66	1.22	3.57	3.11	2.57	1.57		
30	PLACE1003697	7.27	7.99	9.8	8.23	6.06	6.42		
	PLACE1003704	3.12	3.97	5.17	5.96	7.25	5.97	*	+
	PLACE1003709	0.89	2.63	0.8	1.19	1.24	2.44		
	PLACE1003711	0.74	5.48	1.35	1.87	1.8	1.39		
	PLACE1003723	1.07	6.99	4.7	4.2	5.31	4.16		
35	PLACE1003724	3.31	10.74	9.1	9.11	11.79	10.49		
	PLACE1003737	2.14	2.21	4.72	3.35	3.1	3.29		
	PLACE1003738	1.06	1.94	3.13	3.96	3.92	3.41		
	PLACE1003742	2.25	3.58	5.71	6.81	6.18	2.85		
	PLACE1003744	6.13	8.86	14.6	16.21	17.96	19.13	*	+
40	PLACE1003758	0.85	4.55	0.96	2	1.46	1.16		
	PLACE1003760	13.44	18.68	27.23	31.82	20.52	22.79		
	PLACE1003762	1.45	4.97	3.7	3.77	3.78	3.49		
	PLACE1003765	1.18	5.23	3.45	2.01	3.1	2.11		
	PLACE1003768	0.36	1.14	1.36	1.45	2.75	1.07		
45	PLACE1003771	1.28	1.94	2.07	1.84	3.13	1.43		
	PLACE1003772	34.15	38.19	97.86	62.42	64.06	52.43		
	PLACE1003783	1.48	3.02	2.22	18.65	19.53	16.61	**	+
	PLACE1003784	0.69	3.92	0.87	2.09	2.19	2.68		
50	PLACE1003788	0.4	4.92	1.06	1.85	1.71	0.32		
	PLACE1003795	1.01	4.1	3.57	4.73	4.38	3.54		
	PLACE1003827	13.83	20.46	20.72	22.48	30.84	25.92		
	PLACE1003833	0.98	1.49	3.9	3.65	4.33	3.31		
	PLACE1003839	22.55	19.18	52.95	50.39	56.11	43.86		
55	PLACE1003845	6.09	6.88	11.72	24.98	19.99	10.6		
	PLACE1003850	3.16	4.84	7.19	5.45	5.95	6.39		



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	PLACE1003852	0.25	3.36	1.09	0.99	1.58	1.05		
	PLACE1003858	1.34	4.42	1.99	2.04	1.85	2.92		
	PLACE1003861	0.95	4.51	1.63	2.98	2.78	1.73		
5	PLACE1003864	0.94	5.5	2.74	2.88	3.86	2.69		
	PLACE1003870	3.84	3.4	13.2	10.71	16.12	12.03		
	PLACE1003885	1.33	1.42	1.59	3.07	3.76	2.38	*	+
	PLACE1003886	4.56	6.01	5.75	9.27	6.87	4.3		
10	PLACE1003888	0.75	3.79	1.96	2.87	3.42	2.68		
	PLACE1003892	4.93	6.91	20.79	17.21	22.33	14.87		
	PLACE1003900	2.27	5.92	7.17	6.34	9.75	6.6		
	PLACE1003902	1.91	7.39	5.25	5.43	8.07	6.29		
	PLACE1003903	0.42	5.07	2.94	2.55	3.5	2.59		
15	PLACE1003915	8.15	7.04	10.78	8.31	9.79	9.84		
	PLACE1003918	1.88	2.45	4.75	3.47	6.26	3.75		
	PLACE1003923	2.06	3.73	5.63	2.7	5.54	3.32		
	PLACE1003932	3.99	5.16	5.47	4.06	7.58	5.09		
	PLACE1003936	1.02	3.82	2.81	3.63	2.42	2.78		
20	PLACE1003966	3.11	7.43	7.76	4.89	7.32	4.21		
	PLACE1003968	1.68	5.68	5.94	3.33	4.26	4.57		
	PLACE1004018	25.49	33.73	48.16	32.56	40.53	28.62		
	PLACE1004020	8.91	10.18	13.26	11.42	18.03	24.15		
	PLACE1004028	0.41	2.55	1.3	1.38	1.23	1.91		
25	PLACE1004034	3.56	4.53	5.22	8.42	9.03	13.04	*	+
	PLACE1004042	17.25	20.19	68.35	79.51	93.32	79.44	*	+
	PLACE1004078	1.14	4.1	3.3	4.95	6.51	4.45		
	PLACE1004103	5.54	10.93	13.98	13.77	15.09	14.14		
30	PLACE1004104	5.94	12.29	27.78	24.18	34.98	29.71		
	PLACE1004113	1.37	3.7	3.28	2.75	3.27	1.29		
	PLACE1004114	1.12	2.55	2.23	2.84	2.49	2.93		
	PLACE1004118	1.58	3.52	2.09	2.74	3.64	2.5		
	PLACE1004128	4.4	6.84	5.66	6.61	8.13	9.01		
35	PLACE1004130	2.25	4.83	8.35	6.86	9.26	6.73		
	PLACE1004149	3.59	7.3	9.86	10.23	13.29	10.12		
	PLACE1004156	3.61	7.91	10.12	11.66	17.62	13.31		
	PLACE1004160	5.45	9.54	14.36	13.1	19.65	14.53		
	PLACE1004161	2.2	4.86	3.54	4.85	5.73	7.48		
40	PLACE1004166	5.61	5.81	9.91	8.3	8.66	11.2		
	PLACE1004168	3.35	4.97	3.73	4.73	6.65	6.79		
	PLACE1004170	0.78	3.28	1.93	2.98	3.42	2.76		
	PLACE1004178	0.83	5.23	2.37	2.4	2.59	2.36		
	PLACE1004183	0.89	7.99	4.41	3.53	4.32	4.84		
45	PLACE1004197	0.64	5.14	1.55	1.73	3.54	1.65		
	PLACE1004199	1.66	4.52	4.09	3.78	5.88	4.35		
	PLACE1004203	1.8	3.57	4.17	2.43	3.62	2.83		
	PLACE1004242	3.8	5.64	11.04	8.55	8.14	8.64		
	PLACE1004249	31.4	56.31	117.88	127.93	152.54	151.22	*	+
50	PLACE1004255	0.79	2.65	1.26	2.59	2.15	1.93		
	PLACE1004256	9.06	11.68	13.63	14.66	14.18	23.37		
	PLACE1004257	2.63	7.95	6.48	7.89	8.8	8.64		
	PLACE1004258	1.87	5.21	3.13	4.59	3.15	3.11		
	PLACE1004270	0.72	3.8	2.5	2.7	4.01	1.65		
55	PLACE1004272	1.34	3.68	3.73	3.86	5.38	6.15		

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	PLACE1004273	92.91	89.59	212.62	212.05	129.56	99.82		
	PLACE1004274	2.09	3.61	6.51	6.42	7.14	6.74		
5	PLACE1004277	2.3	4.4	5.76	6.45	7.7	6.04		
	PLACE1004279	0.54	3.39	2.23	3.16	2.64	2.02		
	PLACE1004282	2.43	8.25	6.62	4.22	5.56	4.49		
	PLACE1004284	4.59	11.31	7.84	7.38	8.16	7.15		
	PLACE1004289	1.28	7.85	2.46	3.06	3.63	2.1		
10	PLACE1004299	0.33	6.41	1.38	1.54	2.67	1.83		
	PLACE1004302	1.01	2.98	3.27	2.41	2.45	1.12		
	PLACE1004305	1.11	2.09	1.9	1.9	1.82	1.78		
	PLACE1004316	2.3	4.48	5.4	6.06	3.85	4.52		
	PLACE1004322	2.49	3.41	5.25	6.35	7.14	5.75	*	+
15	PLACE1004325	2.43	6.38	3.84	3.85	3.66	4		
	PLACE1004332	1.21	7.18	2.8	3.72	3.46	3.01		
	PLACE1004336	2.87	9.6	5.36	6.88	9.21	6.71		
	PLACE1004346	0.47	7.22	2.58	1.87	2.54	1.69		
	PLACE1004358	1.3	2.41	2.41	2.46	2.09	2.03		
20	PLACE1004376	11.07	10.15	23.35	19.16	17.04	16.46		
	PLACE1004384	0.65	3.46	1.46	1.92	2.48	2.1		
	PLACE1004385	1.4	2.89	1.69	3.52	1.88	2.67		
	PLACE1004388	1.79	5.73	4.27	3.44	4.87	3.04		
	PLACE1004405	2.16	8.39	4.42	13.36	14.48	16.74	**	+
25	PLACE1004407	5.05	13.12	13.37	11.2	16.24	11.85		
	PLACE1004424	0.37	5.78	0.85	1.7	1.81	1.58		
	PLACE1004425	1.14	1.94	3.57	3.28	3.27	3.44		
	PLACE1004427	1.96	3.31	4.56	4.67	4.22	3.24		
30	PLACE1004428	0.88	2.05	2.17	2.66	2.08	2.62		
	PLACE1004433	5.7	8.3	10.82	12.94	15.67	12.05	*	+
	PLACE1004435	0.72	4.17	1.43	1.95	1.9	2.15		
	PLACE1004437	4.05	7.68	14.2	11.07	13.01	12.37		
	PLACE1004441	7.82	11.68	34.06	30.75	43.19	26.41		
35	PLACE1004446	1.5	4.36	0.9	1.03	1.35	1.39		
	PLACE1004450	0.33	1.46	1.34	2.57	1.71	0.7		
	PLACE1004451	0.51	1.45	2.14	1.89	2.69	0.88		
	PLACE1004456	8.22	9.7	10.97	16.68	10.4	4.18		
	PLACE1004458	3.39	4.81	3.66	7.77	7.05	8.24	**	+
40	PLACE1004460	0.84	4.58	2.1	2.91	2.69	1.75		
	PLACE1004467	5.31	6.81	10.65	7.67	10.14	10.48		
	PLACE1004471	2.65	5.93	6.64	6.79	7.34	6.14		
	PLACE1004473	1.16	4.66	3.5	3.18	3.23	3.21		
	PLACE1004475	14.03	16.41	32.49	31.09	32.51	18.17		
45	PLACE1004482	8.37	6.7	10.79	10.04	9.76	9.15		
	PLACE1004491	0.39	2.51	1.49	1.19	2.68	1.3		
	PLACE1004492	61.52	74.8	127.94	129.92	127.64	123.82		
	PLACE1004506	10.71	14.35	14.4	8.45	11.13	10.03		
	PLACE1004507	2.9	7.37	5.09	7.15	6.87	6.18		
50	PLACE1004510	2.51	6.23	6.33	6.59	7.8	8.16		
	PLACE1004516	0.98	7.36	2.12	2.79	3.78	2.22		
	PLACE1004518	1.64	1.78	3.03	2.41	3.88	2.83		
	PLACE1004519	0.17	0.82	0.62	1.43	2.79	1.51	*	+
	PLACE1004520	6.08	8.09	10.06	7.44	9.11	2.52		
55	PLACE1004530	33.19	43.86	68.13	41.86	27.72	38.09		

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	PLACE1004545	1.13	3.83	2.12	3.03	3.31	3.65	
	PLACE1004547	5	7.61	7.82	8.66	11.2	10.28	
	PLACE1004548	1.69	6.73	4.43	6.93	8.48	6.5	
5	PLACE1004550	2.27	6.24	6.67	5.92	6.78	6.15	
	PLACE1004551	0.8	2.16	1.62	2.14	2.21	1.95	
	PLACE1004559	2.9	2.89	5.11	4.45	6.75	4.82	
	PLACE1004562	8.67	11.27	16.07	13.01	14.38	13.34	
	PLACE1004564	1.84	5.19	4.36	4.64	5.98	4.49	
10	PLACE1004604	1.69	4.21	9.88	2.49	4.34	1.97	
	PLACE1004611	2.73	5.87	4.89	3.86	4.17	3.99	
	PLACE1004629	9.42	15.75	19.92	23.93	30.49	29.01	* +
	PLACE1004630	16.66	20.82	35.1	16.76	23.04	19.17	
15	PLACE1004637	5.03	8.82	10.34	6.61	9.17	8.29	
	PLACE1004645	36.5	39.28	92.04	85.16	87.94	74.59	
	PLACE1004646	1.07	2.91	2.87	3.68	2.19	2.28	
	PLACE1004648	0.8	3.42	2.52	2.53	3.15	1.22	
	PLACE1004655	45.95	58.09	130.94	112.14	126.25	99.01	
20	PLACE1004658	2.4	7.34	6.31	6.64	8.37	6	
	PLACE1004664	1.26	4.83	1.3	3.02	2.65	1.89	
	PLACE1004672	2.32	6.79	8.02	6.3	7.51	7.14	
	PLACE1004674	9.4	11.97	14.7	8.3	9.75	15.25	
	PLACE1004681	1.97	3.84	5.62	5.05	5.69	4.39	
25	PLACE1004686	2.74	4.33	7.46	9.22	10.77	8.59	* +
	PLACE1004690	10.64	13.43	19.62	21.75	19.21	31.72	
	PLACE1004691	1.14	6.71	3.71	2.92	4.13	2.75	
	PLACE1004693	1.34	7.54	4.89	3.91	4.59	5.97	
	PLACE1004701	13.01	18.45	24.24	25.21	24.46	25.1	
30	PLACE1004705	1.29	3.33	2.27	1.8	1.96	1.47	
	PLACE1004708	37.69	46.37	80.19	41.34	39.66	50.98	
	PLACE1004716	6.37	8.81	11.08	4.22	12.55	14.26	
	PLACE1004722	1.31	3.05	2.6	2.26	3.28	2.51	
35	PLACE1004736	5.25	7.71	7.6	9.16	8.89	11.63	
	PLACE1004737	5.42	12.71	16.14	8.15	11.23	13.78	
	PLACE1004740	4.88	9.06	8.22	7.37	7.93	8.2	
	PLACE1004743	1.31	4.04	3.1	1.97	4	3.55	
	PLACE1004751	0.98	2.89	2.88	2.75	3.74	3.06	
40	PLACE1004757	3.45	4.34	10.53	8.4	9.6	7.22	
	PLACE1004761	6.41	7.32	12.59	9.99	10.44	9.72	
	PLACE1004773	1.05	2.34	1.7	1.94	2.31	2.72	
	PLACE1004775	0.35	3.26	1.37	1.29	2.14	1.07	
	PLACE1004777	2.1	7.57	2.97	3.68	4.25	4.4	
45	PLACE1004793	0.83	4.58	1.37	1.9	2.06	1.25	
	PLACE1004796	6.65	8.7	13.08	7.79	8.57	7.88	
	PLACE1004804	0.99	4.46	3.25	2.44	2.38	3.22	
	PLACE1004813	4.55	7.11	9.84	6.45	5.19	5.45	
	PLACE1004814	7.16	11.76	17.62	15.83	11.39	10.1	
50	PLACE1004815	0.7	2.81	2.43	3.12	2.61	3.44	
	PLACE1004816	1.16	2.63	2.04	2.36	2.26	1.84	
	PLACE1004824	3.25	7.37	5.27	8.1	9.13	8.85	
	PLACE1004827	1.4	10.89	3.17	2.57	3.05	1.3	
	PLACE1004836	1.72	12.95	4.26	6.25	7.99	4.49	
55	PLACE1004838	1.35	8.81	2.2	2.49	2.34	1.68	

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	PLACE1004840	1.59	2.06	2.21	1.85	2.08	1.37		
	PLACE1004842	0.86	1.98	1.89	1.98	1.78	2.33		
	PLACE1004850	0.81	2.35	1.63	1.83	2.76	2.36		
5	PLACE1004868	0.81	2.97	2.04	1.62	2.23	2		
	PLACE1004885	1.5	7.09	3.51	3.4	6.03	4.77		
	PLACE1004886	1.87	8.53	2.76	3.33	5.12	4.93		
	PLACE1004887	18.14	34.01	58.51	36.9	38.66	30.33		
10	PLACE1004896	8.39	14.15	15.4	9.39	11.14	14.03		
	PLACE1004900	1.75	2.7	6.69	5.66	5.74	4.44		
	PLACE1004902	5.42	6.25	9.27	6.39	4.2	3.6		
	PLACE1004904	1.7	4.66	2.52	6.49	4.78	3.03		
	PLACE1004911	0.69	2.5	1.12	5.95	4.82	6.09	**	+
15	PLACE1004913	3.63	5.72	7.38	4.49	5.45	4.79		
	PLACE1004918	1.3	6.69	2.05	2.39	3.24	2.64		
	PLACE1004930	2.74	8.84	5.93	10.63	16.57	14.71	*	+
	PLACE1004934	1.14	4.3	3.34	2.97	2.03	2.5		
	PLACE1004937	2.1	4.03	4.91	2.74	3.59	2.36		
20	PLACE1004949	4.32	4.98	7.67	8.53	8.48	6.04		
	PLACE1004969	0.74	1.74	1.99	1.39	2.34	1.4		
	PLACE1004970	0.45	2.18	1.2	1.43	1.31	1.01		
	PLACE1004972	1.63	6.56	2.69	5.66	3.17	4.76		
25	PLACE1004974	1.27	5.21	4.2	5.6	5.7	5.62		
	PLACE1004975	0.59	2.84	1.11	1.94	1.98	1.24		
	PLACE1004979	1.58	4.06	4.26	4.91	5.69	4.75		
	PLACE1004982	5.66	6.45	9.74	10.03	10.67	5.65		
	PLACE1004985	1.4	1.47	1.46	2.5	2.17	1.2		
30	PLACE1005003	2.85	4.22	6	6.05	6.37	5.78		
	PLACE1005004	0.47	3.36	0.92	1.5	0.73	0.85		
	PLACE1005005	3.35	6.9	5.32	6.67	9.65	7.17		
	PLACE1005011	6.03	11.12	35.8	37.66	56.97	36.62		
	PLACE1005026	0.79	4.18	2.29	2.44	2.49	2.16		
35	PLACE1005027	2.46	6.72	6.69	5.36	6.92	5.68		
	PLACE1005031	1.21	1.47	3.69	5.72	7.1	4.6	*	+
	PLACE1005036	2.27	3.6	6.83	9.08	8.91	7.53	*	+
	PLACE1005041	2.5	2.84	2.84	5.05	4.41	3.25	*	+
	PLACE1005046	2.23	4.11	4.56	6.04	3.92	4.33		
40	PLACE1005047	0.23	3.19	2.6	1.43	1.23	2.1		
	PLACE1005052	4.24	8.53	6.36	8.08	8.15	8.1		
	PLACE1005055	2.54	7.45	4.66	7.2	6.45	5.62		
	PLACE1005066	4.33	8.26	7.58	12.9	14.14	16.49	**	+
	PLACE1005077	1.17	0.68	1.2	2.1	2.43	1.54	*	+
45	PLACE1005085	1.41	1.97	3.06	3.34	4.14	3.45		
	PLACE1005086	1.93	3.77	5.17	5.62	7.78	4.79		
	PLACE1005088	24.66	32.47	46.03	43.45	31.47	27.46		
	PLACE1005089	1.57	4.78	3.15	2.52	3.67	3.14		
	PLACE1005101	3.37	8.11	5.46	6.11	8.96	6.39		
50	PLACE1005102	2.56	7.14	5.01	4.11	5.51	3.8		
	PLACE1005108	2	6.08	5.87	6.58	6.19	5.09		
	PLACE1005110	1.34	1.89	3.08	1.75	2.75	2.15		
	PLACE1005111	1.31	1.34	1.23	1.45	2.17	1.54		
	PLACE1005123	26.23	26.21	47.58	34.26	49.34	34.98		
55	PLACE1005124	3.2	4.66	4.18	4.2	6.91	5.44		

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	PLACE1005128	9.54	8.89	18.22	16.37	16.36	16.13		
	PLACE1005130	2.65	6.57	5.54	2.84	4.98	3.58		
5	PLACE1005141	6.3	9.92	11.25	16.15	20.75	18.95	**	+
	PLACE1005146	1.3	2.71	3.03	2.17	2.53	2.29		
	PLACE1005152	1.85	3.9	4.56	4.13	4.23	4.79		
	PLACE1005157	2.66	5.19	5.3	4.38	4.09	7.01		
	PLACE1005162	2.79	3.72	9.31	6.57	7.45	7.1		
10	PLACE1005170	17.34	18.92	29.76	21.38	18.18	23.73		
	PLACE1005176	0.57	5.6	1.7	2.33	2.47	1.94		
	PLACE1005181	0.53	5.14	0.96	0.89	1.36	0.37		
	PLACE1005184	4.06	9.09	10.4	8.97	12.82	11.26		
	PLACE1005186	3.5	3.41	8.56	8.05	5.79	5.73		
15	PLACE1005187	2.85	4	4.13	6.1	4.99	4.25		
	PLACE1005189	6.12	7.71	5.34	10.84	10.65	12.22	**	+
	PLACE1005193	1.48	3.78	1.71	3.84	2.91	2.61		
	PLACE1005200	1.35	4.68	2.61	2.47	3.75	3.1		
	PLACE1005206	2.43	6.48	4.26	3.35	3.95	2.95		
20	PLACE1005216	1.53	5.46	4.44	5.6	6.51	4.12		
	PLACE1005223	1.43	6.21	5	4.38	5.66	3.27		
	PLACE1005225	1.36	3.01	3.49	3.33	3.32	4.65		
	PLACE1005232	1.86	3.31	4.87	5.63	6.19	3.88		
	PLACE1005239	1.06	4.3	2.32	2.84	2.86	2.41		
25	PLACE1005243	4.35	7.32	5.41	8.48	7.49	10.75		
	PLACE1005250	4.24	10.31	7.98	4.38	5.9	8.88		
	PLACE1005261	3.21	7.43	4.74	4.78	5.82	3.51		
	PLACE1005266	1.05	4.47	2.82	2.28	4.43	2.76		
	PLACE1005271	4.66	5.31	8.79	5.87	11.16	7.95		
30	PLACE1005277	2.06	3.48	2.35	2.62	1.98	2.64		
	PLACE1005287	3.63	4.31	5.87	2.98	5.06	6.91		
	PLACE1005299	24.16	22.75	48.29	35.17	24.24	41.06		
	PLACE1005305	6.81	8.46	11.13	10.67	11.85	16.25		
35	PLACE1005307	1.59	5.44	4.14	3.15	5.42	4.84		
	PLACE1005308	2.41	4.96	3.95	5.32	5.99	5.79		
	PLACE1005313	1.08	3.83	1.6	1.8	2.05	1.8		
	PLACE1005320	1.36	3.65	3.34	3.39	4.05	2.26		
	PLACE1005327	10.78	8.74	16.8	10.36	7.95	4.43		
40	PLACE1005331	2.28	4.92	5.28	4.66	4.97	3.33		
	PLACE1005335	1.53	3.8	2.24	2.03	3.22	2.42		
	PLACE1005336	9.12	12.58	16.58	16.39	16.99	20.15		
	PLACE1005351	2.62	8.18	10.17	9.28	8.66	9.52		
	PLACE1005366	2.04	6.93	3	2.99	3.71	4.23		
45	PLACE1005373	1.77	6.34	4.44	3.91	5.36	3.37		
	PLACE1005374	3.29	9.47	11.4	7.35	10.22	12.41		
	PLACE1005383	8.16	7.54	12.81	7.21	5.93	4.03		
	PLACE1005388	0.33	2.04	1.56	1.92	3.67	2.2		
	PLACE1005409	2.97	5.02	4.99	3.9	4.23	2.97		
50	PLACE1005410	12.41	16.44	18.89	24.38	20.98	27.1	*	+
	PLACE1005426	5.16	7.48	9.06	5.51	7.67	5.45		
	PLACE1005431	12.6	15.65	22.53	19.64	26.25	23.75		
	PLACE1005453	1.4	10.38	3.93	4.85	4.45	3.28		
	PLACE1005467	3.09	11.87	7	5.57	11.63	7.28		
55	PLACE1005471	1.6	1.94	1.66	2.29	1.52	1.28		

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	PLACE1005476	0.42	1.73	1.24	1.6	1.57	1.46	
	PLACE1005477	1.58	2.26	2.51	3	2.93	2.74	
5	PLACE1005480	0.77	2.01	1.86	1.93	1.4	0.53	
	PLACE1005481	0.44	4.81	2.3	2.77	3.62	2.44	
	PLACE1005494	0.27	6.66	1.68	1.21	1.73	1.06	
	PLACE1005495	3.86	12.83	8.31	6.85	9.25	7.62	
	PLACE1005497	2.27	7.72	3.95	4.24	5.68	5.91	
10	PLACE1005499	5.71	5.86	11.07	10.82	7.9	6.49	
	PLACE1005502	1.59	2.87	3.43	4.07	3.45	1.49	
	PLACE1005513	1.77	4.14	3.35	1.86	2.85	1.98	
	PLACE1005515	2.89	4.76	4.22	4.58	5.29	3.78	
	PLACE1005519	1.04	4.53	3.29	2.85	2.85	2.83	
15	PLACE1005526	0.58	5.55	1.38	1.3	1.59	0.71	
	PLACE1005528	2.08	7.71	5.57	5.94	7.12	5.33	
	PLACE1005530	2.16	7.09	4.32	5.17	8.23	4.67	
	PLACE1005536	1.74	1	2.74	3.12	2.43	2.88	
	PLACE1005539	10.1	11.64	23.77	8.65	8.66	5.22	
20	PLACE1005543	1.7	3.57	5.62	3.54	4.32	2.57	
	PLACE1005544	0.86	3.26	3.15	2.49	2.68	2.27	
	PLACE1005550	4.32	7.61	7.85	10.16	7.25	6.86	
	PLACE1005554	1.15	5.47	2.67	2.17	2.17	1.17	
	PLACE1005557	1.76	7.21	4.95	8.22	7.64	7.7	
25	PLACE1005563	0.51	4	1.89	1.45	2.07	1.06	
	PLACE1005569	0.6	0.5	1.56	1.59	1.81	1.09	
	PLACE1005574	1.07	1.88	2.49	2.48	4.43	2.22	
	PLACE1005584	1.3	2.68	3.91	3.91	5.58	3.03	
30	PLACE1005590	4.28	5.14	8.4	9.87	10.73	8.02	
	PLACE1005595	3.08	4.03	2.89	3.65	3.81	3.89	
	PLACE1005601	2	5.66	4.22	3.77	4	4.02	
	PLACE1005603	1.08	4.9	1.04	2.49	0.95	1.94	
	PLACE1005604	1.2	6.71	2.42	3.6	4.2	3.46	
35	PLACE1005611	2.22	2.3	3.98	5.15	5.65	2.89	
	PLACE1005622	0.65	1.71	1.98	2.94	3.88	1.26	
	PLACE1005623	1.42	3.08	3.27	3.71	3.65	1.61	
	PLACE1005630	3.31	5.81	7.75	87.83	72.15	89.12	** +
	PLACE1005639	0.75	4.36	1.28	1.66	2.02	1.18	
40	PLACE1005646	2.13	5.41	4.31	5.4	5.08	2.55	
	PLACE1005647	2.77	9.69	6.72	7.34	9.11	6.25	
	PLACE1005648	3	8.11	9.21	8.34	10.59	8.22	
	PLACE1005653	1.99	1.43	2.74	2.74	2.13	2.67	
	PLACE1005656	0.92	2.48	2.24	1.68	2.78	1.58	
45	PLACE1005659	0.87	2.64	1.01	1.62	1.84	1.32	
	PLACE1005660	3.91	8.03	5.77	8.87	8.88	8.34	
	PLACE1005664	2.69	6.57	6.14	3.39	4.27	3.19	
	PLACE1005666	0.89	5.91	3.55	4.63	4.93	3.97	
50	PLACE1005669	4.46	10.41	11.39	11.64	13.9	14.6	
	PLACE1005682	1.94	5.27	4.49	6.2	5.2	5.47	
	PLACE1005698	0.6	2.7	2.92	2.01	2.67	2.38	
	PLACE1005708	25.32	34.08	53.46	53.89	59.98	53.76	
	PLACE1005725	3.25	3.75	6.41	5.64	5.82	7.29	
55	PLACE1005727	2.97	4.54	4.15	3.9	3.49	4	
	PLACE1005730	0.77	4.29	3.26	1.1	1.54	1.28	

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	PLACE1005736	5.37	7.55	5.73	9.25	12.55	10.19	*	+
	PLACE1005739	0.81	4.96	1.38	2.46	3.17	1.74		
	PLACE1005745	8.03	7.11	11.52	11.98	6.97	11.44		
5	PLACE1005752	1.31	3.15	2.96	2.55	2.24	1.25		
	PLACE1005755	0.8	2.79	3.02	1.72	3.28	2.27		
	PLACE1005756	10.79	12.06	17.2	18.22	19.3	21.47	*	+
	PLACE1005760	10.22	15.24	68.06	49.69	68.81	53.09		
10	PLACE1005763	1.47	7.04	3.58	3.79	4.63	3.02		
	PLACE1005768	1.25	5.63	3.69	4.58	5.13	4.19		
	PLACE1005771	5.71	13.63	13.7	11.28	17.49	17.27		
	PLACE1005783	1.82	2.44	3.64	3.05	3.71	3.47		
	PLACE1005799	4.79	5.25	8.37	6.12	8.78	8.62		
15	PLACE1005802	1.07	3.78	3.64	2.7	3.64	1.96		
	PLACE1005803	3.06	6.15	4.78	5.6	4.94	7.36		
	PLACE1005804	0.92	8.41	1.33	2	1.91	2.44		
	PLACE1005813	17.23	18.71	78.06	70.01	94.17	74.89		
	PLACE1005815	1.43	5.6	4.38	3.8	5.01	4.1		
20	PLACE1005828	2.11	3.62	4.42	5.34	6.24	3.56		
	PLACE1005833	119.17	92.82	182.22	122	114.37	107.96		
	PLACE1005834	2.04	4.33	3.95	3.55	3.56	2.56		
	PLACE1005835	22.7	19.1	51.52	72.32	60.34	68.56	*	+
	PLACE1005836	2.39	4.21	4.97	2.61	3.83	2.55		
25	PLACE1005845	0.97	5.42	2.66	2.67	3.05	3.65		
	PLACE1005850	1.82	3.91	3.04	2.84	2.85	2.15		
	PLACE1005851	1.03	3.44	1.46	1.2	2.01	1.11		
	PLACE1005856	0.92	4.01	2.42	2.24	3.37	3.37		
	PLACE1005875	1.78	3.89	4.77	3.3	3.48	3.17		
30	PLACE1005876	1.33	3.99	4.76	6.87	6.34	6.9	*	+
	PLACE1005878	1.3	2.67	2.08	3.54	4.46	2.79		
	PLACE1005880	2.36	4.09	4.31	4.16	3.07	3.45		
	PLACE1005884	1.6	4.87	1.89	2.48	2.21	2.73		
	PLACE1005890	1.9	9.57	3.7	2.26	3.09	1.88		
35	PLACE1005898	3.29	10.87	5.34	7.36	8.12	6.36		
	PLACE1005913	1.46	9.31	8.05	4.99	6.47	4.33		
	PLACE1005921	0.99	1.92	2.03	1.49	2.22	0.79		
	PLACE1005923	0.74	1.61	1.17	1.47	2.42	1.43		
40	PLACE1005925	0.83	2.67	3.18	2.19	2.14	1.68		
	PLACE1005927	1.26	2.49	1.93	1.95	2.56	2.3		
	PLACE1005932	2.04	5.66	2.44	2.53	2.32	2.52		
	PLACE1005934	0.88	7.91	3.16	3.9	5.61	4.19		
	PLACE1005936	1.31	8.96	3.02	2.02	2.84	2.3		
45	PLACE1005939	54.61	68.58	111.22	157.61	194.58	212.18	**	+
	PLACE1005951	2.36	3.39	4.98	5.56	4.48	2.35		
	PLACE1005953	1.5	1.64	2.64	2.59	2.43	3.03		
	PLACE1005955	1.64	2.01	3.8	4.07	3.43	2.55		
	PLACE1005966	0.76	3.42	1.69	1.75	2	2.19		
50	PLACE1005968	1.52	4.96	3.2	4.71	5.15	6.12		
	PLACE1005975	2.58	7.11	5.42	6.18	7.01	6.49		
	PLACE1005990	0.7	7.7	1.54	2.1	1.87	0.88		
	PLACE1005997	88.15	118.52	196.48	189.6	226.97	172.1		
	PLACE1006002	3.38	3.97	8.87	8.4	7.71	9.18		
55	PLACE1006003	1.55	3.02	4.83	5.09	4.44	5.33		

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	PLACE1006011	1.85	3.63	3.46	4.48	2.68	1.91		
	PLACE1006017	0.84	2.74	2.81	3.4	3.4	3.58		
	PLACE1006037	2.99	7.05	2.48	6.14	3.64	4.29		
5	PLACE1006040	2.2	7.87	3.97	6.64	6.9	7.77		
	PLACE1006063	0.94	4.64	2.59	2.11	3.15	2.25		
	PLACE1006071	3.06	6.52	4.97	5.36	4.03	4.47		
	PLACE1006073	2.74	3.53	6.43	7.19	6.81	6.93		
10	PLACE1006074	1.4	2.22	3.34	2.62	3.23	1.69		
	PLACE1006076	1.36	2.51	2.98	3.15	2.47	2.75		
	PLACE1006079	1.38	4.32	1.78	2.1	1.1	1.11		
	PLACE1006093	0.49	3.76	1	3.56	3.85	1.83		
	PLACE1006116	2.99	6.44	4.04	5.28	5.01	4.91		
15	PLACE1006119	3.15	6.81	7.07	9.22	10.4	8.03		
	PLACE1006129	2.12	5.6	3.98	6.59	7.62	5.65		
	PLACE1006139	3.44	2.98	6.03	7.77	8.85	5.58		
	PLACE1006143	0.5	1.48	1.87	3.18	4.13	3.17	*	+
	PLACE1006157	1.55	2.54	4.82	2.96	3.9	2.44		
20	PLACE1006159	0.69	3.61	0.94	2.68	1.98	1.04		
	PLACE1006164	0.35	3.18	1.37	1.73	1.85	1.21		
	PLACE1006167	2.18	6.5	3.37	3.95	4.52	3.13		
	PLACE1006170	2.79	6.09	6.09	4.34	5.31	3.68		
	PLACE1006181	2.75	7.34	2.84	5.8	5.51	5.22		
25	PLACE1006187	0.76	1.3	2.15	2.01	2.41	1.48		
	PLACE1006195	0.11	1.24	1.73	1.93	1.93	0.87		
	PLACE1006196	1.8	4.01	4.15	4.32	5.77	2.19		
	PLACE1006197	2.12	5.6	5.24	4	3.47	3.39		
30	PLACE1006198	0.27	3.68	1.21	0.84	1.63	0.5		
	PLACE1006205	0.89	5.59	0.99	2.43	2.18	1.28		
	PLACE1006208	7.28	13.32	13.46	14.09	14.99	12.5		
	PLACE1006211	2.6	8.05	7.92	6.07	9.08	9.35		
	PLACE1006219	6.77	5.77	8.94	14.88	22.25	15.35	*	+
35	PLACE1006223	1.55	1.46	3.19	1.39	3	1.64		
	PLACE1006225	0.56	2.27	1.3	1.04	2.3	0.99		
	PLACE1006236	1.53	3.2	2.92	3.06	5.01	2.29		
	PLACE1006239	0.67	3.62	1.97	2.61	3.66	3.41		
	PLACE1006245	3.86	7.13	5.45	4.43	7.44	3.28		
40	PLACE1006246	1.66	6.56	6.19	5.59	7.66	6.33		
	PLACE1006248	1.58	4.47	5.6	2.77	3.1	2.82		
	PLACE1006262	0.93	2.24	1.49	2.08	1.61	1.4		
	PLACE1006269	2.28	4.71	3.42	2.06	2.47	2.33		
	PLACE1006275	1.6	3.57	3.37	4.12	3.68	3.53		
45	PLACE1006277	1.01	2.42	1.4	1.79	3.01	0.88		
	PLACE1006288	9.32	13.59	22.49	26.85	18.4	25.21		
	PLACE1006290	1.79	6.81	5.99	8.87	7.56	9.13		
	PLACE1006298	1.93	5.52	2.47	3.87	5.08	4.55		
	PLACE1006311	0.65	3.38	1.75	225.97	161.43	251.12	**	+
50	PLACE1006318	3.52	4.03	4.17	4.04	3.17	4.01		
	PLACE1006325	5.43	6.73	6.31	8.09	8.38	8.08	**	+
	PLACE1006331	1.87	3.36	3.21	4.44	3.59	2.56		
	PLACE1006335	1.76	3.64	2.55	4.45	2.98	2.92		
	PLACE1006357	0.27	4.51	1.59	1.7	1.49	1.2		
55	PLACE1006360	1.1	5.11	1.79	2.46	2.74	2.62		



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	PLACE1006364	4.51	8.06	7.29	7.37	9.19	5.75		
	PLACE1006365	1.68	4.65	1.97	1.8	2.12	0.97		
	PLACE1006368	1.53	3.11	2.57	3.01	3.04	4.27		
5	PLACE1006371	1.38	3.2	1.46	1.68	3.01	1.67		
	PLACE1006373	2.21	5.21	5.75	7.83	8.02	7.56	*	+
	PLACE1006382	0.9	4.67	2.81	3.3	1.92	2.95		
	PLACE1006385	1.59	6.33	1.86	2.68	2.59	2.71		
10	PLACE1006391	1.19	5	1.95	1.96	2.79	1.63		
	PLACE1006412	1.88	5.53	5.92	7.07	9.93	5.27		
	PLACE1006414	0.63	3.42	0.95	1.22	1.87	1.6		
	PLACE1006419	7.79	9.8	11.93	5.19	7.29	5.32	*	-
	PLACE1006438	0.99	6.07	3.42	3.29	4.56	5.14		
15	PLACE1006443	2.05	5.01	5.12	5.01	5.31	6.44		
	PLACE1006445	0.84	5.76	3.65	3.53	3.27	3.55		
	PLACE1006447	1.34	5.81	3.28	2.95	3.26	3.96		
	PLACE1006466	0.75	4.38	1.35	1.49	1.66	1.08		
	PLACE1006469	0.67	4.66	2.31	1.65	2.26	1.67		
20	PLACE1006470	2.47	3.71	3.74	5.25	7.02	4.35		
	PLACE1006472	24.4	23.44	52.17	26.23	28.52	9.36		
	PLACE1006476	2.52	4.31	8.67	6.21	7.23	5.93		
	PLACE1006482	1.64	3.35	4.43	4.25	4.67	4.98		
	PLACE1006488	14.12	19.42	32.69	40.76	34.77	41.4	*	+
25	PLACE1006492	2.03	6.41	4.38	4.04	4.98	3.02		
	PLACE1006506	1.78	6.67	4.04	4.41	5.71	4.17		
	PLACE1006515	1.65	5.7	3.08	3.19	2.84	4.08		
	PLACE1006516	1.1	7.32	7.05	4.89	5.69	7.28		
30	PLACE1006520	1.02	2.74	2.12	1.19	3	1.54		
	PLACE1006521	2.4	3.54	6.38	6.49	6.86	5.08		
	PLACE1006529	5.96	7.35	6.96	10.56	8.2	7.93		
	PLACE1006531	1.01	4.31	3.33	1.84	2.05	2.43		
	PLACE1006534	1.68	6.04	2.59	3.01	3.86	3.19		
35	PLACE1006540	2.68	9.7	7.77	8.71	11.21	4.46		
	PLACE1006549	0.6	9.45	2.09	1.6	2.28	1.65		
	PLACE1006550	1.76	8.82	4.07	2.77	2.94	4.14		
	PLACE1006552	1.3	2.48	2.14	1.97	1.3	0.81		
	PLACE1006557	2.38	4.01	3.79	2.84	2.51	2.45		
40	PLACE1006563	2.49	3.44	5.7	4.23	4.15	4.3		
	PLACE1006579	1.53	7.5	4.82	4.88	5.38	5.78		
	PLACE1006594	236.53	241.11	397.64	122.37	278.58	324.29		
	PLACE1006598	0.72	8.53	2.4	1.53	1.58	2.07		
	PLACE1006607	1.47	7.69	4.18	3.45	5.86	4.29		
45	PLACE1006610	9.46	13.73	38.26	27.65	32.76	22.64		
	PLACE1006615	6.22	9.09	18.78	20.25	15.74	15.86		
	PLACE1006617	0.91	1.54	2.66	1.87	2.49	2.09		
	PLACE1006618	5.42	8.01	9.24	5.33	8.59	5.76		
	PLACE1006626	1.53	4.11	1.3	2.47	2.78	1.16		
50	PLACE1006629	0.99	5.05	1.36	2.22	2.56	1.76		
	PLACE1006637	1.29	6.54	3.97	3.77	4.23	4.87		
	PLACE1006640	0.59	5.14	1.17	0.85	2.54	0.94		
	PLACE1006644	1.66	4.46	2.12	2.79	2.49	2.39		
	PLACE1006657	1.28	2.09	2.31	4.55	3.09	2.19		
55	PLACE1006673	2.29	4.73	10.34	11.06	10.89	6.45		

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	PLACE1006678	2.54	2.98	1.44	1.37	1.96	1.39		
	PLACE1006682	3.5	5.93	2.58	15.44	20.96	23.99	**	+
	PLACE1006684	1.12	4.8	1.81	1.64	2.54	1.65		
5	PLACE1006698	1.54	5.86	4.52	2.15	3.57	1.9		
	PLACE1006704	1.81	5.41	2.71	2.93	2.92	2.97		
	PLACE1006708	1.69	5.07	3.49	3.46	4.11	3.7		
	PLACE1006711	14.21	16.18	29.77	24.34	26.25	22.42		
	PLACE1006714	2.27	3.26	4.74	4.57	5.23	3.53		
10	PLACE1006716	1.51	2.75	3.7	6	7.05	3.99		
	PLACE1006731	1.65	3.77	2.83	2.71	4	3.09		
	PLACE1006754	0.43	3.94	1.73	1.8	1.81	0.99		
	PLACE1006760	7.56	10.98	10.08	8.58	8.89	11.31		
15	PLACE1006779	1.44	4.12	2.88	3.19	3.79	2.97		
	PLACE1006782	0.44	5.17	2.42	2.95	1.57	1.15		
	PLACE1006783	9.34	11.46	18.65	157.98	223.05	66.46	*	+
	PLACE1006786	3.31	4.08	6.07	5.9	6.24	3.34		
	PLACE1006792	1.61	3.31	5.38	5.66	3.33	4.18		
20	PLACE1006795	0.89	2.43	0.74	0.81	1.27	1.01		
	PLACE1006800	1.62	4.94	2.53	4.7	4.56	3.93		
	PLACE1006805	3.94	7.79	5.5	10.83	9.8	8.79	*	+
	PLACE1006809	3.55	5.7	5.94	9.58	10.61	8.97	**	+
	PLACE1006815	1.7	7.57	4.1	5.12	5.23	5.8		
25	PLACE1006819	0.33	0.88	0.95	0.89	1.76	0.63		
	PLACE1006820	2.35	2.01	4.91	4.84	6.72	4.18		
	PLACE1006826	2.28	6.22	4.84	7.68	7.62	5.58		
	PLACE1006829	3.76	5.51	6.54	9.49	8.66	8.69	*	+
	PLACE1006853	1.2	4.21	1.97	2.25	2.93	2.88		
30	PLACE1006860	1	4.29	1.62	1.61	2.1	1		
	PLACE1006867	5.65	9.36	11.34	7.04	8.33	7.63		
	PLACE1006875	1.15	6.19	5.66	4.84	4.53	4.63		
	PLACE1006878	1.59	2.84	3.09	2.99	3.22	2.39		
35	PLACE1006883	3.21	5.08	6.78	6.83	7.38	6.19		
	PLACE1006898	1.67	4.23	3.67	3.54	4.77	4.59		
	PLACE1006901	2.59	4.75	4.03	3.71	3.28	4.14		
	PLACE1006904	0.91	3.59	2.7	3.26	2.92	2.04		
	PLACE1006917	3.63	7.13	6.1	5.8	7.21	7.03		
40	PLACE1006932	0.54	5.85	1.29	0.92	1.34	1.19		
	PLACE1006935	1.3	5.46	2.54	1.59	4.03	1.6		
	PLACE1006956	0.92	2.55	3.4	2.55	2.41	2.09		
	PLACE1006958	0.78	2.41	1.35	1.76	4.2	3.39		
	PLACE1006959	4.97	8.48	9.98	11.46	9.58	13.62		
45	PLACE1006961	8.03	9.85	14.42	13.73	11.57	14.2		
	PLACE1006962	2.97	7.44	6.56	5.04	7.26	6.22		
	PLACE1006966	2.02	6.94	3.46	3.15	3.89	2.89		
	PLACE1006979	0.95	4.44	2.03	1.46	2.64	1.77		
	PLACE1006989	2.19	5.05	3.02	3.27	3.9	5.06		
50	PLACE1007001	4.98	6.79	10.71	4.03	7.43	7.38		
	PLACE1007014	1.37	3.03	3.45	1.79	2.18	2.2		
	PLACE1007021	0.74	3.03	2.11	0.75	2.2	1.73		
	PLACE1007026	2.1	9.23	3.93	4.15	4.27	5.42		
55	PLACE1007028	4.12	8.5	10.56	7.89	8.34	9.35		
	PLACE1007038	237.33	267.91	446.14	406.27	622.67	671.17		

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	PLACE1007040	1.55	3.14	2.85	1.57	3.31	2.45		
	PLACE1007045	1.08	3.74	2.85	2.9	5.03	2.74		
	PLACE1007048	147.06	149.67	259.53	121.61	211.26	109.43		
5	PLACE1007053	4.9	6.69	10	3.59	4.91	4.71		
	PLACE1007068	7.56	10.33	62.76	39.52	45.9	36.69		
	PLACE1007070	5.97	10.85	10.28	8.65	9.6	14.3		
	PLACE1007076	8.22	14.4	14.19	16.53	23.62	24.67	*	+
10	PLACE1007077	2.65	6.45	4.01	5.2	5.28	5.43		
	PLACE1007081	0.36	4.47	1.94	1.92	1.92	1.37		
	PLACE1007082	1.23	4.66	4.95	4.32	4.5	3.99		
	PLACE1007092	2.49	4.12	7.26	4.77	5.22	4.34		
	PLACE1007096	0.72	2.19	0.74	1.35	1.63	0.97		
15	PLACE1007097	0.54	2.49	1.35	1.61	1.28	1.04		
	PLACE1007099	1.58	4.66	2.56	2.77	3.64	3.72		
	PLACE1007105	1.18	6.51	3.44	2.65	4.13	2.21		
	PLACE1007108	3.55	13.02	7.41	5.03	6.87	5.75		
20	PLACE1007111	1.33	9.51	1.52	1.74	2.37	1.52		
	PLACE1007112	1.23	7.26	1.79	2.09	3.12	2.36		
	PLACE1007130	0.54	2.02	1.92	0.87	1.47	0.33		
	PLACE1007132	1.46	3.32	4.63	3.58	3.38	2.88		
	PLACE1007140	0.61	2.58	2.41	1.98	1.98	1.32		
25	PLACE1007143	2.79	6.32	4.62	4.9	5.34	5.33		
	PLACE1007169	2.21	8.59	3.46	5.44	8.46	7.99		
	PLACE1007178	0.82	8.66	2.48	3.28	6.28	4.1		
	PLACE1007190	3.31	10.9	6.7	10.51	13.57	11.14		
	PLACE1007201	0.81	5.82	1.41	1.72	3.04	2.51		
30	PLACE1007202	37.76	34.95	76.28	58.23	34.42	37.86		
	PLACE1007226	2.01	2.39	2.73	1.89	3.14	2.29		
	PLACE1007238	1.64	3.07	1.83	2.39	2.73	2.2		
	PLACE1007239	1.81	3.68	2.99	1.76	2.72	2.44		
	PLACE1007242	0.61	5.18	1.87	1.54	1.14	1.67		
35	PLACE1007243	2.21	7.36	2.29	2.24	3.27	3.31		
	PLACE1007247	0.36	6.17	1.71	1.11	1.36	1.34		
	PLACE1007257	1.67	5.33	3.34	3.3	5.27	4.25		
	PLACE1007274	1.46	2.18	4.43	4.38	4.03	4.06		
	PLACE1007276	0.93	2.02	1.1	2.13	2.1	1.74		
40	PLACE1007282	2.51	4.2	5.72	4.28	3.62	4.66		
	PLACE1007286	2.97	4.8	7.85	10.14	12.47	8.79	*	+
	PLACE1007296	10.55	19.45	24.46	31.43	17.57	27.05		
	PLACE1007301	0.65	5.17	1.55	1.19	1.54	1.11		
45	PLACE1007314	3.11	6.61	8.64	7.98	8.96	10.24		
	PLACE1007317	1.19	3.34	1.27	1.88	1.62	1.79		
	PLACE1007329	0.89	0.73	1.78	2.38	2.35	2.09	*	+
	PLACE1007338	3.96	6.47	9.58	11.59	8.93	2.32		
	PLACE1007342	0.71	1.8	1.3	1.1	1.1	0.7		
50	PLACE1007345	1.72	4.57	2.54	2.72	3.6	3.29		
	PLACE1007346	1.43	4.61	3.89	5.77	4.53	4.1		
	PLACE1007359	0.74	4.55	2.16	2.59	2.44	3.53		
	PLACE1007367	4.53	8.63	15.16	12.49	13.49	11.75		
	PLACE1007375	0.36	3.24	2.02	1.75	2.56	1.59		
55	PLACE1007377	1.49	2.01	3.18	3.29	3.96	2.36		
	PLACE1007386	1.55	1.75	1.47	2.37	1.68	1.36		

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	PLACE1007392	1.57	2.99	2.49	2.79	4.48	3.51	
	PLACE1007402	2.41	5.66	3.08	1.52	2.91	1.8	
5	PLACE1007409	1.05	4.57	1.04	2.51	2.68	2.02	
	PLACE1007416	3.45	6.97	6.5	7.05	9.14	6.52	
	PLACE1007420	12.12	12.66	20.8	25.26	23.9	22.88	* +
	PLACE1007431	1.87	7.4	5.51	7.17	5.28	5.91	
	PLACE1007450	0.79	1.22	2.65	3	2.99	2.39	
10	PLACE1007452	0.42	2.36	1.76	2.09	2.98	1.45	
	PLACE1007454	23.74	28.02	76.56	59.97	75.95	46.61	
	PLACE1007460	0.75	3.52	2.35	2.34	1.93	2.58	
	PLACE1007478	0.41	3.07	1.33	1.35	2.18	1.92	
	PLACE1007484	0.6	4.8	2.57	2.56	1.45	1.69	
15	PLACE1007488	0.4	6.24	1.64	1.74	2.61	1.46	
	PLACE1007507	2.91	6.36	4.49	5.31	8.29	8.11	
	PLACE1007511	0.53	1.29	1.06	1.06	1.29	0.42	
	PLACE1007513	10.57	10.43	24.05	12.24	16.88	16.9	
20	PLACE1007524	1.55	3.33	3.53	3.96	4.72	2.96	
	PLACE1007525	1.24	2.95	3.14	2.38	2.85	2.24	
	PLACE1007537	8.6	9.68	49.88	43.78	63.66	40.1	
	PLACE1007544	1.55	6.45	4.97	3.2	3.92	4.61	
	PLACE1007547	1.36	5.03	4.15	2.37	2.84	2.4	
25	PLACE1007557	1.12	3.16	3.14	3.07	3.9	3.41	
	PLACE1007560	9.38	8.86	12.57	11.03	9.62	17.59	
	PLACE1007565	0.37	2.27	1	1	1.16	0.91	
	PLACE1007580	1.06	3.71	3.06	10.8	11.15	13.74	** +
30	PLACE1007583	0.76	3.88	1.78	2.51	2.37	1.09	
	PLACE1007591	0.79	4.62	1.7	2.2	2.53	2.07	
	PLACE1007598	1.13	6.98	3.86	2.71	3.46	4.71	
	PLACE1007610	0.41	5.63	1.28	1.33	3.18	1.5	
	PLACE1007618	1.57	1.91	2.01	1.75	2.2	2.41	
35	PLACE1007621	1.78	2.83	3.64	3.33	3.57	4.38	
	PLACE1007626	23.99	25.61	32.78	30.53	30.94	13.53	
	PLACE1007632	2.03	3.26	2.52	2.65	3.81	4.63	
	PLACE1007635	1.61	4.62	6.42	2.8	4.19	3.37	
	PLACE1007645	10.59	11.55	15.06	9.99	11.58	11.95	
40	PLACE1007649	1.7	5.88	3.47	2.78	4.95	3.13	
	PLACE1007659	1.33	5.85	3.61	4.88	6.22	4.9	
	PLACE1007669	2.01	2.1	3.74	2.97	4.63	4.4	
	PLACE1007677	1.25	2.29	2.81	2.68	3.07	2.91	
	PLACE1007688	3.4	5.69	5.43	1.98	4.53	4.98	
45	PLACE1007690	1.4	4.03	2.12	3.74	3.37	4.61	
	PLACE1007697	0.69	7.13	1.37	1.84	2.56	1.8	
	PLACE1007702	2.03	7.08	5.7	4.03	3.91	4.08	
	PLACE1007705	1.38	3.93	1.59	1.74	4.45	2.75	
	PLACE1007706	3.11	6.08	4.69	5.25	8.84	7.49	
50	PLACE1007725	3.41	4.69	6.65	5.1	3.29	5.39	
	PLACE1007729	0.98	2.65	1.8	2.7	3.11	1.99	
	PLACE1007730	1.25	4.29	3.07	3.66	3.75	4.32	
	PLACE1007737	1.43	4.79	3.39	3.79	4.7	4.17	
55	PLACE1007743	1.38	4.26	2.29	2.3	2.83	2.03	
	PLACE1007746	6.56	9.02	10.42	9.65	13.29	12.97	
	PLACE1007753	0.53	4.48	1.71	1.35	2.86	1.94	

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	PLACE1007769	1.31	4.31	3.5	3.27	4.51	4.58	
	PLACE1007780	5.77	4.63	7.11	6.51	3.75	2.17	
	PLACE1007791	1.82	3.29	3.38	3.16	3.69	2.87	
5	PLACE1007807	0.67	2.79	1.72	2.33	1.76	1.29	
	PLACE1007810	0.39	4.45	2.63	4.11	4.08	3.27	
	PLACE1007814	3.57	5.98	5.04	4.2	4.62	6.3	
	PLACE1007828	2.01	7.64	3.34	2.69	4.64	3.44	
10	PLACE1007829	1.32	6.9	2.88	2.87	4.87	3.06	
	PLACE1007841	1.64	7.26	1.87	2.25	3.14	3.39	
	PLACE1007842	1.1	3.32	2.44	2.09	3.96	1.39	
	PLACE1007843	1.2	1.92	1.43	2.13	1.48	1.86	
	PLACE1007845	1.76	3	4.11	3.45	3.42	2.36	
15	PLACE1007846	0.99	3.26	1.64	2.02	2.73	1.5	
	PLACE1007848	1.09	3.51	2.23	2.39	2.62	2.25	
	PLACE1007852	2.26	7.88	3.82	2.94	4.61	3.24	
	PLACE1007858	3.65	11.57	5.81	61.71	80.46	57.09	** +
	PLACE1007866	19.42	25.98	40.48	43	80.39	56.73	
20	PLACE1007871	8.1	7.9	15.45	16.17	12.35	11.08	
	PLACE1007877	1.09	2.09	1.45	1.4	2.39	1.53	
	PLACE1007878	5.98	9.75	14.61	13.65	7.49	8.9	
	PLACE1007881	0.43	2.66	1.34	1.59	1.94	1.93	
25	PLACE1007885	4.35	7.85	6.76	5.57	6.53	7.01	
	PLACE1007897	0.27	6.51	1.85	1.72	1.53	1.41	
	PLACE1007908	3.14	12.29	5.73	5.96	7.9	8.24	
	PLACE1007922	6.08	11.75	8.75	5.24	7.15	4.54	
	PLACE1007946	1.07	2.03	1.86	2.71	2.28	1.94	
30	PLACE1007950	6.98	7.6	18.21	16.17	19.34	12.63	
	PLACE1007954	-0.03	2.45	1.15	2.46	1.57	1.51	
	PLACE1007955	0.92	4.01	2.17	2.05	2.52	3.05	
	PLACE1007956	0.6	3.61	2.91	2.35	2.1	2.22	
	PLACE1007958	0.75	6.31	1.34	0.79	1.21	0.8	
35	PLACE1007965	0.64	5.88	3.25	3.38	2.91	2.17	
	PLACE1007969	1.09	6.37	3.06	2.35	3.29	2.21	
	PLACE1007971	2.73	4.17	5.21	6.1	4.41	5.92	
	PLACE1007990	1.95	2.33	2.31	3.22	3.09	1.88	
	PLACE1008000	0.32	2.16	1.98	1.85	1.27	0.66	
40	PLACE1008002	0.99	3.38	1.7	1.81	2.04	0.51	
	PLACE1008037	0.57	4.19	1.7	4.59	2.86	2.02	
	PLACE1008044	1.42	5.81	2.46	4.18	4.93	4.16	
	PLACE1008045	0.4	4.07	1.54	1.75	2	1.65	
45	PLACE1008080	2.05	6.08	3.22	4.23	4.03	4.78	
	PLACE1008092	1.56	1.56	1.48	1.48	2.98	1.86	
	PLACE1008095	0.59	2.14	1.48	2.38	2.73	1.23	
	PLACE1008105	0.95	1.76	1.71	2.24	2.71	0.74	
	PLACE1008107	0.27	2.33	0.7	1.72	1.44	1.68	
50	PLACE1008111	1.73	5.01	2.12	4.57	5.4	4.04	
	PLACE1008113	5.88	9.24	12.48	16.57	20.29	19.24	* +
	PLACE1008122	1.22	5.54	2.55	1.61	1.57	1.5	
	PLACE1008129	1.5	5.64	2.8	2.43	5.36	2.91	
	PLACE1008132	5.51	4.47	8.34	6.61	11.2	7.63	
55	PLACE1008137	0.96	1.82	1.02	2.12	3.88	0.8	
	PLACE1008174	0.77	3.16	2.43	5.12	4.39	2.46	

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	PLACE1008177	1.62	4.87	3.09	3.79	3.26	3.77		
	PLACE1008181	1.76	3.87	1.6	2.06	2.43	1.43		
5	PLACE1008195	2.66	6.08	2.97	4.34	4.14	3.9		
	PLACE1008198	1.06	5.56	2.52	2.55	3.31	1.54		
	PLACE1008201	1.22	4.45	3.58	5.92	7.69	5.64	*	+
	PLACE1008209	2.35	2.29	4.46	2.51	5.31	4.44		
	PLACE1008226	1.8	2.35	5.25	4.72	5.68	7.08		
10	PLACE1008227	0.77	2.67	3.02	2.38	4.6	3.54		
	PLACE1008231	1.26	3.85	1.85	1.05	1.83	0.78		
	PLACE1008238	1.22	3.21	2.9	2.47	2	1.72		
	PLACE1008244	1.01	4.69	1.56	1.68	3.2	1.56		
	PLACE1008249	0.8	4.94	2.55	1.22	2.17	2.01		
15	PLACE1008266	11.31	18.61	43.04	60.04	82.48	59.04	*	+
	PLACE1008273	1.47	3.95	3.81	3.53	3.8	4.47		
	PLACE1008275	1.59	3.67	2.17	2.62	2.57	2.34		
	PLACE1008280	0.85	2.6	1.84	2.42	2.48	2.36		
	PLACE1008282	4.71	8.19	6.89	7.27	9.02	6.38		
20	PLACE1008297	2.32	4.7	3.36	2.89	3.42	3.21		
	PLACE1008303	1.65	6.68	1.24	4.12	3.83	2.65		
	PLACE1008309	0.43	6.52	0.82	1.77	1.5	1.29		
	PLACE1008315	5.3	5.93	8.61	4.92	4.79	9.83		
	PLACE1008329	0.47	2.23	2.06	2.32	2.8	2.49		
25	PLACE1008330	0.72	4.06	3.16	2.48	3.36	2.96		
	PLACE1008331	0.84	5.01	2.1	4.5	2.17	2.91		
	PLACE1008351	4.34	8.66	7.41	7.91	7.31	7.1		
	PLACE1008356	1.56	8.23	1.93	2.86	4.16	3.35		
30	PLACE1008359	1.57	4.11	2.89	2	2.97	2.94		
	PLACE1008368	2.27	6.38	7.43	5.72	7.33	6.95		
	PLACE1008369	0.57	2.46	1.45	1.12	1.59	1.68		
	PLACE1008392	0.8	3.09	2.54	2.44	3.22	3.24		
	PLACE1008394	2.08	4.84	3.75	3.98	5.03	4.76		
35	PLACE1008398	5.32	9.36	11.44	11.36	11.3	12.33		
	PLACE1008401	1.19	7.06	3.21	2.82	3.43	3.33		
	PLACE1008402	3.21	6.45	7.2	7.23	10.15	9.26		
	PLACE1008405	10.3	10.95	18.42	17.17	18.82	20.4		
	PLACE1008409	1.88	5.19	5.69	4.97	5.41	5.65		
40	PLACE1008420	1.4	1.87	1.96	2.67	2.69	2.27	*	+
	PLACE1008424	0.88	2.69	2.54	1.69	2.34	1.71		
	PLACE1008426	0.98	2.58	1.58	1.7	2.66	2.32		
	PLACE1008429	0.92	3.17	2.14	1.91	3.4	1.84		
	PLACE1008430	1.63	4.85	3.04	2.93	3.52	3		
45	PLACE1008437	0.87	3.64	3.01	2.83	1.82	1.57		
	PLACE1008453	1.16	4.8	1.02	1.64	2.06	1.17		
	PLACE1008454	2.14	6.46	9.23	5.46	9.02	5.92		
	PLACE1008455	2.06	4.33	7.2	5.26	6.68	4.87		
50	PLACE1008457	0.51	2.6	2.01	2.28	2.43	2.47		
	PLACE1008465	0.49	2.41	1.72	1.56	2.13	0.48		
	PLACE1008469	2.42	4.36	5.32	5.16	4.75	7.1		
	PLACE1008488	0.81	5.48	1.97	2.44	2.03	1.8		
	PLACE1008519	1.48	10.85	6.17	4.41	4.99	4.51		
55	PLACE1008524	1.04	11.09	1.72	2	3.22	2.02		
	PLACE1008531	0.64	8.37	1.92	1.33	2.05	1.72		

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	PLACE1008532	2.12	3	5.51	5.66	4.72	4.19		
	PLACE1008533	2.01	4	4.07	5.53	5.18	3.77		
	PLACE1008542	1.61	2.36	0.96	2.05	2.1	1.72		
5	PLACE1008549	0.96	3.06	0.67	1.45	2.1	1.53		
	PLACE1008560	1.18	4.23	2.28	2.29	3.93	3.47		
	PLACE1008567	0.87	7.26	1.85	2.33	3.67	2.38		
	PLACE1008568	2.37	10.67	5.49	2.97	7.47	4.21		
10	PLACE1008569	3.94	10.32	6.74	6.1	8.6	7.6		
	PLACE1008584	0.88	1.4	1.58	2.86	3.38	1.31		
	PLACE1008585	4.96	4.8	7.56	11.08	4.84	3.57		
	PLACE1008603	5.9	7.25	31	30.55	43.67	29.76		
	PLACE1008621	0.55	2.28	0.95	0.72	1.89	1.16		
15	PLACE1008625	0.64	4.01	0.9	1.18	1.41	2.03		
	PLACE1008626	0.55	6.06	0.9	1.03	0.83	0.95		
	PLACE1008627	0.46	8.32	1.86	1.87	3.34	2.7		
	PLACE1008629	3.22	9.18	5.84	5.44	6.75	4.41		
	PLACE1008630	1.68	3.39	4.23	4.21	3.01	3.51		
20	PLACE1008643	1.31	0.93	1.98	1.72	2.34	1.94		
	PLACE1008650	0.25	3.05	1.62	2.23	1.63	1.24		
	PLACE1008657	1.17	2.39	2.51	2.34	4.04	2.91		
	PLACE1008664	0.91	5.93	2.37	2.91	2.51	1.13		
25	PLACE1008693	0.97	4.93	3.09	2.53	3.81	2.2		
	PLACE1008696	0.88	3.84	2.21	2.26	2.11	1.47		
	PLACE1008715	1.05	4.71	2.11	1.34	2.65	2.65		
	PLACE1008716	2.48	3.94	4.19	5.75	6.9	7.07	*	+
	PLACE1008722	3.85	4.34	7.37	7.64	7.19	3.45		
30	PLACE1008738	5.17	9.13	12.7	9.49	5.83	4.8		
	PLACE1008742	6.57	6.87	14.66	14.94	15.06	12.41		
	PLACE1008744	3.52	6.98	5.61	5.83	4.55	2.74		
	PLACE1008748	0.63	4.39	2.75	2.44	1.67	1.61		
	PLACE1008757	0.99	4.74	4.51	2.77	5.74	2.17		
35	PLACE1008766	2.66	6.75	3.77	3.51	6.47	4.06		
	PLACE1008785	1.39	1.68	2.6	3.26	3.8	3.89	*	+
	PLACE1008790	1.57	1.8	2.29	3.5	5.39	2.96		
	PLACE1008798	1.71	3.82	4.45	6	5.93	3.32		
40	PLACE1008807	1.34	3.95	1.61	2.54	2.62	1.8		
	PLACE1008808	1.6	4.53	3.01	4.24	3.69	5.04		
	PLACE1008813	1.38	4.85	1.97	1.9	1.95	2.3		
	PLACE1008836	1.34	5.81	3.68	3.89	6.17	4.1		
	PLACE1008851	1.21	6.65	3.94	4.85	10.04	4.54		
45	PLACE1008854	0.56	0.48	1.14	1.16	1.41	1.6		
	PLACE1008864	1.98	1.92	2.96	2.73	2.65	2.49		
	PLACE1008867	1.2	6.57	6.22	6.43	5.71	4.82		
	PLACE1008876	11.7	16.5	27.29	26.74	20.94	23.24		
	PLACE1008887	1.37	4.31	1.44	3.26	2.07	3.28		
50	PLACE1008902	1.33	5.62	2.93	3.17	4.58	2.06		
	PLACE1008911	4.04	8.56	10.48	11.31	13.99	15.66		
	PLACE1008917	0.6	4.53	2.72	1.7	2.9	1.71		
	PLACE1008920	0.75	0.77	0.87	0.61	1.58	1.44		
	PLACE1008925	0.25	0.9	1.04	0.94	1.91	0.84		
55	PLACE1008930	4.12	7.32	9.83	5.11	10.36	7.17		
	PLACE1008934	0.9	3.42	2.9	2.89	2.28	1.7		

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	PLACE1008941	1.57	4.14	2.8	2.06	2.59	4.05		
	PLACE1008947	2.3	5.41	5.51	3.96	5.84	5.16		
5	PLACE1008984	1.26	6.31	3.25	3.1	3.93	3.19		
	PLACE1008985	0.94	2.75	2.74	2.84	2.43	2.7		
	PLACE1008994	0.27	1.72	0.65	1.11	0.78	0.68		
	PLACE1009020	0.46	3.49	2.42	2.49	3.1	2.16		
	PLACE1009027	0.89	2.7	1.59	2.24	1.75	2.09		
10	PLACE1009039	-0.06	3.31	3.42	2.39	1.59	1.49		
	PLACE1009045	1.53	6.33	6.05	23.13	20.76	22.2	**	+
	PLACE1009048	0.41	5.97	2.3	0.61	1.04	0.54		
	PLACE1009050	0.97	4.9	1.68	1.07	1.47	1.55		
	PLACE1009060	5.61	8.4	9.51	10.74	8.55	11.96		
15	PLACE1009067	1.14	2.8	2.03	1.6	2.34	3.4		
	PLACE1009071	1.44	4.05	3.9	3.79	7.24	9.82		
	PLACE1009090	1.27	6.46	2.35	3.11	4.73	2.86		
	PLACE1009091	5.58	10.22	38.11	38.77	49.35	36.29		
	PLACE1009094	0.26	5.68	1.88	1.67	5.04	1.71		
20	PLACE1009099	1	5.52	3.47	3.49	3.36	3.84		
	PLACE1009110	1.59	5.82	1.16	1.68	4.3	4.39		
	PLACE1009111	1.88	5.24	2.65	3.95	3.77	2.88		
	PLACE1009113	2.24	3.52	3.62	6.14	4.87	7.29	*	+
25	PLACE1009130	4.46	6.8	7.84	6.68	9.36	10.47		
	PLACE1009150	0.88	3.54	1.95	3.23	3.3	3.01		
	PLACE1009155	1.11	5.06	2.98	4.46	4.43	3.87		
	PLACE1009158	1.06	5.77	1.95	1.77	2.35	2.88		
	PLACE1009166	0.76	4.8	1.53	1.59	2.16	1.3		
30	PLACE1009172	1.43	3.96	2.45	2.26	5.85	2.61		
	PLACE1009174	1.13	3.45	2.42	1.67	3.02	2.38		
	PLACE1009183	1.62	3.54	4.47	4.1	6.33	8.06		
	PLACE1009186	1.04	5.07	2.3	2.46	2.86	2.91		
	PLACE1009190	0.75	2.32	1.44	1.53	1.9	1.65		
35	PLACE1009196	0.81	4.01	2.73	2.24	2.38	1.99		
	PLACE1009200	1.01	4.44	2.94	2.84	4.39	2.91		
	PLACE1009217	2.55	4.91	3.43	4.46	7.29	7.23		
	PLACE1009230	1.9	5.55	6.63	5.63	9.16	9.46		
	PLACE1009236	4.97	7.07	12.6	8.21	10.79	7.13		
40	PLACE1009246	11.71	11.96	24.75	14.59	16.36	9.05		
	PLACE1009265	6.95	7.82	14.01	15.61	5.19	12.17		
	PLACE1009279	0.67	2.07	2.46	1.93	2.54	1.63		
	PLACE1009298	5.54	9.92	9.52	10.21	11.25	17.55		
	PLACE1009308	1.13	6.82	2.04	2.48	2.48	2.34		
45	PLACE1009319	2.04	9.25	3.15	2.92	3.54	2.5		
	PLACE1009328	1.04	5.78	1.81	2.98	3.39	2.17		
	PLACE1009335	1.38	6.55	4.72	2.24	3.21	3.01		
	PLACE1009338	2.56	4.14	5.1	3.24	4.3	1.57		
50	PLACE1009344	0.73	2.45	1.08	1.31	1.55	0.84		
	PLACE1009355	5.41	7.37	9.95	13.44	10.76	13.55	*	+
	PLACE1009368	1.3	2.56	2.41	2.43	2.32	2.19		
	PLACE1009375	1.21	6.41	3.05	3.04	4.46	2.53		
	PLACE1009388	1.18	8.68	3.01	3.46	4.53	2.72		
55	PLACE1009398	1.19	9.2	3.74	3.17	4.28	3.96		
	PLACE1009404	2.78	9.18	4.51	5.33	6.73	6.94		



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	PLACE1009410	1.27	2.35	2.33	2.51	2.31	1.44		
	PLACE1009417	0.95	2.25	4.34	2.55	3.08	1.71		
	PLACE1009424	1.88	3.61	3.18	2.85	3.24	3.93		
5	PLACE1009434	0.84	3.94	2.91	1.29	1.82	2.19		
	PLACE1009443	1.21	7.2	2.55	2.42	3.43	3.17		
	PLACE1009444	1.33	7.71	4.05	2.51	3.17	3.79		
	PLACE1009459	0.23	7.99	1.55	1.71	1.83	0.86		
10	PLACE1009460	1.75	6.84	3.26	5.15	4.31	4.08		
	PLACE1009468	0.99	2.83	3.42	4.43	4.42	2.97		
	PLACE1009476	0.21	1.21	0.73	1.05	0.67	1.33		
	PLACE1009477	1.35	3.13	2.67	3.06	2.35	2.2		
	PLACE1009493	0.87	3.35	0.94	1	1.87	1.41		
15	PLACE1009502	0.76	4.64	2.13	1.19	1.89	1.66		
	PLACE1009524	1.32	4.22	1.63	0.94	2.14	1.6		
	PLACE1009527	0.95	4.51	2.11	1.64	2.55	1.28		
	PLACE1009531	20.82	28.24	41.52	46.25	43.25	49.96		
	PLACE1009535	1.1	1.56	2.68	2.42	2.15	1.11		
20	PLACE1009539	2.15	3.41	4.18	3.88	2.65	2.57		
	PLACE1009540	5.89	8	11.66	14.8	4.47	3.84		
	PLACE1009542	1.11	3.37	1.42	1.51	2.06	1.44		
	PLACE1009546	0.62	5.27	0.97	2.24	1.64	1.25		
25	PLACE1009556	0.35	4.46	3.46	3.36	2.86	3.16		
	PLACE1009569	0.05	3.93	2.46	3.34	2.7	3.11		
	PLACE1009571	1.67	4.27	2.52	3.04	2.85	2.67		
	PLACE1009573	3.81	2.97	6.73	6.92	8.12	6.49		
	PLACE1009576	1.92	2.51	4.3	2.73	3.66	2.08		
30	PLACE1009580	1.42	1.81	1.74	2.73	3.47	2.33	*	+
	PLACE1009581	0.89	4.25	2.03	2.91	4.38	2.74		
	PLACE1009587	0.96	4.91	2.29	2.43	3.2	1.99		
	PLACE1009593	2.71	6.73	4.37	4.94	6.85	5.03		
	PLACE1009595	1.81	5.44	2.66	2.67	5	2.79		
35	PLACE1009596	1.57	6.83	2.6	3.44	3.97	2.7		
	PLACE1009600	3.03	4.27	4.48	5.48	9.14	4.42		
	PLACE1009604	2.32	4.64	5.02	4.22	6.11	3.23		
	PLACE1009607	1.29	2.48	3.18	3.19	4.17	3.18		
40	PLACE1009613	1.94	5.23	2.94	2.65	3.08	2.23		
	PLACE1009621	1.66	6.72	3.32	8.21	8.67	8.06	*	+
	PLACE1009622	1.78	5.93	3.78	3.9	4.1	3.9		
	PLACE1009624	1.16	5.77	3.42	3.2	3.65	3.5		
	PLACE1009637	2	6.88	3.36	3.07	4.59	3.91		
45	PLACE1009639	1.94	1.76	4.15	3.44	3.67	4.99		
	PLACE1009654	20.88	17.13	34.95	14.94	24.53	20.64		
	PLACE1009659	2.77	6.78	7.45	6.38	8.38	6.55		
	PLACE1009665	1.04	4.21	1.93	1.19	2.72	1.93		
	PLACE1009669	7.73	9.64	14.54	9.85	16.89	8.82		
50	PLACE1009670	1.76	5.36	2.54	2.77	4.47	4.01		
	PLACE1009708	2.1	5.57	5.09	3.64	6.54	5.84		
	PLACE1009721	1.34	4.28	3.56	5.78	5.81	3.01		
	PLACE1009731	1.36	3.59	3	3.58	6.53	5		
	PLACE1009735	1.94	3.94	3.21	5.16	7.52	4.78		
55	PLACE1009737	1.89	4.29	2.95	4.83	5.61	5.47	*	+
	PLACE1009741	1.3	4.32	3.45	2.09	5.03	3.07		

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	PLACE1009752	1.34	5.64	2.65	2.3	3.33	1.68	
	PLACE1009763	3.95	9.73	6.82	7.13	7.44	8.39	
5	PLACE1009766	1.46	6.98	3.32	3.07	5.19	3.75	
	PLACE1009772	0.48	5.19	0.6	1.01	2.46	0.89	
	PLACE1009782	0.91	2.39	2.03	2.88	2.91	3.74	
	PLACE1009794	2.58	4.45	5.11	3.54	3.66	5.03	
	PLACE1009798	1.59	5.37	4	6.26	5.57	5.67	
10	PLACE1009845	1.05	6.02	2.92	2.79	3.39	3.92	
	PLACE1009849	0.96	6.61	2.35	1.79	3.41	2.59	
	PLACE1009857	0.79	4.86	1.45	1.19	1.27	1.56	
	PLACE1009861	1.43	4.67	3.87	4.1	3.47	3.11	
	PLACE1009872	53.53	52.43	88.5	74.95	49.47	81.73	
15	PLACE1009877	5.45	7.59	12.08	10.03	10.3	12.32	
	PLACE1009879	0.82	3.28	1.59	1.55	2.99	1.34	
	PLACE1009886	0.68	4.04	1.53	1.62	3.04	1.72	
	PLACE1009888	1.03	7.4	3.23	5.34	5.84	7.94	
	PLACE1009908	1.56	7.63	8.64	3.37	6.71	5.9	
20	PLACE1009919	4.5	7.53	8.26	5.84	10.72	10.15	
	PLACE1009921	0.96	3.94	3.32	1.63	4.28	2.47	
	PLACE1009923	3.82	5.56	6.85	6.32	8.13	5.57	
	PLACE1009924	3.01	2.49	4.53	4.43	4.31	1.04	
	PLACE1009925	0.61	2.77	1.84	2.51	2.2	2.5	
25	PLACE1009931	2.78	5.21	9	8.71	6.93	8.09	
	PLACE1009935	0.74	3.71	2.1	1.19	1.08	1.5	
	PLACE1009947	0.47	3.83	1.64	1.51	2.46	2.03	
	PLACE1009961	0.43	4.08	1.39	1.69	2.18	1.9	
	PLACE1009971	0.92	4.9	1.98	1.35	1.74	1.45	
30	PLACE1009982	40.34	48.71	89.8	53.8	57.87	66.96	
	PLACE1009992	0.94	1.9	2.59	1.47	2.52	0.68	
	PLACE1009995	6.47	10.83	15.72	7.79	9.03	11.23	
	PLACE1009997	0.55	3.7	3.03	2.76	3.2	2.64	
35	PLACE1010002	1.4	4.14	2.82	2.89	3.04	3.46	
	PLACE1010011	2.09	8.13	3.85	4.4	5.21	4.68	
	PLACE1010013	0.18	12.85	1.74	0.92	1.81	0.68	
	PLACE1010021	3.18	11.98	5.42	4.12	4.13	6.06	
	PLACE1010023	2.15	8.45	5.16	5.62	6.52	6.14	
40	PLACE1010031	4.6	4.35	7.23	6.79	4.91	1.82	
	PLACE1010039	1.17	3.3	1.45	1.28	1.23	1.19	
	PLACE1010045	1.1	2.83	3.66	2.52	3.55	2.64	
	PLACE1010053	1.42	3.56	1.65	2.21	2.76	2.37	
	PLACE1010060	1.63	6.1	4.13	4.11	4.6	4.05	
45	PLACE1010069	0.41	7.96	2.32	1.48	2.91	1.3	
	PLACE1010070	0.92	8.04	1.5	0.45	1.78	1.09	
	PLACE1010074	5.25	11.67	11.8	12.32	9.51	11.22	
	PLACE1010076	12.75	11.95	29.01	19.58	15.88	16.82	
	PLACE1010078	2.96	2.42	4.36	4.64	4.39	3.85	
50	PLACE1010081	2.74	4.1	3.7	6.85	7.81	4.59	*
	PLACE1010083	0.69	2.53	1.51	1.22	1.86	2.26	
	PLACE1010089	1.86	4.89	3.35	3.45	3.47	3.48	
	PLACE1010096	2.17	7.73	2.91	3.43	4.19	3.2	
	PLACE1010102	3.89	10.9	5.33	7.1	9.64	7.57	
55	PLACE1010105	2.98	7.46	4.93	7.31	9.04	9.82	

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	PLACE1010106	2.46	2.95	4.48	5.47	4.88	5.8	*	+
	PLACE1010130	0.53	1.79	1.17	2.27	2.55	1.23		
	PLACE1010132	2.49	4.65	5.3	5.07	4.39	4.19		
5	PLACE1010134	0.8	3.32	1.15	1.97	2.31	1.67		
	PLACE1010139	6.67	10.51	12.98	14.99	16.1	14.58		
	PLACE1010148	0.96	5.07	1.62	1.48	1.9	1.97		
	PLACE1010152	3.11	5.68	5.16	6.33	6.64	5.76		
10	PLACE1010155	3.8	6.17	6.52	16.85	20.56	20.32	**	+
	PLACE1010156	13.71	15.43	32.21	132.45	85.59	134.99	**	+
	PLACE1010161	1.9	2.81	5.05	3.29	2.92	1.97		
	PLACE1010181	0.73	2.22	1.51	2.58	1.99	2.53		
	PLACE1010194	0.64	3.35	1.03	2.26	2.14	1.64		
15	PLACE1010202	0.4	4.14	1.2	2.91	1.65	2.16		
	PLACE1010231	1.1	3.78	2.39	1.31	2.99	2.73		
	PLACE1010235	1.26	4.24	1.94	2.68	2.42	3.16		
	PLACE1010237	1.01	3.4	2.1	1.14	1.97	0.87		
	PLACE1010251	0.59	0.98	1.95	2.57	3.18	1.62		
20	PLACE1010261	0.97	2.63	2.07	2.69	1.69	1.55		
	PLACE1010270	0.76	2.7	1.3	1.39	2.33	1.42		
	PLACE1010273	0.97	3.27	0.46	1.48	2.25	1.5		
	PLACE1010274	6.28	9.23	9.66	10.49	12.18	14.28		
	PLACE1010277	6.03	10.14	12.68	14.6	16.06	15.84	*	+
25	PLACE1010293	1.8	5.68	3.55	3.65	3.37	3.96		
	PLACE1010297	5.17	11.37	21	24.84	32.59	22.06		
	PLACE1010300	4.18	4.78	8.22	8	9.95	6.87		
	PLACE1010310	16.52	14.75	49.45	70.74	71	77.01	*	+
	PLACE1010321	2.03	4.92	2.46	3.37	4.99	2.73		
30	PLACE1010324	0.88	3.49	1.56	1.12	1.54	1.2		
	PLACE1010329	0.73	4.64	1.95	2.56	3.37	1.96		
	PLACE1010330	3.78	9.09	7.29	2.42	10.45	7.67		
	PLACE1010335	6.43	11.15	7.43	13.15	17.89	19.1	*	+
	PLACE1010341	0.19	4.81	1.24	1.07	3.13	1.54		
35	PLACE1010342	0.77	0.9	0.75	0.48	2.12	0.8		
	PLACE1010346	1.47	1.73	3.61	2.96	4.47	1.71		
	PLACE1010362	1.31	2.69	2.22	2.18	3.49	3.31		
	PLACE1010364	0.78	2.56	1.65	1.19	2.32	1.49		
40	PLACE1010368	1.66	5.44	3.51	3.41	3.87	4.48		
	PLACE1010373	9.05	10.48	16.82	12.13	15.45	12.28		
	PLACE1010383	1.91	5.52	5.13	5.58	6.39	4.9		
	PLACE1010385	0.3	3.01	1.07	0.04	0.6	0.9		
	PLACE1010389	6.28	7.98	13.24	22.3	13.64	22.94	*	+
45	PLACE1010401	0.73	2.72	1.32	1.99	2.87	2.21		
	PLACE1010410	3.15	4.83	6.71	4.78	7.55	7.32		
	PLACE1010418	1.88	4.73	4.2	4.71	5.14	4.66		
	PLACE1010425	0.93	4.78	1.43	1.78	1.96	2.15		
	PLACE1010443	6.98	13.83	51.39	36.22	63.67	48.93		
50	PLACE1010445	0.95	5.02	0.68	2.69	3.81	2.44		
	PLACE1010481	1.19	2.06	2.46	1.75	2	1.85		
	PLACE1010482	28.99	29.39	53.06	31.75	19.63	40.44		
	PLACE1010491	3.36	6.4	5.38	4.96	5.98	3.26		
	PLACE1010492	4	4.75	5.95	5.57	8.15	7.77		
55	PLACE1010509	0.8	4.32	3.15	3.09	3.01	2.99		

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	PLACE1010518	3.33	6.72	6.58	7.3	8.25	8.24		
	PLACE1010522	2.3	5.96	4.35	1.87	3.52	2.64		
	PLACE1010529	1.8	6.5	3.84	5.43	8.44	7.2		
5	PLACE1010547	0.79	1.57	1.76	1.51	1.93	2.45		
	PLACE1010560	0.63	2.51	2.06	3.31	2.2	2.51		
	PLACE1010562	0.74	2.68	1.65	1.64	2.1	1.63		
	PLACE1010579	1.11	7.13	2.63	3.45	4.67	3.26		
10	PLACE1010580	1.35	9.12	3.79	3.27	2.49	4.52		
	PLACE1010599	3.56	6.07	7.94	8.32	9.26	8.13		
	PLACE1010606	1.17	4.42	1.64	3.39	4.17	3.51		
	PLACE1010616	1.84	3.72	5.49	4.09	8.09	6.81		
	PLACE1010622	2.1	3.43	3.91	5.07	4.74	4.69	*	+
15	PLACE1010624	1.43	3.35	3.98	4.21	6.17	5.22		
	PLACE1010628	1.37	3.97	2.83	2.14	3.63	4.22		
	PLACE1010629	1.08	4.64	2.24	3.01	3.3	3.5		
	PLACE1010630	1.64	4.77	3.69	4.22	4.78	5.29		
	PLACE1010631	0.5	5.35	2.64	1.55	1.66	2.67		
20	PLACE1010651	14.24	15.75	24.44	37.62	40.09	52.12	*	+
	PLACE1010661	1.62	4.09	2.28	3.56	6.43	3.22		
	PLACE1010662	1.32	2.48	1.6	2.98	2.3	1.61		
	PLACE1010668	12.87	15.91	27.82	37.63	30.53	28.75		
25	PLACE1010702	1.46	2.34	4.24	3.59	3.6	3.2		
	PLACE1010709	79.16	78.33	115.91	107.07	96.3	133.25		
	PLACE1010713	7	10.81	14.7	9.14	8.16	15.14		
	PLACE1010714	0.82	7.41	1.58	1.75	2.04	1.47		
	PLACE1010716	0.71	6.19	4.31	2.08	2.3	1.93		
30	PLACE1010717	0.9	6.49	2.13	2.17	3.9	2.61		
	PLACE1010720	14.03	17.05	53.79	46.72	50.7	41.49		
	PLACE1010739	0.9	1.2	1.11	1.73	1.21	1.93		
	PLACE1010743	1.09	2.3	1.99	2.63	2.05	2.21		
	PLACE1010752	0.87	2.92	1.85	1.76	2.05	1.53		
35	PLACE1010761	3.6	8.83	13.51	12.07	16.4	17.08		
	PLACE1010771	1.41	6.89	5.03	6.13	10.3	5.42		
	PLACE1010784	0.9	9.66	1.97	2.07	1.72	1.34		
	PLACE1010786	1.21	8.77	2.83	2.91	3.68	2.21		
	PLACE1010789	0.6	1.16	1.52	1.8	1.89	1.17		
40	PLACE1010800	2.18	2.86	3.25	3.95	3.24	2.93		
	PLACE1010802	2.97	4.63	5.31	5.72	4.27	3.3		
	PLACE1010811	0.89	2.19	1.96	1.83	1.75	2.18		
	PLACE1010813	8.89	13.3	55.85	48.82	72.26	46.7		
	PLACE1010827	1.54	6.43	3.94	4.3	5.52	4.81		
45	PLACE1010833	0.93	8.13	2.63	2.68	3.64	2.09		
	PLACE1010839	1.57	6.22	3.21	4.22	6.72	4.13		
	PLACE1010856	7.58	8.94	12.34	8.02	6.53	8.59		
	PLACE1010857	3.41	3.81	7.63	8.24	5.98	4.56		
	PLACE1010870	1.3	2.24	2.05	1.62	2.38	1.94		
50	PLACE1010877	1.67	4.66	2.69	2.77	3.92	2.62		
	PLACE1010882	0.49	4.8	0.99	1.74	1.27	0.51		
	PLACE1010891	1.1	7.73	1.12	1.85	1.73	0.95		
	PLACE1010896	1.19	5.29	3.18	3.98	3.05	3.47		
55	PLACE1010900	7.41	13.29	27.9	23.88	20.99	18.85		
	PLACE1010916	1.55	1.18	2.06	1.89	1.9	2.2		

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	PLACE1010917	-0.04	0.82	0.36	1.05	2.25	0.56		
	PLACE1010924	1.15	2.31	1.55	1.11	1.88	0.92		
5	PLACE1010925	2.76	5.36	2.17	4.92	6.32	4.16		
	PLACE1010926	1.8	5.73	4.31	5.37	4.35	4.45		
	PLACE1010942	1.7	6.25	5.63	5.53	7.88	7.69		
	PLACE1010943	7.38	10.43	17.12	24.62	29.5	31.96	**	+
	PLACE1010944	4.33	7.39	9.3	13.11	11.44	15.58	*	+
10	PLACE1010947	1.43	0.9	2.41	2.57	2.8	2.25		
	PLACE1010954	3.56	2.92	7.4	7.92	8.55	7.64		
	PLACE1010960	2.06	3.44	6.07	4.23	7.89	2.6		
	PLACE1010965	2.33	3.81	3.54	6.09	4.92	5.03	*	+
	PLACE1010968	1.55	4.69	1.38	4.95	6.51	3.68		
15	PLACE1010978	3.63	6.12	7.05	9	8.94	6.45		
	PLACE1010982	2.23	5.77	5.6	4.74	5.66	4.88		
	PLACE1010990	0.88	5.4	2.04	3.11	3.03	2.19		
	PLACE1011017	5.6	3.78	22.57	25.64	35.47	20.97		
20	PLACE1011019	1.1	1.5	2.48	3.78	4.42	0.88		
	PLACE1011026	4.17	4.93	6.23	6	5.19	2.74		
	PLACE1011032	0.89	3.95	2.03	1.44	1.58	0.56		
	PLACE1011041	1.07	4.13	1.03	1.69	1.22	1.43		
	PLACE1011045	1.49	5.62	2.36	3.26	3.67	4.45		
25	PLACE1011046	0.83	5.25	1.79	2.57	3.17	1.87		
	PLACE1011054	2.33	5.33	6.64	5.26	7.29	5.05		
	PLACE1011056	5.78	5.43	16.22	14.56	19.78	15.67		
	PLACE1011057	2	2.18	3.5	3.29	5.68	3.9		
	PLACE1011059	0.93	1.37	1.56	1.74	2.96	1.79		
30	PLACE1011066	4.49	5.74	6.76	5.38	7.72	5.49		
	PLACE1011087	7.6	7.04	16.48	12.43	17.42	9.79		
	PLACE1011090	2.98	6.14	6.74	3.36	4.13	3.26		
	PLACE1011109	1.99	7.29	4.29	4.08	7.96	3.83		
	PLACE1011114	1.62	4.4	3.13	3.33	4.68	3.29		
35	PLACE1011116	4.89	5.94	6.66	7.43	6.81	8.98		
	PLACE1011122	0.93	2.52	1.84	2.1	1.61	1.64		
	PLACE1011133	0.83	2.22	3.03	3.48	3.52	2.77		
	PLACE1011134	12.47	15.29	66.86	44.95	68.68	51.65		
	PLACE1011143	0.68	4.53	1.48	1.84	2.62	1.41		
40	PLACE1011146	0.91	5.93	1.74	1.97	3.23	2.36		
	PLACE1011160	1.67	7.36	3.81	3.42	4.53	4.24		
	PLACE1011165	1.77	2.34	3.39	2.15	3.39	3.8		
	PLACE1011181	5.25	8.31	37.21	29.38	38.44	30.55		
	PLACE1011185	2.47	4	3.57	4.66	5.15	4.8	*	+
45	PLACE1011186	13.16	12.8	16.45	21.18	25.69	28.83	*	+
	PLACE1011203	1.08	4.64	2.19	1.75	2.94	1.96		
	PLACE1011214	9.02	16.55	59.24	46.39	62.58	47.89		
	PLACE1011219	1.41	4.91	3.6	3.26	4.96	2.9		
50	PLACE1011221	2.68	5.47	6.15	6.23	8.57	7.51		
	PLACE1011229	1.38	4.2	2.69	2.43	2.43	3.09		
	PLACE1011231	0.53	1.5	1.62	1.84	2.59	2.4		
	PLACE1011236	5.69	7.9	43.53	33.48	56.77	44.25		
	PLACE1011247	8.36	10.08	19.16	24.17	26.33	29.74	*	+
55	PLACE1011263	0.57	6.43	4.23	2.62	4.11	5.09		
	PLACE1011273	0.72	3.62	1.17	2.01	1.64	1.72		

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	PLACE1011278	2.42	5	6.12	3.98	4.84	4.31		
	PLACE1011289	2.73	5.84	7.57	6.34	6.13	6.08		
5	PLACE1011291	3.2	5.19	8.31	7.32	8.04	7.95		
	PLACE1011296	0.93	2.45	1.94	1.76	2.63	2.05		
	PLACE1011310	1.72	2.64	3.36	4.51	2.77	4.48		
	PLACE1011311	1.8	3.97	6.33	7.8	9.34	6.73		
	PLACE1011321	1.29	4.77	3.5	3.3	2.63	3.33		
10	PLACE1011325	0.63	4.2	1.84	2	2.74	1.59		
	PLACE1011332	5.65	10.55	9.4	14.8	14.57	15.04	*	+
	PLACE1011340	0.86	4.88	3.38	3.81	4.71	3.47		
	PLACE1011353	5.39	5.53	8.39	10.06	8.58	4.43		
15	PLACE1011360	1.09	3.29	2.18	2.11	3.06	2.41		
	PLACE1011364	4.88	5.69	7.92	6.34	4.57	4.57		
	PLACE1011365	0.92	3.36	2.95	3.01	3.6	2.06		
	PLACE1011371	9.37	10.69	63.06	56.51	87.51	64.33		
	PLACE1011375	1.62	9.37	3.35	2.61	2.74	1.62		
20	PLACE1011386	3.91	12.96	4.18	6.88	5.51	5.93		
	PLACE1011399	1.52	10.14	4.27	2.12	4.22	3.77		
	PLACE1011406	1.25	2.05	1.81	5.03	3.26	2.38		
	PLACE1011407	0.64	2.05	2.58	2.08	2.19	2.02		
	PLACE1011419	2.83	3.2	6.02	6.23	4.18	3.72		
25	PLACE1011433	3.09	4.43	6.13	3.41	4.74	4.99		
	PLACE1011440	0.77	5.81	2.48	2.1	2.24	2.27		
	PLACE1011452	1.06	8.86	2.43	2.87	2.71	2.68		
	PLACE1011465	0.09	8.53	1.96	1.04	1.68	0.85		
	PLACE1011472	1.52	7.67	3.98	0.97	2.87	1.59		
30	PLACE1011477	11.18	12.29	54.35	31.86	55.86	45.67		
	PLACE1011478	1.24	1.64	3.11	5.03	3.02	3.01		
	PLACE1011492	2.24	3.54	5.01	5.45	6.74	5.27		
	PLACE1011498	0.57	2.77	0.98	1.18	1.69	1.15		
	PLACE1011501	0.49	4.67	1.8	4.87	5.63	7.5		
35	PLACE1011503	0.44	5.37	0.79	0.5	0.82	0.35		
	PLACE1011509	1.1	7.8	3.38	4.62	5.08	5.74		
	PLACE1011514	5.86	11.61	11.98	13	17.7	13.17		
	PLACE1011516	10.37	13.29	18.32	18.32	8.08	3.63		
40	PLACE1011520	0.34	0.95	1.34	1.3	1.73	1.01		
	PLACE1011538	52.87	99.27	185.04	129.45	86.87	63.9		
	PLACE1011555	0.87	2.88	2.83	1.55	2.03	1.48		
	PLACE1011561	3.2	4.53	1.98	6.81	5.31	3.08		
	PLACE1011563	1.35	4.74	3.49	2.52	2.64	2.87		
45	PLACE1011567	1.04	4.94	3.36	2.75	4.19	2.77		
	PLACE1011569	0.32	4.35	2.77	2.38	2.46	2.28		
	PLACE1011576	3.25	1.88	7.94	7.85	9.1	8.03		
	PLACE1011586	3.24	2.5	6.22	4.43	4.35	2.94		
	PLACE1011635	1.85	2.56	4.53	9.96	12.43	8.71	**	+
50	PLACE1011641	0.43	2.9	0.9	1.71	1.18	1.19		
	PLACE1011642	5.05	6.96	10.37	12.13	10.86	10.09		
	PLACE1011643	1.29	3.69	1.14	2.38	2.28	2.14		
	PLACE1011646	8.68	12.8	30.53	39.05	54.16	37.76	*	+
	PLACE1011649	1.35	5.7	3.88	4.5	4.61	5.46		
55	PLACE1011650	1.15	1.45	2.54	2.47	3.24	3.75		
	PLACE1011661	1.02	2.26	2.8	3.95	5.92	3.46		

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	PLACE1011664	2.21	3.18	3.99	5.31	3.93	1.73		
	PLACE1011672	0.88	4.14	0.72	2.69	3.57	2.04		
	PLACE1011675	0.51	2.31	1.32	1.66	0.99	0.83		
5	PLACE1011682	2.04	4.56	2.23	2.22	4.03	2.12		
	PLACE1011708	1.1	5.89	3.8	5.5	8.12	4.66		
	PLACE1011719	1.07	4.58	1.66	3.55	3.88	3.03		
	PLACE1011725	1.23	1.19	2.72	3.73	5.19	4.3	*	+
10	PLACE1011729	0.86	1.03	1.8	2.38	3.26	1.22		
	PLACE1011741	2.36	3.67	3.64	4.16	2.52	4.23		
	PLACE1011749	1.58	3.89	4.09	3.49	4.85	3.27		
	PLACE1011757	20.92	30.53	55.88	56.6	55.88	49.59		
	PLACE1011762	0.4	4.34	2.69	3.91	2.14	2.3		
15	PLACE1011778	0.51	4.39	1.99	1.34	2.02	1.34		
	PLACE1011783	2.59	4.63	5.46	4.8	8.41	5.55		
	PLACE1011795	0.74	1.28	2.24	1.47	1.8	1.22		
	PLACE1011810	9.28	10.82	19.51	13.32	17.73	15.47		
	PLACE1011824	5.38	8.17	38.05	25.52	42.89	16.75		
20	PLACE1011825	10.61	16.39	22.6	17.63	18.92	16.07		
	PLACE1011835	24.64	32.67	47.67	32.09	26.75	37.23		
	PLACE1011836	18.11	18.97	31.43	33.14	47.23	13.95		
	PLACE1011847	2.67	6.74	6.42	5.34	7.18	5.84		
	PLACE1011855	0.9	6.06	3.53	3.23	4.47	3.49		
25	PLACE1011858	5.83	7.44	9.37	6.88	6.25	8.35		
	PLACE1011874	1.35	3.14	3.55	4.18	5.28	4.65		
	PLACE1011875	0.57	2.29	1.11	2.66	2.48	2.64		
	PLACE1011877	3.8	5.03	4.4	7.67	6.8	9.97	*	+
30	PLACE1011891	0.17	3.81	1.31	1.13	1.34	1.26		
	PLACE1011896	-0.1	5.22	1.45	-0.19	1.07	0.32		
	PLACE1011920	0.21	5.87	1.04	1.1	1.92	1.76		
	PLACE1011922	2.4	4.18	4.72	3.72	2.88	3.98		
	PLACE1011923	3.42	4.82	7.51	8.09	5.38	12.28		
35	PLACE1011937	3.16	2.24	3.76	3.81	5.58	4.64		
	PLACE1011939	14.93	17.81	26.01	41.75	45.05	47.88	**	+
	PLACE1011940	6.13	7.58	12.68	5.73	7	7.23		
	PLACE1011962	3.28	7.83	7.35	6.39	8.38	8.01		
	PLACE1011964	0.39	5.05	1.66	1.04	1.95	1.46		
40	PLACE1011978	1.55	4.65	3.35	4.48	5.91	5.14		
	PLACE1011980	2.1	4.62	6.07	3.95	4.91	5.35		
	PLACE1011981	5.77	7.28	38.2	27.22	35.24	34.99		
	PLACE1011982	0.83	3.1	2.23	1.82	2.59	1.57		
	PLACE1011995	0.81	3.4	3.73	2.51	3.59	2.86		
45	PLACE1012023	1.38	5.37	1.87	2.09	2.46	1.91		
	PLACE1012026	1.95	5.72	4.23	6.08	9.51	9.8		
	PLACE1012031	2.49	5.81	4.54	4.34	6.35	4.03		
	PLACE20000003	1.18	3.64	6.86	7.38	8.12	8.92		
	PLACE20000005	1.16	2.41	2.16	2.76	2.03	1.89		
50	PLACE20000006	2.52	4.13	15.6	11.34	16.58	13.4		
	PLACE20000007	0.96	4.85	4.24	3.94	5.13	3.33		
	PLACE20000011	1.72	3.27	3.34	4.3	5.06	3.62		
	PLACE20000014	4.04	5.93	23.94	27.19	30.87	30.97	*	+
	PLACE20000015	1.27	4.79	3.52	2.77	3.31	2.69		
55	PLACE20000017	0.48	4.78	2.15	2.65	2.56	2.45		

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	PLACE2000021	1.99	5.06	4.09	3.72	6.24	5.61
	PLACE2000022	1.8	2.8	4.31	3.35	4.64	2.71
5	PLACE2000030	9.37	11.08	71.38	55.43	60.32	35.97
	PLACE2000032	1.23	2.89	3.51	3.53	3.24	2.32
	PLACE2000033	3.29	6.3	12.11	12.49	14.25	9.37
	PLACE2000034	0.6	4.3	1.92	1.79	2.19	2.44
	PLACE2000039	2.75	8.06	3.92	6.27	8.01	4.81
10	PLACE2000043	7	11.08	22.94	19.27	26.58	17.38
	PLACE2000044	0.63	6.92	1.12	1.8	1.71	1.29
	PLACE2000047	0.84	5.25	5.15	5.4	6.46	7.32
	PLACE2000050	1.48	2.68	4.78	2.92	2.98	1.2
	PLACE2000061	0.47	2.07	1.17	0.95	1.34	0.25
15	PLACE2000062	1.99	2.83	4.12	4.89	4.4	3.09
	PLACE2000072	0.78	2.45	1.57	1.85	1.62	1.69
	PLACE2000073	0.89	5.86	2.86	2.8	2.61	3.07
	PLACE2000097	8.54	19.93	23.93	27.69	35.36	26.36
	PLACE2000100	1.87	7.79	3.53	4.23	6.29	4.22
20	PLACE2000103	1.03	7.44	2.25	3.51	5.17	4.38
	PLACE2000106	1.53	2.42	4.19	5.71	3.29	4.01
	PLACE2000111	2.05	3.17	4.37	4.07	6.6	4.75
	PLACE2000115	0.3	2.06	0.75	0.31	1.29	0.97
25	PLACE2000118	10.15	17.04	21.09	13.73	15.21	22.01
	PLACE2000124	10.14	17.83	62.13	53.2	98.37	62.96
	PLACE2000132	0.06	6.26	1.48	0.99	1.5	1.56
	PLACE2000136	0.55	7.94	0.91	1.47	1.37	1.02
	PLACE2000137	0.96	4.46	2.4	2.65	4.12	3.14
30	PLACE2000140	2.91	5.24	14.34	13.2	12.08	9.43
	PLACE2000147	1.49	1.52	2.83	1.06	0.97	1.12
	PLACE2000153	0.3	3.44	2.15	1.69	2.45	1.95
	PLACE2000164	0.66	2.78	1.13	2.66	1.62	1.62
	PLACE2000170	1.54	6.18	4.69	5.26	9.09	6.24
35	PLACE2000172	0.33	4.34	2.15	1.25	1.93	2.43
	PLACE2000173	0.92	4.97	3.37	3.33	3.71	2.74
	PLACE2000174	1.17	4.68	2.43	1.85	2.89	2.05
	PLACE2000176	1.22	1.57	2.58	3.28	2.27	1.42
	PLACE2000187	1.01	2.08	2.55	3.45	3.66	2.19
40	PLACE2000216	7.03	9.28	11.47	14.09	9.13	3.68
	PLACE2000219	0.69	4.02	2.72	3.55	3.58	2.3
	PLACE2000221	2.49	6.81	6.53	7.22	9.33	8.56
	PLACE2000223	0.72	3.2	1.71	1.16	1.05	0.48
	PLACE2000231	1.02	3.97	3.11	3.43	2.61	2.47
45	PLACE2000235	1.82	5.27	6.17	6.02	7.45	6.97
	PLACE2000246	1.93	2	6.06	4.58	5.09	3.93
	PLACE2000264	0.67	1.39	1.85	2.45	3.74	3 * +
	PLACE2000274	0.65	2.4	2.12	3.09	4.11	2.1
	PLACE2000287	0.81	4.44	1.49	2	2.59	1.34
50	PLACE2000296	1.01	4.56	1.55	2.5	3.16	1.69
	PLACE2000302	1.34	4.67	2.86	3.52	3.35	3.45
	PLACE2000305	3.09	6.65	5.42	6.3	7.15	5.02
	PLACE2000317	0.92	6.34	2.26	3.15	2.95	2.4
	PLACE2000324	1.19	1.25	3.09	4.2	5.84	3.3
55	PLACE2000334	3.52	5	6.6	7.33	8.12	5.88



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	PLACE2000335	1.47	4.35	4.24	5.68	6.25	4.76		
	PLACE2000340	0.64	3.47	1.63	1.58	1.52	1.65		
	PLACE2000341	4.21	7.87	28.81	18.94	32.45	19.16		
5	PLACE2000342	2.07	5.11	4.32	4.84	5.82	4.49		
	PLACE2000347	1.24	5.26	5.58	7.83	6.22	7.55		
	PLACE2000357	8.49	13.56	15.35	17.83	18.98	21.24	*	+
	PLACE2000358	2.87	3.65	8.67	4.88	7.63	4.37		
10	PLACE2000359	1.27	1.79	4.45	3.28	6.65	3.61		
	PLACE2000366	1.93	3.14	3.22	3.99	5.6	4.17		
	PLACE2000371	4.29	5.2	6.08	5.95	9.06	7.32		
	PLACE2000373	1.91	4.8	5.98	5.69	6.29	4.19		
	PLACE2000374	1.86	5.17	2.78	1.62	2.79	1.49		
15	PLACE2000379	0.34	4.85	1.32	1.28	0.92	0.04		
	PLACE2000386	39.29	43.92	84.66	87.53	104.55	76.56		
	PLACE2000388	1.96	3.35	3.89	2.78	3.48	3.49		
	PLACE2000392	33.29	39.2	59.56	42.5	52.12	58.24		
	PLACE2000394	1.26	3.27	3.01	5.69	4.35	4.34	*	+
20	PLACE2000398	0.73	3.88	2.36	2.03	3.59	1.35		
	PLACE2000399	3.7	6.82	7.01	7.15	7	6.79		
	PLACE2000402	2.15	6.88	3.84	2.86	3.68	3.9		
	PLACE2000404	5.2	9.96	10.67	10.03	11.04	6.47		
	PLACE2000411	3.21	7.2	5.21	5.27	5.73	6.68		
25	PLACE2000418	0.73	2.28	2.41	2.22	3.07	2.37		
	PLACE2000419	0.99	2.32	2.54	4.95	4.55	3.29	*	+
	PLACE2000425	1.26	3.98	3.11	4.28	4.81	5.2		
	PLACE2000427	0.7	5.13	3.27	2.54	3.04	2.47		
	PLACE2000433	0.77	7.05	2.6	2.33	3.09	2.46		
30	PLACE2000435	0.48	5.19	1.49	1.69	1.63	1.5		
	PLACE2000438	1.61	4.74	3.66	2.33	2.81	3.15		
	PLACE2000450	3.01	4.38	5.67	6.51	7.39	5.63		
	PLACE2000455	0.24	2.62	1.24	1.65	2	1.82		
	PLACE2000458	0.38	3.3	1.81	1.06	2.7	1.24		
35	PLACE2000464	2.15	4.91	5.3	7.43	9.68	8.83	*	+
	PLACE2000465	1.43	6.72	6	6.51	8.27	6.31		
	PLACE2000473	120.94	179.35	328.3	214.7	297.75	279.74		
	PLACE2000477	0.43	3.87	1.34	1.13	2.22	0.97		
	PLACE3000004	2.22	4.63	6.39	5.27	7.51	5.2		
40	PLACE3000009	19.91	19.71	105.63	77.3	140.99	92.95		
	PLACE3000020	10.03	9.03	49.6	36.74	46.52	23.82		
	PLACE3000029	6.59	9.63	24.88	14.88	18.47	20.04		
	PLACE3000038	0.52	2.37	2.47	1.44	2.4	2.05		
45	PLACE3000052	5.13	7.95	23.92	25.01	29.61	24.94		
	PLACE3000059	0.57	5	2.42	0.75	2.8	1.27		
	PLACE3000067	2.51	5.79	7.44	5.66	8.53	7.75		
	PLACE3000069	1.95	5.61	3.58	5.24	3.79	4.55		
	PLACE3000070	2.57	5.57	9.04	9.5	10.42	10.57		
50	PLACE3000103	3.85	7.84	11.87	6.6	8.32	4.37		
	PLACE3000119	1.59	2.74	3.15	3.24	3.67	2.95		
	PLACE3000121	7.58	8.44	38.1	30.63	42.28	32.64		
	PLACE3000124	1.53	4.54	5.95	6.35	7.75	7.18		
	PLACE3000135	0.69	5.46	1.1	0.76	0.9	0.59		
55	PLACE3000136	0.77	10.46	4.46	2.12	2.77	2.01		

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	PLACE3000142	0.7	9.94	1.75	1.53	2.76	1.13		
	PLACE3000145	8.69	17.55	55.33	42.85	49.12	39.96		
	PLACE3000147	15.7	12.92	39.97	64.96	54.76	30.34		
5	PLACE3000148	0.7	2.08	1.48	0.82	1.4	1.38		
	PLACE3000154	0.48	1.86	0.67	1.5	0.87	0.44		
	PLACE3000155	1.28	4.26	2.53	3.97	4.76	3.04		
	PLACE3000156	1.11	7.96	2.07	1.96	3.4	2.81		
10	PLACE3000157	0.92	8.37	1.75	2.06	3.02	2.72		
	PLACE3000158	1.73	8.82	5.05	3.81	5.63	4.77		
	PLACE3000160	8.11	15.22	19.5	33.66	34.71	33.78	**	+
	PLACE3000169	2.15	2.65	6.87	4.3	5.11	5.12		
	PLACE3000181	1.06	2.14	3.94	3.22	2.62	3		
15	PLACE3000194	0.31	2.83	1.77	1.89	2.58	2.42		
	PLACE3000197	1.18	2.66	2.09	2.42	2.46	2.21		
	PLACE3000199	0.22	4.8	1.63	0.55	0.86	0.43		
	PLACE3000205	11.79	17.95	57.49	51.4	63.83	42.63		
	PLACE3000207	3.37	6.91	7.13	6.7	8.92	6.23		
20	PLACE3000208	2.26	4.96	2.66	5.28	5.97	5.84		
	PLACE3000213	4.79	5.55	10.8	5.12	5.16	5.05		
	PLACE3000215	1.88	5.02	5.71	4.74	5	3.03		
	PLACE3000218	0	1.63	1.18	0.97	0.62	0.31		
25	PLACE3000220	1.96	3.55	4.58	6.74	7.52	6.69	*	+
	PLACE3000221	14.42	25.34	40.15	43.8	51.16	36.99		
	PLACE3000225	1.15	4.68	3.11	2.11	2.67	1.28		
	PLACE3000226	1.37	5.65	5.16	3.78	7.42	3.68		
	PLACE3000230	0.83	3.46	1.36	2	2.8	1.73		
30	PLACE3000231	1.31	1.97	2.37	4.86	3.95	4.12	**	+
	PLACE3000235	1.12	1.75	3.89	3.95	4.21	3.39		
	PLACE3000242	2.6	5.11	9.24	9.46	10.97	8.29		
	PLACE3000244	1.05	3.2	1.81	1.85	1.81	0.64		
	PLACE3000253	0.7	3.75	1.64	2.67	2.11	1.27		
35	PLACE3000254	2.5	4.75	4.04	6.19	6.09	5.75	*	+
	PLACE3000271	2.67	6.06	6.81	10.96	10.99	9.5	*	+
	PLACE3000276	1.1	5.78	2.27	1.48	1.9	1.78		
	PLACE3000304	5.55	4.69	10.81	11.19	11.49	10.5		
	PLACE3000309	0.43	1.67	1.87	2.43	2.94	2.78	*	+
40	PLACE3000310	2.19	2.19	3.73	4.84	4.81	3.4		
	PLACE3000320	1.02	3.65	1.8	2.54	2.37	2.32		
	PLACE3000322	1.31	4.23	6.63	7.5	7.8	6.09		
	PLACE3000330	24.05	24.44	41.08	31.87	35.83	29.17		
45	PLACE3000331	1.21	5.86	4.14	4.34	5.7	4.31		
	PLACE3000336	2.61	6.99	4.42	4.24	5.72	5.11		
	PLACE3000339	7.36	5.1	11.41	16.25	18.28	17.37	**	+
	PLACE3000341	1.65	1.32	2.41	4.08	4.35	3.65	**	+
	PLACE3000350	5.88	6.4	12.86	15.45	18.5	15.41	*	+
	PLACE3000352	1.54	3.88	2.13	2.37	2.25	1.71		
50	PLACE3000353	5.38	9.72	11.8	19.12	22.98	15.5	*	+
	PLACE3000362	0.62	4.92	4.72	3.61	5.33	3.39		
	PLACE3000363	2.19	5.13	2.32	1.89	3.28	2.07		
	PLACE3000365	1.34	6.11	3.37	3.34	4.05	2.12		
55	PLACE3000373	0.89	1.52	3.66	2.93	6.08	2.3		
	PLACE3000374	1.07	1.85	2.91	2.72	2.99	2.15		

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	PLACE3000387	0.31	3.32	1.04	1.24	1.65	1.29	
	PLACE3000388	1.18	3.22	1.94	2.76	3.49	2.22	
	PLACE3000399	2.12	4.66	6.28	7.42	9.84	6.05	
5	PLACE3000400	3.08	5.44	11.87	7.97	10.77	7.82	
	PLACE3000401	7.52	11.42	18.59	22.61	29.55	23.4	* +
	PLACE3000402	1.79	3.21	3.4	2.19	1.74	1.79	
	PLACE3000405	3.37	3.74	5.82	5.54	7.22	6.01	
10	PLACE3000406	2.1	2.91	3.11	3.48	3.68	2.42	
	PLACE3000413	1.18	2.72	2.69	1.71	2.06	1.52	
	PLACE3000416	1.05	4.03	4.04	3.43	2.67	2.72	
	PLACE3000425	1.21	6.27	4.33	3.98	6.36	3.92	
	PLACE3000437	4.79	10.85	29.89	16.69	25.26	19.14	
15	PLACE3000455	2.97	8.07	10.62	8.97	10.39	7.91	
	PLACE3000475	16.52	19.2	47.35	40.22	39.77	34.21	
	PLACE3000477	5.44	4.79	5.56	8.05	5.52	8.42	
	PLACE4000003	0.38	2.97	1.61	3.14	2.33	2.31	
	PLACE4000008	15.19	11.38	16.76	13.05	14.26	8.84	
20	PLACE4000009	1.17	6.19	3.39	3.93	3.37	1.82	
	PLACE4000014	1.31	5.12	1.77	2.16	3.03	2.19	
	PLACE4000029	6.33	8.48	35.37	23.93	32.21	24.25	
	PLACE4000034	2.27	6.24	5.22	6.46	6.52	4.91	
	PLACE4000049	3.39	3.35	5.21	3.85	5.82	4.86	
25	PLACE4000052	1.41	3.36	2.2	2.62	2.64	2.02	
	PLACE4000062	1.6	4.94	5.06	4.25	5.06	3.71	
	PLACE4000063	2.59	6.87	5.19	4.86	4.81	3.73	
	PLACE4000089	1.52	6.31	3.35	2.81	3.91	2.84	
	PLACE4000093	0.44	5.6	1.61	1.28	1.65	1.98	
30	PLACE4000100	2.72	6.13	4.75	4.33	3.62	3.94	
	PLACE4000103	0.63	4.48	5.64	4.4	5.67	2.9	
	PLACE4000106	3.2	5.33	6.63	7.1	5.13	7.21	
	PLACE4000128	1.93	3.97	4.88	4.15	4.96	4.4	
	PLACE4000129	0.74	3.26	1.64	1.57	2.11	1.78	
35	PLACE4000131	7.14	10.85	41.43	32.45	41.08	31.22	
	PLACE4000147	0.34	3.65	0.54	0.45	0.93	0.61	
	PLACE4000156	2.47	6.08	8.06	7.83	13.47	9.07	
	PLACE4000175	0.72	4.08	1.48	0.98	0.91	0.84	
	PLACE4000190	14.55	18.47	70.34	49.15	74.82	60.76	
40	PLACE4000192	1.3	2.27	3.6	2.36	2	1.25	
	PLACE4000206	5.35	6.65	12.44	7.13	7.1	6.02	
	PLACE4000211	3.34	4.64	22.23	11.68	12.35	13.44	
	PLACE4000214	0.86	3.61	2.68	2.08	2.53	1.69	
45	PLACE4000222	0.93	5.28	4.36	4.13	4.75	3.5	
	PLACE4000223	0.46	4.51	1.79	1.37	1.22	0.38	
	PLACE4000229	1.9	5.79	2.11	2.81	3.36	3.48	
	PLACE4000230	1.11	5.89	6.51	3.61	6.81	5.15	
	PLACE4000233	1.26	3.02	5.66	2.92	2.98	3.51	
50	PLACE4000239	2.35	3.68	4.17	4.19	3.97	3.35	
	PLACE4000247	0.52	2.37	3.38	2.64	3.1	2.35	
	PLACE4000250	1.18	3.24	2.35	3.33	3.68	2.8	
	PLACE4000252	1.06	4.99	2.25	1.92	1.75	1.64	
	PLACE4000259	4.42	11.95	18.1	14.47	22.09	14.02	
55	PLACE4000261	0.87	10.29	1.07	2.03	1.9	1.12	

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	PLACE4000264	15.86	24.96	36.9	11.96	21.82	22.51	
	PLACE4000269	3.48	3.71	7.95	4.62	4.55	2.85	
5	PLACE4000270	0.43	1.42	1.87	1.75	1.83	0.59	
	PLACE4000281	17.84	20.97	44.05	32.93	28.37	28.87	
	PLACE4000300	0.67	2.06	2.04	3.21	2.88	3.58	* +
	PLACE4000320	1.33	5.86	3.1	2.84	5.32	3.21	
	PLACE4000323	1.63	7.43	5.13	4.03	4.65	4.82	
10	PLACE4000326	1.8	10.98	5.67	5.72	8.73	5.59	
	PLACE4000344	0.22	5.75	2.62	1.66	1.6	1.18	
	PLACE4000347	4.7	3.82	13.93	16.83	16.75	17.36	* +
	PLACE4000354	3.18	6.29	10.68	5.17	2.81	2.79	
	PLACE4000367	0.79	2.97	1.71	0.87	1.3	1.38	
15	PLACE4000369	1.35	3.97	2.36	1.99	1.96	0.82	
	PLACE4000379	2.44	6.66	5.44	5.94	7.55	5.07	
	PLACE4000387	0.88	5.86	2.11	1.28	0.84	1.12	
	PLACE4000392	0.42	5.58	1.32	1.81	1.02	1.63	
20	PLACE4000399	10.99	17.08	75.17	59.11	80.22	58	
	PLACE4000401	0.72	0.7	1.53	1.17	0.83	1.4	
	PLACE4000403	3.15	4.13	8.51	5.29	6.38	5.87	
	PLACE4000411	2.22	2.28	4	2.27	2.6	1.82	
	PLACE4000415	0.7	3.55	2.8	1.16	1.86	0.78	
25	PLACE4000416	25.49	29.13	33.54	23.65	21.92	24.83	
	PLACE4000424	1.61	5.59	3.33	3.27	3.92	2.51	
	PLACE4000431	3.89	7.39	21.01	17.68	28.21	16.79	
	PLACE4000443	0.07	4.33	2.15	1.52	2.83	1.14	
	PLACE4000445	3.94	5.43	9.98	7.62	6.99	6.27	
30	PLACE4000450	2.99	3.65	23.28	15.51	24.53	16.04	
	PLACE4000455	5.18	7.39	9.55	8	7.21	4.63	
	PLACE4000465	1.39	4.34	3.26	4.15	6.07	4.34	
	PLACE4000466	120.96	98.04	201.25	113.83	170.96	145.31	
	PLACE4000472	3.12	9.6	10.17	10.92	13.21	9.22	
35	PLACE4000487	3.18	7.83	16.5	14.66	16.62	15.05	
	PLACE4000489	0.93	4.69	3.41	1.95	3.88	1.69	
	PLACE4000494	1.15	1.6	4.07	2.74	3.1	2.08	
	PLACE4000502	6.3	5.39	10.92	11.65	15.08	6.37	
	PLACE4000521	2.5	3.44	16.06	12.78	20.63	11.2	
40	PLACE4000522	5.07	6.17	9.07	12.43	8.68	14.11	
	PLACE4000537	0.98	4.28	1.27	1.67	1.61	1.22	
	PLACE4000548	1.99	5.69	2.46	3.04	3.68	2.32	
	PLACE4000558	0.87	6.72	1.97	3.15	2.41	2.15	
	PLACE4000581	2.1	7.22	7.04	3.9	5.96	5.44	
45	PLACE4000590	0.4	0.61	0.15	0.4	0.81	-0.25	
	PLACE4000593	2.94	2.98	5.22	4.44	5.82	3.83	
	PLACE4000612	0.68	3.33	3.33	1.5	3.02	2.74	
	PLACE4000638	1.25	4.24	0.84	1.2	1.44	1.58	
	PLACE4000650	0.82	4.67	1.02	1.43	1.11	1.16	
50	PLACE4000651	2.42	6.4	7.48	5	7.01	6.07	
	PLACE4000654	0.98	5.7	2.47	1.35	2.48	1.47	
	PLACE4000670	0.5	4.06	2.92	0.76	1.29	0.67	
	PLACE4000685	6.35	8.68	13.83	13.46	14.26	13.77	
	PLACE4000687	0.37	3.02	1.11	2.2	1.4	1.12	
55	PLACE5000003	1.1	2.74	3.31	3.21	3.55	3.07	

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	PLACE5000005	12.43	16.53	27.36	24.54	24.57	24.76	
	PLACE5000019	0.4	4.15	1.13	0.59	1.89	0.79	
	PLACE5000021	0.74	4.59	1.61	0.39	0.93	0.32	
5	PLACE5000022	1.2	6.11	2.25	3.17	2.76	2.09	
	PLACE5000024	1.77	2.58	2.27	2.92	3.39	3.84	* +
	PLACE5000036	1.81	3.24	3.11	2.41	3.19	2.84	
	PLACE5000059	14.41	17.79	26.55	25.98	30.03	34.87	
10	PLACE5000076	1.41	3.61	2.22	4.04	3.96	2.54	
	PLACE5000117	7.44	12.48	15.66	16.87	18.78	20.64	
	PLACE5000143	0.85	6.45	2.11	1.67	2.85	2.73	
	PLACE5000152	0.42	4.49	1.23	1.61	1.95	1.57	
	PLACE5000154	18.23	23.5	45.06	21.81	25.65	31.8	
15	PLACE5000155	3.35	2.81	5.51	3.94	2.78	4.87	
	PLACE5000165	3.78	4.4	6.67	4.51	5.99	5.82	
	SKNMC1000004	9.7	11.62	16.77	10.19	12.16	13.96	
	SKNMC1000011	1.82	8.58	4.12	5.89	3.95	6.77	
	SKNMC1000013	0.51	6.69	1.13	1.21	2.14	1.44	
20	SKNMC1000014	1.28	4.18	3.22	3.77	6.37	3.96	
	SKNMC1000018	3.42	5.19	5.25	5.51	5.68	3.44	
	SKNMC1000020	0.95	4.03	3.46	3.6	4.68	4.56	
	SKNMC1000046	2	3.17	3.48	3.95	3.26	2.55	
25	SKNMC1000050	4.99	8.04	10.32	5.4	6.28	6.12	
	SKNMC1000062	9.79	12.6	20.18	19.2	15.42	18.73	
	SKNMC1000075	1.45	4.3	2.01	1.98	1.89	2.92	
	SKNMC1000082	1.12	4.39	2.13	1.85	1.78	2.39	
	SKNMC1000091	4.54	7.52	7.95	11.74	12.86	12.77	** +
30	SKNMC1000099	0.33	4.29	1.98	1.32	0.65	1.18	
	SKNMC1000104	1.13	4.24	3.45	1.47	3.14	2.43	
	SKNMC1000113	0.97	1.83	1.2	1.74	2.63	0.89	
	SKNMC1000119	1.73	2.64	5.07	4.48	5.34	4.67	
	SKNMC1000142	0.04	2.87	0.99	1.27	0.75	1	
35	SKNMC1000170	0.91	4.75	2.34	1.71	1.49	1.11	
	SKNMC1000178	3.02	8.39	7.08	5.77	9.65	9.02	
	SKNMC1000194	0.63	9.82	1.51	0.61	1.73	1.3	
	SKNMC1000198	1.35	11.01	3.33	2.65	2.1	2.88	
	SKNMC1000225	1.35	6.44	2.97	2.39	3.4	3.26	
40	SKNMC1000249	0.49	2.14	0.75	0.57	0.51	0.52	
	SPLEN1000007	0.74	2.15	2.11	1.7	2.26	1.99	
	SPLEN1000012	0.39	1.9	1.72	1.19	0.8	0.84	
	SPLEN1000014	1.78	4.4	4.9	5.75	4.33	3.99	
	SPLEN1000036	4.95	11.64	24.32	20.56	27.73	21.68	
45	SPLEN1000059	0.04	6.69	1.06	0.91	1.79	1.47	
	SPLEN1000068	1.68	10.81	5.71	5.79	5.17	5.64	
	SPLEN1000072	1	8.5	4.7	2.82	3	2.21	
	SPLEN1000101	20.01	18.4	45.64	29.93	25.24	12.63	
	SPLEN1000108	0.56	1.54	0.98	0.75	1.11	0.76	
50	SPLEN1000113	1.33	2.27	3.04	2.72	4.13	3.04	
	SPLEN1000114	2.97	4.19	6.03	3.59	4.76	6.32	
	SPLEN1000132	0.85	4	1.72	2.25	2.67	1.99	
	SPLEN1000135	3.13	8.76	14.93	11.12	15.28	10.52	
	SPLEN1000136	12.41	21.47	15.14	20.24	27.48	21.8	
55	SPLEN1000141	2.26	7.07	10.79	4.03	5.41	4.51	

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	SPLEN1000164	2.49	3.79	8.58	3.98	5.88	7.61		
	SPLEN1000166	0.4	2.9	2.96	1.67	1.19	1.68		
5	SPLEN1000175	2.16	4.48	6.1	5.65	4.12	4.15		
	SPLEN1000182	0.98	2.66	0.23	0.83	0.6	0.67		
	SPLEN1000185	3.41	8.49	8.54	11.38	10.43	11.95		
	THYMU1000004	10.22	14.07	20.43	22.34	22.76	23.6		
	THYMU1000009	9.48	10.13	14.9	13.48	23.86	22.1		
10	THYMU1000015	8.87	10.42	16.18	19.25	22.21	20.8	*	+
	THYMU1000016	6.24	5.96	13.03	10.3	8.45	9.38		
	THYMU1000023	0.77	1.86	3.6	5.22	3.68	3.6		
	THYMU1000034	0.16	1.77	1.8	0.79	0.88	0.14		
	THYMU1000035	0.62	2.8	0.97	1.17	0.95	1.31		
15	THYMU1000037	1.53	4.15	2.11	2.06	2.81	1.45		
	THYMU1000042	5.97	10.24	12.23	12.03	13.98	13.28		
	THYMU1000047	2.72	6.03	6.72	6.04	7.77	7.23		
	THYMU1000080	0.56	4.31	2.6	3.26	1.85	2.11		
20	THYMU1000094	2.77	3.47	7.91	9.17	8.35	4.55		
	THYMU1000109	17.28	14.34	111.37	98.05	142.29	93.04		
	THYMU1000127	2.75	5.95	10.76	8.18	9.98	6.74		
	THYMU1000130	2.5	4.4	4.55	6.69	6.07	4.94		
	THYMU1000137	3.53	7.18	10.26	12.67	18.55	13.05	*	+
25	THYMU1000146	4.37	8.38	6.52	8.29	7.46	7.74		
	THYMU1000159	5.43	9.51	16.37	12.4	15.15	13.27		
	THYMU1000163	5.85	12.26	37.58	45.53	58.37	36.93		
	THYMU1000167	2.39	3.02	4.73	4.89	6.79	3.97		
	THYMU1000186	0.69	1.05	1.45	1.31	2.45	0.66		
30	THYRO1000017	0.94	3.45	2.54	2.02	3.54	2.11		
	THYRO1000026	1.56	5.63	4.02	3.96	4.82	3.36		
	THYRO1000034	0.49	4.16	1.59	1.99	2	1.82		
	THYRO1000035	0.86	4.84	1.34	2.29	2.48	2.11		
	THYRO1000036	0.93	8.32	4	3.08	4.36	5.59		
35	THYRO1000040	2.58	7.02	4.76	4.66	4.83	4.93		
	THYRO1000061	2.01	1.91	3.07	3.53	3.8	2.61		
	THYRO1000067	1.98	2.8	5.12	3.37	4.14	3.3		
	THYRO1000070	1.26	2.09	3.59	2.65	3.85	3.45		
	THYRO1000072	1.33	3.37	4.22	2.54	4.08	2.06		
40	THYRO1000084	8.07	12.69	22.39	2.99	5.61	4.42		
	THYRO1000085	1.44	5.66	3.99	2.42	3.86	2.85		
	THYRO1000086	-0.05	5.46	1.74	0.89	1.18	1.15		
	THYRO1000087	0.72	3.86	1.01	0	0.58	0.17		
	THYRO1000092	2.32	5.1	4.66	3.75	4.43	4.5		
45	THYRO1000093	0.35	3.24	0.83	1.54	1.27	0.95		
	THYRO1000099	0.45	2.53	2.73	2.8	1.67	2.39		
	THYRO1000107	0.5	2.95	2.7	2.86	3.22	2		
	THYRO1000111	0.85	4.58	1.78	1.4	2.06	2.36		
	THYRO1000121	1.33	5.72	2.52	1.94	2.4	2.95		
50	THYRO1000124	0.27	5.55	0.64	0.86	0.89	0.64		
	THYRO1000129	0.36	2.1	0.11	0.94	1.11	0.92		
	THYRO1000130	1.82	3.11	3.13	3.85	3.01	2.39		
	THYRO1000132	2.4	3.62	9.43	11.14	6.99	6.26		
55	THYRO1000134	1.5	4.07	3.22	4.06	3.65	3.73		
	THYRO1000144	1.72	4.78	3.15	7.87	7.09	2.33		

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	THYRO1000155	1.6	4.1	1.45	1.77	1.9	2.23		
	THYRO1000156	1.13	6.53	3.62	2.45	4.29	2.58		
	THYRO1000163	3.62	8.42	5.28	4.76	6.63	2.24		
5	THYRO1000173	1.19	4.45	2.26	3.33	1.36	2.75		
	THYRO1000186	1.98	3.24	7.86	6.91	6.84	6.35		
	THYRO1000187	2.7	3.58	5.3	4.92	6.24	5.22		
	THYRO1000190	1.12	3.32	2.94	3.73	4.55	2.71		
	THYRO1000196	0.3	5.28	0.81	0.66	1.21	0.52		
10	THYRO1000197	2.05	7.28	4.69	4.08	6.24	3.89		
	THYRO1000199	0.76	6.28	4.13	1.93	2.08	1.98		
	THYRO1000206	8.47	6.92	9.25	8.44	11.6	7.5		
	THYRO1000221	1.9	3.17	4.42	4.02	5.87	4.54		
15	THYRO1000222	3.65	4.26	4.23	4.68	4.96	4.93	*	+
	THYRO1000228	0.81	3.67	2.85	2.24	3.04	2.94		
	THYRO1000241	1.76	3.7	6.29	4.62	5.54	4.01		
	THYRO1000242	0.63	4.16	4.46	2.49	2.56	2.62		
	THYRO1000246	1.61	5.5	3.9	3.43	4.7	3.91		
20	THYRO1000253	1.07	4.05	1.73	1.99	3.35	2.31		
	THYRO1000270	1.15	5.12	1.39	1.22	2.5	1.26		
	THYRO1000279	0.42	2.84	0.25	0.65	1.01	0.58		
	THYRO1000285	2.75	4.65	7.31	7.03	7.75	4.88		
	THYRO1000288	7.76	7.59	11.77	5.68	5.07	7.22		
25	THYRO1000296	4.18	6.04	6.22	7.4	11.24	8.96	*	+
	THYRO1000320	1.54	5.83	4.97	3.65	4.45	3.34		
	THYRO1000322	1.1	5.48	2.48	1.76	3.93	1.76		
	THYRO1000327	1.75	7.69	4.77	6.21	5.23	4.41		
	THYRO1000343	2.5	6.12	5.35	5.06	5.04	6.13		
30	THYRO1000345	1.36	7.34	11.92	7.82	5.84	9.49		
	THYRO1000358	1.82	3.39	3.08	1.92	2.32	1.54		
	THYRO1000368	0.76	2.39	2.73	1.43	2.82	0.58		
	THYRO1000375	3.2	7.03	4.79	7.38	6.09	9.77		
35	THYRO1000381	0.92	2.88	2.19	3.87	3.11	2.74		
	THYRO1000387	0.98	6.66	3.22	2.53	3.56	2.51		
	THYRO1000394	1.31	9.88	4.59	4.29	5.19	2.61		
	THYRO1000395	0.8	10.44	2.26	1.97	2.07	2.02		
	THYRO1000400	0.57	8.1	2.82	2.35	2.96	2.52		
40	THYRO1000401	0.86	1.94	2.5	1.87	1.16	1.57		
	THYRO1000407	1.97	2.3	1.36	1.37	1.58	0.55		
	THYRO1000420	1.8	2.67	4.46	3.52	3.53	3.39		
	THYRO1000438	1.78	4.37	3.26	2.94	3.33	3.15		
	THYRO1000452	2.62	7.99	6.45	3.71	5.75	4.38		
45	THYRO1000455	0.32	6.67	2.31	0.25	0.97	0.87		
	THYRO1000471	0.99	8.03	2.05	1.11	2.08	1.02		
	THYRO1000481	1.33	6.23	4.68	3.79	3.45	4.55		
	THYRO1000484	1.2	1.42	2.41	2.35	3	2.21		
	THYRO1000488	1.18	2.64	2.44	1.49	2.02	1.7		
50	THYRO1000501	1.12	4.01	2.73	3	1.92	1.82		
	THYRO1000502	0.34	3.7	1.69	1.79	1.44	1.2		
	THYRO1000505	0.13	4.64	1.19	1.14	1.02	0.6		
	THYRO1000535	11.1	20.54	39.24	54.13	69.59	62.96	*	+
	THYRO1000556	1.89	6.36	4.13	3.77	5.17	3.69		
55	THYRO1000558	0.25	2.82	1.12	1.16	0.81	0.61		

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	THYRO1000569	2.88	4.12	6.05	5.78	4.46	4.88
	THYRO1000570	2.31	3.28	8.46	8.53	6.04	3.49
5	THYRO1000572	0.43	2.04	1.11	0.17	0.97	-0.42
	THYRO1000573	0.69	4.02	1.73	2.02	2.2	1.78
	THYRO1000577	1.06	5	1.34	0.96	1.22	0.71
	THYRO1000580	0.79	3.72	3.01	2.82	2.2	1.79
	THYRO1000584	2.18	6.88	8.8	7.57	6.61	7.58
10	THYRO1000585	4.83	9.37	9.83	5.76	6.27	9.52
	THYRO1000596	0.22	0.93	1.19	0.44	1.36	0.21
	THYRO1000602	2.08	2.95	4.01	4.05	4.65	4.97
	THYRO1000605	0.37	3.01	0.98	2.13	2.14	1.56
	THYRO1000615	1.02	3.62	1.24	1.55	1.36	1.29
15	THYRO1000625	0.71	5.48	2.28	2.46	2.9	1.78
	THYRO1000636	3.67	5.65	6.9	6.53	7.84	6.67
	THYRO1000637	0.91	3.96	1.71	1.18	2.03	1.54
	THYRO1000641	0.38	4.19	2.49	1.36	1.67	1.64
20	THYRO1000657	2.99	3.69	5.42	7.67	12.28	3.86
	THYRO1000658	2.68	3.62	5.39	5.4	5.55	6.09
	THYRO1000662	1.1	3.19	2.09	2.42	2.69	1.66
	THYRO1000666	0.57	3.19	2.28	1.63	1.48	1.43
	THYRO1000676	1.37	4.53	2.01	1.75	1.83	1.56
25	THYRO1000678	0.52	5.86	0.99	1.29	1.4	0.53
	THYRO1000684	0.95	4.98	2.94	1.92	2.65	1.47
	THYRO1000694	2.08	6.64	4.65	2.8	2.48	3.59
	THYRO1000699	2.98	2.14	5.55	4.86	7.08	7.12
	THYRO1000712	1.88	4.25	5.9	6.25	6.75	7.78
30	THYRO1000715	5.74	5.67	27.37	21.74	28.63	16.99
	THYRO1000716	0.92	3.26	3.2	1.88	1.78	1.35
	THYRO1000717	1.58	5	4.36	2.98	4.63	1.91
	THYRO1000723	0.6	4.54	1.6	0.55	1.06	0.85
	THYRO1000734	-0.01	4.81	1.89	1.49	1.73	1.07
35	THYRO1000748	0.98	5.51	5.23	2.35	3.85	3.18
	THYRO1000755	1.74	3.26	4.32	4.33	3.47	4.38
	THYRO1000756	2.79	4.24	3.24	3.46	4.2	3.41
	THYRO1000776	0.48	2.17	3.02	3.36	3.99	3.34
	THYRO1000777	1.81	3.39	4.54	4.99	2.05	2.37
40	THYRO1000779	1.45	3.55	0.88	0.18	1.01	-0.26
	THYRO1000782	3.92	10.13	12.52	10.76	15.05	14.05
	THYRO1000783	0.12	5.51	1.2	1.11	1.41	0.92
	THYRO1000786	6.65	9.54	19.71	15.74	7.92	13.7
	THYRO1000787	0.23	1.88	1.67	1.31	1.54	0.78
45	THYRO1000792	1.51	3.13	2.29	3.09	3.13	2.11
	THYRO1000793	0.11	3.13	0.84	1.51	1.86	1.16
	THYRO1000795	1.23	6.03	3.54	2.76	3.1	3.05
	THYRO1000796	0.6	7.73	2.44	2.26	2.95	1.66
	THYRO1000798	1.89	5.82	2.51	2.59	3.57	3.53
50	THYRO1000800	9.26	17.2	24.74	17.74	20.68	21.06
	THYRO1000805	0.49	3.04	1.08	0.72	2.66	1.38
	THYRO1000815	2.54	3.49	9.48	7.61	5.47	7.87
	THYRO1000829	5.55	7.83	10.57	3.78	8.32	10.01
55	THYRO1000835	0.96	3.2	1.93	1.07	2.36	1.8
	THYRO1000843	1.09	11.48	3.56	3.69	4.41	3.62



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	THYRO1000846	0.76	5.71	1.32	2.67	1.62	1.26	
	THYRO1000852	1.59	6.02	5.63	2.8	4.7	3.32	
	THYRO1000855	3.14	5.02	6.63	9.03	15.1	10.07	* +
5	THYRO1000865	1.86	4.3	11.97	10.01	11.47	8.95	
	THYRO1000866	7.47	6.29	12.66	4.49	7.87	6.01	
	THYRO1000881	5.62	7.3	10.93	15.65	26.64	29.58	* +
	THYRO1000894	0.33	3.95	1.36	1.75	1.48	1	
	THYRO1000895	0.58	4.43	1.42	1.62	1.46	0.82	
10	THYRO1000916	1.22	5.49	3.43	2.43	3.13	2.29	
	THYRO1000917	16.19	25.26	34.11	30.37	37.42	35.89	
	THYRO1000926	0.78	3.13	1.27	1.76	1.57	0.82	
	THYRO1000934	0.08	3.1	1.34	0.43	1.38	1.46	
15	THYRO1000951	0.52	2.46	1.26	2.33	2.11	1.9	
	THYRO1000952	2.25	3.81	6.01	2.38	2.53	2.24	
	THYRO1000956	0.06	2.55	1.81	1.16	1.5	0.87	
	THYRO1000960	0.5	6.72	2.89	1.85	2.79	1.48	
	THYRO1000961	1.67	7.77	3.56	4.73	5.26	4.64	
20	THYRO1000964	0.42	11.59	0.76	1	1.27	1.06	
	THYRO1000971	1.82	9.9	3.56	3.29	3.33	2.19	
	THYRO1000974	2.87	8.83	7.53	9.87	11.79	8.71	
	THYRO1000975	1.5	2.19	3.8	4.02	3.68	3.68	
	THYRO1000983	6.42	8.31	11.63	12.67	8.49	7.12	
25	THYRO1000984	2.4	2.83	3.03	3.29	2.98	3.26	
	THYRO1000988	1.36	4.14	3.23	3.48	3.68	2.67	
	THYRO1000991	1.22	4.71	2.05	1.76	2.22	3.2	
	THYRO1000999	0.87	9.64	3.26	1.96	3.14	2.26	
	THYRO1001003	2.97	8.43	4.42	3.1	4.52	3.56	
30	THYRO1001015	0.6	6.29	2.04	2.22	1.79	1.66	
	THYRO1001016	1.73	2.26	3.34	2.06	1.85	1.24	
	THYRO1001022	0.9	1.86	0.86	1.68	1.25	1.41	
	THYRO1001031	4.65	3.97	4.55	5.03	7.03	6.16	
	THYRO1001033	1.18	3.34	2.46	2.86	3.45	2.02	
35	THYRO1001062	1.21	5.4	4.14	2.9	4.31	2.62	
	THYRO1001063	0.5	8.74	2.38	2.37	2.09	2.84	
	THYRO1001071	0.12	7.45	0.88	1.33	0.68	0.76	
	THYRO1001080	2.56	6.75	5.11	4.96	4.31	4.78	
	THYRO1001093	0.77	1.63	3.24	5.11	1.74	1.5	
40	THYRO1001100	0.52	1.89	2.05	1.89	1.21	0.78	
	THYRO1001102	2.61	3.6	5.7	4.4	4.95	6.93	
	THYRO1001104	3.67	6.54	6.55	8.77	8.01	11.18	
	THYRO1001109	1.81	6.02	2.68	3.06	2.58	1.99	
45	THYRO1001113	11.41	17.42	32	21.81	26.65	18.72	
	THYRO1001120	1.65	6.22	5.27	4.78	5.8	3.72	
	THYRO1001121	1.57	4.28	4.19	3.92	2.72	3	
	THYRO1001128	1.64	2.77	5.86	3.52	3.19	5.09	
	THYRO1001133	1.14	3.02	7.23	6.54	4.54	4.12	
50	THYRO1001134	2.97	4.78	1.63	3.14	2.83	1.38	
	THYRO1001142	0.3	2.69	0.63	1.3	1.71	0.22	
	THYRO1001173	8.37	12.87	7.72	11.14	9.92	10.62	
	THYRO1001175	3.26	6.63	5.51	3.46	4.62	3.52	
	THYRO1001177	1.36	5.85	5.93	4.66	7.27	7.97	
55	THYRO1001189	2.74	6.93	11.42	7.84	7.27	9.94	

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	THYRO1001194	1.05	2.62	4.96	4.89	4.57	2.31	
	THYRO1001204	2.17	3.58	4.27	4.03	4.74	4	
	THYRO1001205	5.76	10.65	20.23	18.54	19.57	20.9	
5	THYRO1001213	1.21	4.69	4.44	3.12	3.21	2.33	
	THYRO1001224	3.59	8.25	6.37	9.92	12.69	10.55	* +
	THYRO1001237	2.82	6.25	4.99	3.61	4.53	4.46	
	THYRO1001242	9.74	11.65	19.04	20.02	19.98	20.46	
10	THYRO1001258	2.08	5.45	3.58	3.33	2.05	2.66	
	THYRO1001262	0.86	2.64	3.38	2.36	3.61	2.69	
	THYRO1001266	0.15	2.39	1.02	0.97	1.64	0.66	
	THYRO1001271	1.85	4.12	4.12	2.46	2.77	2.97	
	THYRO1001287	7.3	8.3	39.26	30.14	43.68	26.2	
15	THYRO1001290	0.38	3.25	1.14	1.15	1.35	0.36	
	THYRO1001291	0.96	7.17	4.38	4.31	4.97	3.5	
	THYRO1001297	3.05	8.04	6.14	6.85	7.47	9.18	
	THYRO1001302	1.72	5.59	5.17	3.8	3.71	3.5	
	THYRO1001313	1.61	2.33	2.91	2.91	2.62	1.48	
20	THYRO1001320	1.76	2.52	5.31	5.07	5.74	4.83	
	THYRO1001321	2.25	2.65	4.3	2.48	4.23	4.23	
	THYRO1001322	1.34	3.93	3.34	1.75	2.67	2.01	
	THYRO1001327	1.29	6.01	4.18	1.4	3.89	2.49	
	THYRO1001336	1.89	6.84	6.72	4.62	4.43	4.18	
25	THYRO1001347	0.43	4.12	3.35	1.85	2.81	0.65	
	THYRO1001358	2.57	5.74	4.52	4.3	5.75	5.1	
	THYRO1001363	0.8	2.15	1.52	2.09	2.24	2.28	
	THYRO1001365	0.86	3	1.6	2.19	2.6	1.96	
30	THYRO1001374	1.85	4.45	12.86	9.4	13.01	6.21	
	THYRO1001401	1.76	5.33	4.89	5.39	7.86	6.29	
	THYRO1001403	1.26	5.15	3.22	3.22	4.42	3.94	
	THYRO1001405	6.99	12.5	10.86	6.69	8.56	10.63	
	THYRO1001406	15.73	14.87	27.69	21.36	22.77	21.36	
35	THYRO1001411	4.49	5.46	10.08	8.93	12.44	8.12	
	THYRO1001420	11.55	15.25	47.52	42.01	44.49	49.87	
	THYRO1001426	3.42	5.56	8.83	9.32	12.77	11.18	
	THYRO1001430	6.97	6.54	10.84	11.13	11.7	13.81	
	THYRO1001434	0.68	5.19	2.11	2.08	4.23	1.73	
40	THYRO1001456	1.74	6.05	2.63	2.89	2.66	2.4	
	THYRO1001457	1.71	4.72	2.04	2.95	4.7	2.67	
	THYRO1001458	0.95	5.44	6.11	6.13	9.17	7.23	
	THYRO1001459	4.54	5.07	9.42	7.18	9.87	14.21	
	THYRO1001471	0.91	2.07	1.93	2.36	2.91	1.64	
45	THYRO1001478	0.58	3.09	1.34	0.95	2.61	2.75	
	THYRO1001480	5.4	10.53	13.62	14.79	15.94	15.57	
	THYRO1001481	2.95	8.64	7.24	4.91	7.76	7.13	
	THYRO1001487	1.36	5.51	3.52	4.1	2.67	3.48	
	THYRO1001495	2.06	5.57	5.43	5.06	9.4	7.55	
50	THYRO1001498	5.39	8.08	13.42	11.59	16.38	19.6	
	THYRO1001510	1.67	2.88	1.59	1.65	2.57	3.35	
	THYRO1001512	26.7	26.97	110.28	56.03	90.95	68.54	
	THYRO1001519	5.92	7.77	11.05	8.91	5.75	10.38	
55	THYRO1001522	2.02	4.7	5.79	4.15	4.69	5.51	
	THYRO1001523	1.83	4.92	3.73	4.38	4.07	4.26	

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	THYRO1001526	26.21	28.22	44.73	34.28	47.64	46.52	
	THYRO1001529	1.64	5.27	2.8	2.32	2.42	2.98	
	THYRO1001534	1.41	4.01	4.96	5.1	5.9	4.54	
5	THYRO1001537	7.4	5.17	12.33	5.97	7.42	7.23	
	THYRO1001541	2.14	3.88	8.27	7.76	8.7	6.73	
	THYRO1001545	1.26	3.84	2.9	4.95	3.57	3.16	
	THYRO1001559	4.52	6.34	8.04	9.06	10.5	10.54	* +
10	THYRO1001563	9.49	14.06	15.89	10	15.49	22.09	
	THYRO1001570	2.01	8.2	3.85	4.25	5.17	3.41	
	THYRO1001573	1.15	5.77	2.22	1.47	2.87	2.67	
	THYRO1001584	2.47	8.54	8.38	5.14	7.81	7.29	
	THYRO1001593	4.27	5.67	11.17	9.5	10.93	9.52	
15	THYRO1001595	3.14	4.53	7.06	5.97	6.35	7.29	
	THYRO1001596	4.71	5.48	7.44	6.45	5.86	2.51	
	THYRO1001602	1.49	3.26	3.52	4.95	5.22	3.41	
	THYRO1001605	1.58	4.48	3.22	3.2	3.43	2.42	
	THYRO1001608	1.87	9.45	5.1	5.04	8.23	4.7	
20	THYRO1001617	6.06	13.68	11.47	9.75	10.87	9.61	
	THYRO1001634	1.87	9.08	3.46	2.93	5.59	2.05	
	THYRO1001637	3.51	3.13	9.65	8.72	7.94	9.07	
	THYRO1001641	2.57	3.73	5.09	4.03	3.08	2.94	
	THYRO1001656	1.59	2.94	4.16	2.82	5.36	2.33	
25	THYRO1001658	22.34	29.19	40.11	34.98	33.16	42.01	
	THYRO1001661	1.4	5.83	2.31	2.93	3.31	2.05	
	THYRO1001671	0.67	7.36	2.68	1.89	1.34	1.8	
	THYRO1001672	1.1	9.24	2.1	1.14	1.52	1.66	
30	THYRO1001673	1.59	7.6	3.49	2.86	4.74	2.16	
	THYRO1001677	1.6	2.27	3.87	3.03	3.54	3.36	
	THYRO1001683	12.71	17.66	29.06	24.4	15.4	16.72	
	THYRO1001700	1.39	2.52	2.67	2.09	1.58	1.37	
	THYRO1001702	11.83	15.98	16.19	15.63	14.35	14.29	
35	THYRO1001703	1.63	6.74	4.25	4.72	3.27	4.21	
	THYRO1001706	1.7	6.47	3.01	2.96	5.6	3.53	
	THYRO1001721	1.84	5.66	3.2	2.73	6.37	2.77	
	THYRO1001725	5.3	6.55	9.69	8.97	8.65	8.29	
	THYRO1001730	17.72	20.4	40.1	30.61	26.56	34.8	
40	THYRO1001738	1.35	3.18	4.65	3.52	2.82	1.78	
	THYRO1001743	0.19	2.13	1.85	1.8	1.64	1.06	
	THYRO1001745	0.47	2.88	1.55	1.05	1.2	1.27	
	THYRO1001746	1.9	6.25	4.04	6.12	4.01	3.88	
	THYRO1001770	15.49	20.38	35.39	41.65	44.42	40.17	* +
45	THYRO1001772	1.12	4.88	3.64	4.78	4.24	3.06	
	THYRO1001778	3.89	6.68	9.89	14.67	13.47	14.25	* +
	THYRO1001793	3.85	3.77	9.43	10.3	10.42	4.92	
	THYRO1001796	1.35	2.28	2.28	3.45	4.22	3.24	* +
50	THYRO1001800	1.82	2.99	2.75	4.17	5.12	2.09	
	THYRO1001803	3.42	6.03	5.21	4.31	4.14	3.42	
	THYRO1001809	1.6	4.26	3.4	5.9	4.23	3.39	
	THYRO1001817	8.69	18.33	24.88	22.11	22.77	25.27	
	THYRO1001819	4.68	8.46	9.01	7.84	10.46	6.77	
55	THYRO1001828	21.89	24.53	104.32	106.68	121.95	68.55	
	THYRO1001854	6.67	6.12	12.45	13.43	15.86	13.31	

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	THYRO1001895	0.85	1.31	2.52	3.54	4.31	1.28	
	THYRO1001907	2.16	3.08	3.37	3.9	4.53	2.74	
	TRACH1000006	2.51	5.87	6.63	4.34	3.46	3.22	
5	TRACH1000013	1.53	4.65	3.68	2.55	3.33	2.65	
	TRACH1000074	2.65	6.75	6.09	7.5	7.26	4.77	
	TRACH1000095	0.28	5.66	2.23	2.46	1.48	1.11	
	TRACH1000102	2.42	6.66	4.09	5.79	5.04	3.65	
10	TRACH1000108	1.1	1.01	2.05	1.75	2.49	1.09	
	TRACH1000126	0.96	1.75	2.71	1.82	3.79	2.54	
	TRACH1000146	1.3	2.67	2.31	3.02	5.18	3.75	
	TRACH1000160	0.61	4.06	1.5	1.47	1.76	0.72	
	TRACH1000184	4.45	7.16	10.16	7.47	8.73	5.69	
15	VESEN1000004	0.69	5.55	3.19	2.56	2.95	2.02	
	VESEN1000007	0.93	5.32	2.94	2.38	3.45	2.94	
	VESEN1000013	5.96	10.11	16.78	10.76	11.25	13.88	
	VESEN1000028	5.2	7.5	9.88	13.18	11.71	14.08	* +
	VESEN1000059	1.55	2.88	2.1	3.38	2.82	2.27	
20	VESEN1000100	1.96	3.22	3.35	3.49	4.58	3.59	
	VESEN1000107	0.88	4.84	2.88	3.12	2.9	2.48	
	VESEN1000117	1.63	6.43	2.46	2.16	2.7	1.79	
	VESEN1000122	1.52	5.34	1.24	4.79	4.51	4.5	
25	VESEN1000137	0.76	5.47	1.92	1.75	3.33	1.65	
	VESEN1000195	7.79	7.93	11.67	8.42	7.51	10.27	
	VESEN1000215	1.48	3.03	2.06	2.67	3.84	1.87	
	VESEN1000279	8.71	11.32	18.49	22.93	23.38	34.68	* +
	VESEN1000363	3.52	6.07	9.99	7.2	9.06	4.59	
30	VESEN1000388	2.55	6.48	3.31	4.17	3.75	6.7	
	VESEN1000394	0.44	7.11	2.33	2.37	2.55	2.36	
	VESEN1000410	1.11	5	1.78	2.36	2.71	3.69	
	VESEN1000411	2.37	4.95	5.08	6.76	7.55	9	* +
	VESEN1000415	1.54	2.64	4.03	5.57	3.92	5.29	
35	VESEN1000440	7	5.53	7.81	3.79	9.4	12.22	
	VESEN1000452	1.22	3.65	2.33	2.91	3.97	4.11	
	VESEN1000539	191.54	185.28	334.6	389.84	403.89	547.31	* +
	VESEN1000554	0.67	6.47	1.43	1.47	2.55	1.58	
	VESEN1000557	4.22	7.94	7.73	6.55	9.07	10	
40	VESEN1000575	7.49	9.75	16.33	11.95	11.73	14.8	
	VESEN1000585	1.69	4.49	3.37	2.53	2.93	3.08	
	VESEN1000592	1.58	2.31	1.58	2.02	1.83	1.46	
	VESEN1000658	1.96	3.56	4.45	5.86	3.91	4.91	
45	VESEN1000669	8.43	10.02	16.35	15.06	14.17	15.51	
	VESEN1000743	0.97	3.3	2.52	1.99	3.37	3.21	
	VESEN1000752	37.43	51.51	72.35	49.32	57.03	57.96	
	VESEN1000761	13.48	18.17	19.37	24.6	33.21	31.28	* +
	VESEN2000039	10.45	15.98	15.56	13.56	18.3	20.1	
50	VESEN2000102	0.4	3.99	1.6	1.21	1.51	1.61	
	VESEN2000164	2.45	3.52	4.8	5.55	4.36	3.66	
	VESEN2000175	0.57	2.64	1.94	3.03	2.05	2.59	
	VESEN2000186	3.77	5.53	6.53	6.68	3.87	2.47	
	VESEN2000199	8.94	13.26	21.75	19.58	24.45	24.12	
55	VESEN2000200	0.5	4.97	2.78	3.03	3.1	1.6	
	VESEN2000204	0.48	12.7	1.02	0.98	1.2	0.33	

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	VESEN2000218	6.66	20.26	19.48	21.37	20.75	18.86		
	VESEN2000230	0.84	7.4	1.45	2.74	1.7	2.41		
	VESEN2000272	2.29	4	8.92	7	8.31	5.88		
5	VESEN2000299	1.99	2.97	3.2	3.3	3.77	3.31		
	VESEN2000323	4.51	8.12	8.37	8.91	9.5	9.36		
	VESEN2000327	3.16	5.8	4.42	3.62	7.66	5.07		
	VESEN2000328	5.44	8.02	11.88	8.73	15.35	14.36		
10	VESEN2000330	6.39	15.42	14.7	14.59	27.73	18.86		
	VESEN2000336	0.82	8.97	2.54	3.46	3.83	2.88		
	VESEN2000354	1.56	8.24	2.48	1.53	2.71	2.1		
	VESEN2000378	7.17	8.87	14.57	13.23	11.14	10.3		
	VESEN2000379	19.87	23.02	44.55	49.13	42.81	32.61		
15	VESEN2000397	0.72	2.38	1.24	1.36	2.06	1.54		
	VESEN2000416	2.83	3.88	4.41	5.74	5.31	5.71	*	+
	VESEN2000420	1.08	3.58	1.94	0.95	1.21	1.13		
	VESEN2000430	0.51	6.68	1.53	2.06	1.79	1.8		
	VESEN2000448	0.51	6.87	1.73	2.12	2.69	1.5		
20	VESEN2000449	2.43	8.07	6.59	8.3	11.31	8.21		
	VESEN2000456	0.74	0.87	2.11	1.54	1.22	0.87		
	VESEN2000562	4.07	3.42	17.42	13.67	22.82	14.47		
	VESEN2000573	0.18	1.75	1.75	1.04	1.21	1.13		
	VESEN2000604	1.73	3.44	2.24	2.04	1.67	2.15		
25	VESEN2000614	4.16	9.02	14.64	13.54	16.27	12.27		
	VESEN2000638	0.48	5.92	1.98	1.33	1.91	1.68		
	VESEN2000641	0.83	3.69	1.34	1.95	2.21	1.43		
	VESEN2000645	2.18	5.29	5.38	5.91	5.73	5.5		
30	Y79AA1000013	2.57	2.7	4.33	3.45	3.8	3.94		
	Y79AA1000030	1.79	4.06	4.52	3.24	3.85	2.47		
	Y79AA1000033	2.87	6	8.4	8.37	10.17	5.83		
	Y79AA1000037	1.38	3.36	5.71	4.84	6.82	4.49		
	Y79AA1000041	1.05	5.16	3.79	4.73	3.65	2.06		
35	Y79AA1000059	1.69	5	4.09	3.88	4.51	2.82		
	Y79AA1000065	24.06	28.99	52.25	82.48	101.48	98.73	**	+
	Y79AA1000081	39.47	49.78	73.62	113.19	114.49	98.22	**	+
	Y79AA1000127	4.08	4.21	5.8	8.42	10.03	7.39	*	+
	Y79AA1000130	2.24	2.48	5.76	6.61	8.1	8.03	*	+
40	Y79AA1000131	507.64	569.21	946.04	769.75	725.35	342.07		
	Y79AA1000134	1.99	4.93	4.21	5.63	4.75	5.38		
	Y79AA1000143	3.58	8.79	4.83	9.98	10.98	11.04	*	+
	Y79AA1000144	4.63	10.79	10.59	11.02	11.62	11		
	Y79AA1000150	18.39	22.18	84.69	93.5	117.62	78.89		
45	Y79AA1000153	183.67	191.4	436.64	423.46	442.52	386.45		
	Y79AA1000166	2.13	2.25	4.15	3.52	4.97	3.6		
	Y79AA1000179	2.58	3.76	4.2	6.85	7.58	3.89		
	Y79AA1000181	1.96	3.92	4.2	4.82	5.66	3.79		
	Y79AA1000202	22.93	24.47	55.57	91.68	86.86	83.22	**	+
50	Y79AA1000207	5.22	7.51	9.82	14.95	16.24	12.62	*	+
	Y79AA1000214	14.94	22.18	33.76	50.43	60.78	41.96	*	+
	Y79AA1000222	11.8	14.89	21.69	49.21	58.01	68.86	**	+
	Y79AA1000226	11.04	14.94	34.41	22.86	33.54	30.03		
	Y79AA1000227	5.95	4.52	7.25	8.98	9.51	9.62	*	+
55	Y79AA1000230	1.09	1.49	2.02	2.07	2.88	2.59		

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	Y79AA1000231	5.99	9.04	15.81	14.63	23.77	17.1		
	Y79AA1000239	15.47	20.55	25.65	18.95	24.01	22.11		
5	Y79AA1000258	2.64	5.17	6.72	5.87	4.95	5.84		
	Y79AA1000268	2.65	5.48	5.09	4.33	5.76	4.01		
	Y79AA1000269	4.32	7.88	7.86	8	6.86	8.24		
	Y79AA1000270	5.28	8.35	11.58	13.17	17.58	16.23	*	+
	Y79AA1000280	1.74	4.17	4.9	5.29	3.1	5.27		
10	Y79AA1000285	3.44	4.21	5.91	4.01	6.86	5.22		
	Y79AA1000295	0.75	3.06	4.85	4.32	4.23	4.45		
	Y79AA1000307	2.88	3.91	5.06	9.35	7.58	11.25	*	+
	Y79AA1000313	3.11	9.02	9.85	10.61	12.84	13.36		
	Y79AA1000314	4.23	10.74	9.19	6.93	6.53	7.51		
15	Y79AA1000328	4.65	10.05	2.64	7.73	9.28	8.68		
	Y79AA1000334	1.43	4.22	3.55	2.68	2.81	3.46		
	Y79AA1000342	10.65	10.05	26.47	23.7	19.13	28.35		
	Y79AA1000346	7.61	8.17	7.9	20.1	22.06	20.18	**	+
20	Y79AA1000347	6.94	7.96	12.42	18.78	16.47	18.48	**	+
	Y79AA1000349	6.93	9.63	12.67	12.31	11.96	14.75		
	Y79AA1000355	3.17	8.28	8.94	8.84	13.55	8.77		
	Y79AA1000368	5.24	8.39	24.43	22.48	35.67	22.55		
	Y79AA1000388	22.9	32.66	62.37	94.17	128.35	109.08	**	+
25	Y79AA1000392	3.02	6.81	3.76	3.42	2.73	3.78		
	Y79AA1000405	3.98	5.97	8.25	7.14	8.17	9.32		
	Y79AA1000410	6.01	7.87	15.72	13.79	17.05	14.95		
	Y79AA1000420	1.54	4.78	3.13	3.32	3.95	5.1		
	Y79AA1000423	1.38	7.08	5.59	5.22	6.04	10.27		
30	Y79AA1000426	3.61	9.44	8.66	4.24	4.43	5.22		
	Y79AA1000432	0.8	4.79	2.16	1.91	2.01	2.34		
	Y79AA1000453	23.94	30.67	47.79	39.74	50.65	58.24		
	Y79AA1000465	4.12	6.02	6.65	4.77	4.14	7.69		
	Y79AA1000469	11.59	9.61	18.04	13.82	16.21	17.18		
35	Y79AA1000480	1.24	4.37	2.78	3.33	3.57	2.79		
	Y79AA1000502	5.31	7.97	12.58	10.49	11.35	15.26		
	Y79AA1000521	1.24	4.4	4.13	2.51	3.61	2.7		
	Y79AA1000534	3.22	8.13	8.92	11.97	14.41	13.46	*	+
40	Y79AA1000538	3.58	6.95	8.79	9.52	12.12	8.41		
	Y79AA1000539	12.76	14.96	53.11	42.61	68.56	50.97		
	Y79AA1000540	1.32	3.59	1.61	2.54	2.97	3.21		
	Y79AA1000560	160.46	140.99	339.33	380.8	313.21	220.43		
	Y79AA1000574	1	2.92	1.65	1.98	2.04	1.59		
45	Y79AA1000584	2.07	4.55	4.97	4.62	5.39	4.04		
	Y79AA1000589	10.74	13.67	81.43	59.09	95.35	68.5		
	Y79AA1000598	1.43	7.64	2.17	1.85	3.88	3.18		
	Y79AA1000600	2.7	10.02	7.93	13.64	15.64	12.84	*	+
	Y79AA1000609	1.18	5.16	1.44	2.28	2.77	1.55		
50	Y79AA1000618	1.85	10.59	5.76	7.4	9.5	9.37		
	Y79AA1000627	1.91	3.93	4.57	3.27	3.02	2.43		
	Y79AA1000636	5.16	5.7	9.9	15.57	11.52	5.38		
	Y79AA1000649	9.45	10.97	12.73	18.7	11.56	20.54		
	Y79AA1000656	15.32	20.21	96.75	80.17	115.97	82.61		
55	Y79AA1000673	1.02	5.86	2.14	1.39	3.13	2.4		
	Y79AA1000674	11.88	21.96	78.28	59.4	98.22	62.67		

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	Y79AA1000678	2.48	8.91	3.88	3.01	4.15	2.45	
	Y79AA1000682	17.99	53.99	93.7	102.53	110.87	118.22	
	Y79AA1000683	1.87	2.66	3.21	4.27	2.59	2.17	
5	Y79AA1000697	21.76	27.52	43.01	21.93	24.76	27.31	
	Y79AA1000700	5.07	7.1	7.08	7.51	6.93	9.97	
	Y79AA1000702	5.13	14.57	13.31	41.48	56.57	63.15	** +
	Y79AA1000704	1.34	5.24	1.14	1.5	2.1	1.18	
10	Y79AA1000705	1.86	9.7	6.24	6.06	7.98	6.45	
	Y79AA1000717	6.18	12.39	9.42	9.73	11.1	8.7	
	Y79AA1000722	5.61	8.6	8.65	26.26	34.81	34.31	** +
	Y79AA1000724	6.42	9.77	18.55	26.57	21.7	11.95	
	Y79AA1000726	0.77	1.24	0.83	1.46	2.01	0.71	
15	Y79AA1000734	2.05	4.46	4.92	3.57	3.3	2.94	
	Y79AA1000748	0.88	4.38	1.77	2.14	2.99	1.56	
	Y79AA1000750	4.17	8.47	20.58	18.11	20.02	18.62	
	Y79AA1000752	1.25	5.13	2.33	2.23	3.38	3.38	
	Y79AA1000774	2.11	6.23	4.24	4.28	5.79	4.21	
20	Y79AA1000776	1.2	4.37	1.9	2.13	1.83	2.11	
	Y79AA1000777	4.36	5.84	9.63	10.05	6.99	6.01	
	Y79AA1000778	1.72	3.77	3.79	3.87	4.19	1.44	
	Y79AA1000782	2.08	4.18	3.72	3.53	2.89	2.96	
	Y79AA1000784	7.04	10.01	7.78	13.87	15.58	14.26	** +
25	Y79AA1000794	0.61	5.21	1.88	2.92	1.69	1.23	
	Y79AA1000800	1.59	5.44	3.82	3.38	2.97	3.39	
	Y79AA1000802	0.64	4.18	1.15	2.52	1.77	2.1	
	Y79AA1000805	2.29	4.03	2.63	2.43	2.11	2.6	
30	Y79AA1000814	2.73	3.9	4.14	4.98	7.09	6.76	* +
	Y79AA1000823	7.91	9.99	12.07	12.02	12.42	6.56	
	Y79AA1000824	0.98	2.47	1.84	2.75	2.26	0.79	
	Y79AA1000827	1.6	4.02	7.27	6.71	8.91	6.14	
	Y79AA1000831	7.04	10.49	17.32	26.61	30.43	27.82	** +
35	Y79AA1000833	62.14	67.46	191.76	270.42	308.16	248.21	* +
	Y79AA1000850	1.69	5.68	2.72	4.92	4.59	4.21	
	Y79AA1000856	3.49	6.78	6.31	9.28	6.01	8.51	
	Y79AA1000862	2.22	2.76	2.44	3.08	2.87	2.59	
	Y79AA1000876	7.46	10.04	17.91	27.36	27.61	25.46	** +
40	Y79AA1000888	4.59	5.07	28.1	24.51	38.78	22.48	
	Y79AA1000902	4.65	5.74	8.44	12.18	12.32	7.68	
	Y79AA1000935	3.53	5.99	6.69	8.28	10.07	9.18	* +
	Y79AA1000959	0.74	6.29	4.35	6.71	5.77	6.07	
	Y79AA1000962	1.22	4.45	3.18	2.9	2.41	1.79	
45	Y79AA1000963	18.6	26.86	35.93	31.61	42.17	49.13	
	Y79AA1000966	18.52	19.25	98.18	77.47	116.12	61.1	
	Y79AA1000967	8.62	8.82	33.82	34.47	40.36	29.3	
	Y79AA1000968	3.32	5.67	6.89	8.86	9.4	7.96	* +
50	Y79AA1000969	0.91	3.18	3.04	2.66	2.91	1.41	
	Y79AA1000976	1.43	4.72	3.02	2.55	3.51	1.43	
	Y79AA1000978	1.99	5.6	7.26	6.9	10.54	5.56	
	Y79AA1000985	9.39	12.84	40.49	38.26	44.3	27.89	
	Y79AA1000989	21.59	22.49	46.19	51.84	58.65	55.19	* +
55	Y79AA1000991	22.11	22.21	110.42	72.46	96.96	82.23	
	Y79AA1001013	59.2	62.64	140.9	174.85	214.13	201.9	* +

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	Y79AA1001014	2.27	4.16	4.1	4.8	5.2	6.55		
	Y79AA1001019	3.37	5.89	7.74	9.24	9.02	9.43	*	+
5	Y79AA1001020	5.37	7.82	9.43	12.31	11.11	10.86	*	+
	Y79AA1001023	0.83	6.11	2.29	1.22	1.95	1.54		
	Y79AA1001030	4.23	8.79	10.87	11.14	10.72	12.43		
	Y79AA1001035	0.19	2.88	0.03	14.44	8.19	17.16	*	+
	Y79AA1001041	1.78	2.46	2.36	2.93	2.45	2.78		
10	Y79AA1001043	11.65	12.62	15.22	8.64	12.01	14.71		
	Y79AA1001048	1.1	4.78	3.73	4.05	4.52	4.21		
	Y79AA1001056	4.56	7.82	11.04	8.27	7.11	9.94		
	Y79AA1001061	1.53	7.79	5.28	6.13	7.46	6.66		
	Y79AA1001062	2.62	6.14	5.02	4.44	6.01	4.67		
15	Y79AA1001068	3.46	6.39	7.29	6.61	8.69	7.05		
	Y79AA1001073	8.19	13.08	17.46	24.14	22.1	29.81	*	+
	Y79AA1001077	7.1	7.08	17.15	14.69	14.74	17.08		
	Y79AA1001078	3.11	8.34	11.07	5.01	12.15	12.92		
	Y79AA1001081	3.59	5.61	4.94	9.62	9.98	10.5	**	+
20	Y79AA1001088	27.75	38.61	69.33	93.1	88.97	113.04	*	+
	Y79AA1001089	4.64	7.8	11.92	22.67	22.6	27.73	**	+
	Y79AA1001090	1.38	4.15	2.2	3.58	2.83	2.35		
	Y79AA1001105	3.7	5.23	15.81	12.52	22.1	13.35		
	Y79AA1001142	8.53	13.38	15.85	14.28	11.42	22.32		
25	Y79AA1001145	2.22	4.68	5.13	4.97	6.26	5.87		
	Y79AA1001162	2.27	2.91	1.62	1.62	4.56	4		
	Y79AA1001167	0.86	2.76	2.38	1.12	2.35	0.77		
	Y79AA1001176	0.57	3.33	1.14	2.02	1.68	0.88		
	Y79AA1001177	1.21	5.5	2.22	2.35	3.01	1.99		
30	Y79AA1001179	6.81	8.66	16.73	22.82	22.64	20.07	*	+
	Y79AA1001185	1.33	5.3	4.55	3.65	4.49	5.8		
	Y79AA1001201	5.69	11.3	16.13	14.57	15.21	19.38		
	Y79AA1001205	1.87	3.28	2.85	5.87	4.85	4.09	*	+
	Y79AA1001211	1.64	4.75	6.93	4.83	4.36	4.15		
35	Y79AA1001212	3.55	6.93	15.91	13.74	15	11.65		
	Y79AA1001216	52.59	51.46	93.73	76.52	97.53	109.55		
	Y79AA1001228	6.1	11.21	9.34	8.99	12.19	10.24		
	Y79AA1001233	0.68	11.46	2.39	0.92	1.66	1.09		
40	Y79AA1001236	4.46	12.86	9.25	11.4	10.66	13.08		
	Y79AA1001239	4.62	13.93	9.94	11.53	12.15	12.94		
	Y79AA1001240	8.74	8.6	13.75	9.13	6.68	3.01		
	Y79AA1001255	10.37	12.22	22.61	12.47	7.51	6.57		
	Y79AA1001264	3.63	5.15	4.49	7.73	8.59	8.75	**	+
45	Y79AA1001272	10.81	13.63	17.47	21.56	20.67	21.32	*	+
	Y79AA1001281	0.45	4.95	1.89	1.42	1.81	0.95		
	Y79AA1001299	2.49	11.34	9.06	9.9	9.26	9.81		
	Y79AA1001312	2.49	10.36	5.17	2.15	4.77	4.14		
	Y79AA1001319	3.34	11.88	5.27	7.23	6.05	7.15		
50	Y79AA1001323	1.22	1.16	2.09	1.11	1.55	0.89		
	Y79AA1001328	2.04	3.18	3.62	4.66	4.48	4.05	*	+
	Y79AA1001343	154.19	151.55	345.05	304.88	394.54	265.65		
	Y79AA1001351	0.81	2.77	1.67	0.03	1.26	0.96		
	Y79AA1001364	1.65	6.07	4.03	3.39	4.43	3.6		
55	Y79AA1001367	2.16	7.41	2.93	3.09	5.34	3.19		



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	Y79AA1001384	0.5	5.14	1.98	0.73	1.15	0.94	
	Y79AA1001391	0.59	3.73	2.88	1.35	1.65	1.2	
	Y79AA1001394	3.12	4.66	12.92	10.94	9.56	10.94	
5	Y79AA1001402	2.77	3.7	5.95	5.65	5.09	4.14	
	Y79AA1001410	0.82	2.78	2.33	2.06	2.31	2.25	
	Y79AA1001414	2.76	7.5	7.59	11.08	10.73	10.06	* +
	Y79AA1001426	0.61	4.36	2.61	1.5	1.43	1.82	
	Y79AA1001427	14.22	13.44	86.36	59.92	88.36	63.53	
10	Y79AA1001430	11.28	16.98	20.98	29.04	34.03	34.38	** +
	Y79AA1001439	16.22	21.53	33.42	45.02	43.74	43.1	* +
	Y79AA1001485	1.65	2.51	4.38	4.85	3.88	3.57	
	Y79AA1001493	1.29	2.3	3.43	2.43	2.35	2.46	
15	Y79AA1001511	4.79	8.57	11.05	9.39	9.11	6.47	
	Y79AA1001523	2.64	6.57	5.08	8.74	7.37	6.1	
	Y79AA1001530	7.46	11.69	22	41.43	36.37	36.07	** +
	Y79AA1001532	5.12	7.35	6.69	10.49	14.82	12.9	* +
	Y79AA1001533	1.84	4.89	2.53	4.15	4	4.19	
20	Y79AA1001541	2.82	5.89	7.54	7.23	5.08	7.34	
	Y79AA1001548	4.25	4.84	9.82	10.46	7.37	7.1	
	Y79AA1001555	2	2.55	3.65	4.7	5.28	4.25	* +
	Y79AA1001562	7.76	10.11	17.15	14.07	16.16	10.83	
	Y79AA1001581	2	5.05	4.47	5.1	7.01	3.54	
25	Y79AA1001585	3.18	7.38	10.96	9.72	10.93	8.05	
	Y79AA1001592	2.61	7.38	5.97	8.15	8	7.02	
	Y79AA1001594	0.76	4.73	3.85	1.96	3.24	1.73	
	Y79AA1001603	56.74	70.81	153.14	131.56	112.16	107.66	
	Y79AA1001613	3.74	3.52	14.81	13.12	15.36	10.66	
30	Y79AA1001630	0.71	2.36	1.73	1.14	2.64	0.67	
	Y79AA1001647	1.96	3.57	2.47	4.14	4.32	2.65	
	Y79AA1001664	4.67	8.39	11.43	8.96	10.01	8.73	
	Y79AA1001665	1.39	6.4	3.73	4.67	4.71	3.75	
	Y79AA1001679	8.92	15.94	20.71	20.53	26.67	25.35	
35	Y79AA1001692	1.87	5.55	3.95	3.99	3.95	3.51	
	Y79AA1001696	1.97	6.49	2.77	1.83	2.63	2.55	
	Y79AA1001705	6.09	6.44	10.39	7.62	7.92	7.85	
	Y79AA1001711	16.17	12.34	29.74	13.73	23.83	21	
	Y79AA1001717	0.72	2.99	1.29	1.68	3.13	1.14	
40	Y79AA1001719	2.5	5.79	6.44	6.15	6.07	6.43	
	Y79AA1001727	6.87	12.13	14.99	8.73	14.71	8.77	
	Y79AA1001750	10.21	13.63	21.67	21.92	32.29	24.33	
	Y79AA1001760	25.24	27.31	122.97	113.56	155.17	83.24	
	Y79AA1001777	1.17	3.59	1.6	2.49	1.75	1.28	
45	Y79AA1001781	0.31	2.3	0.42	1.62	1.84	1.42	
	Y79AA1001787	1	3.94	3.54	5.51	5.18	5.15	
	Y79AA1001793	16.23	15.19	91.7	60.44	87.21	75.35	
	Y79AA1001795	1.23	3.84	2.24	2.05	2.45	2.8	
50	Y79AA1001799	4.9	8.35	6.99	10.7	10.72	11.26	* +
	Y79AA1001800	2.25	8.3	10.1	8.49	10.51	9.9	
	Y79AA1001801	1.77	6.44	4.87	7.67	5.91	7.33	
	Y79AA1001803	0.74	2.15	1.72	1.85	1.68	1.17	
	Y79AA1001805	6.05	6.88	12.15	10.21	8.32	11.15	
55	Y79AA1001807	3.37	6.33	12.56	11.76	17.8	16.79	

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	Y79AA1001827	1.7	4.41	3.12	3.43	3.6	2.52		
	Y79AA1001846	1.82	6.52	5.51	6.52	5.09	5.07		
5	Y79AA1001848	0.86	5.57	2.75	5.98	4.78	5.14		
	Y79AA1001853	1.38	6.16	2.76	3.24	4.56	3.63		
	Y79AA1001863	0.86	5	2.53	2.93	3.83	3.85		
	Y79AA1001866	2.29	3.2	5.81	3.53	3.98	3.46		
	Y79AA1001874	0.12	2.18	-0.21	1.17	0.75	0.51		
10	Y79AA1001875	9.33	12.67	13.09	11.05	17.79	18.63		
	Y79AA1001907	68.02	70.94	96.4	118.34	86.75	104.86		
	Y79AA1001908	0.64	8.4	2.29	1.92	2.59	2.31		
	Y79AA1001923	1.61	6.64	3.03	3.86	3.76	3.35		
	Y79AA1001927	19.1	22.05	36.94	42.46	45.29	48.81	*	+
15	Y79AA1001930	4.07	6.65	8.07	7.92	12.42	12.21		
	Y79AA1001932	2.84	4.41	8.47	11.51	9.1	8.57		
	Y79AA1001933	2.14	3.27	3.69	4.34	7.99	6.65	*	+
	Y79AA1001942	1.58	3.45	2.69	2.94	2.13	2.41		
	Y79AA1001963	9.6	9.37	46.06	38.48	49.64	47.27		
20	Y79AA1001968	18.61	27.73	37.44	42.93	44.16	55.23	*	+
	Y79AA1001983	1.81	6.35	4.28	3.97	5.86	4.47		
	Y79AA1002000	2.55	5.35	4.55	4.42	3.21	2.83		
	Y79AA1002004	13.1	18.87	27.47	23.72	29.45	40.93		
25	Y79AA1002008	2.51	3.73	3.79	4.54	2.19	2.85		
	Y79AA1002012	1.37	3.22	2.81	3.22	2.29	2.87		
	Y79AA1002017	1.34	2.53	2.46	3.51	3.07	2.82		
	Y79AA1002022	2.99	4.94	5.93	7.32	7.51	6.01		
	Y79AA1002027	2.02	6.33	2.67	2.69	4.03	4.09		
30	Y79AA1002050	2.53	8.12	4.22	6.68	6.91	5.11		
	Y79AA1002058	13.69	21.8	70.12	59.07	70.89	55.33		
	Y79AA1002060	6.38	13.17	20.54	17.14	21.12	24.23		
	Y79AA1002062	4.33	5.18	8.15	8.54	6.66	5.51		
	Y79AA1002065	33.54	39.97	72.6	49.46	30.04	41.81		
35	Y79AA1002067	10.11	11.64	17.24	16.25	9.42	8.13		
	Y79AA1002069	0.97	1.79	0.54	1.55	1.44	0.66		
	Y79AA1002070	10.16	33.47	44.36	52.16	71.15	73.35	*	+
	Y79AA1002074	38.55	74.38	179.6	165.55	282.48	224.96		
	Y79AA1002076	0.48	9.71	2.89	2.86	3.34	1.91		
40	Y79AA1002083	1.2	7.48	2.03	2.73	1.75	2.06		
	Y79AA1002084	1.79	2.59	4.54	3.73	3.73	2.98		
	Y79AA1002086	0.96	1.78	1.71	2.77	1.88	1.43		
	Y79AA1002087	11.18	14.9	27.67	33.34	30.01	23.08		
	Y79AA1002089	1.18	3.46	2.13	1.46	2.92	3.26		
45	Y79AA1002093	2.19	5.48	5.25	5.28	5.68	6.17		
	Y79AA1002101	1.11	8.58	2.98	6.54	5.58	6.6		
	Y79AA1002103	1.47	10.22	3.39	4.43	6.49	4.7		
	Y79AA1002115	4.34	9.78	7.37	7.45	7.03	6.95		
50	Y79AA1002121	1.55	2.16	2.18	1.67	2.55	2.31		
	Y79AA1002125	6.67	7.08	9.29	8.81	6.4	7.6		
	Y79AA1002129	1.64	6.23	7.84	5.41	2.2	4.93		
	Y79AA1002131	0.9	3.25	0.78	0.77	1.29	1.15		
	Y79AA1002139	0.69	5.02	1.04	1.83	1.53	1.34		
55	Y79AA1002144	25.99	29.62	51.01	42.61	51.16	43.17		
	Y79AA1002177	1.72	5.97	4.33	4.79	3.09	4.73		

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	Y79AA1002183	10.44	13.89	17.69	27.61	29.67	28.92	**	+
	Y79AA1002202	3.97	7.15	8.34	18.27	10.12	17.85	*	+
	Y79AA1002204	0.53	0.99	1.56	1.7	2.2	1.54		
5	Y79AA1002206	2.63	5.36	7.28	4.35	2.95	1.49		
	Y79AA1002208	4.26	6.54	3.94	6.88	6.3	3.96		
	Y79AA1002209	1.8	6.34	2.88	4.38	3.74	4.57		
	Y79AA1002210	0.41	4.14	2.09	1.8	2.24	1.65		
10	Y79AA1002211	2.25	5.39	3.85	5.71	5.3	4.5		
	Y79AA1002213	1.15	4.13	6.53	7.38	7.54	7.43		
	Y79AA1002215	18.7	18.69	26.61	17.72	15.59	9.62		
	Y79AA1002220	3.78	3.38	2.87	4.89	4.19	4.14	*	+
	Y79AA1002226	8.54	8.9	9.75	13.06	14.2	4.41		
15	Y79AA1002229	1.35	3.88	3.38	2.95	2.79	2.67		
	Y79AA1002234	3.24	6.82	3.94	4.29	7.74	6.88		
	Y79AA1002235	5.6	7.55	6.43	8.78	9.74	9.47	*	+
	Y79AA1002246	0.59	5.06	2.41	3.94	2.54	4.27		
	Y79AA1002258	0.72	7.26	2.92	3.99	4.19	2.7		
20	Y79AA1002279	17.79	19.12	27.8	16.52	19.13	11.5		
	Y79AA1002292	1.68	2.1	3.22	2.96	3.91	2.73		
	Y79AA1002298	0.76	2.52	1.32	2.03	2.77	1.06		
	Y79AA1002307	1.05	4.35	1.79	0.76	1.05	1.2		
25	Y79AA1002309	1.15	4.19	2.3	2.21	1.78	2.55		
	Y79AA1002311	2.84	7.35	3.43	5.71	6.04	5.45		
	Y79AA1002334	1.72	6.54	2.95	4.77	4.19	3.35		
	Y79AA1002351	1.27	5.5	2.89	3.5	3.38	3.06		
	Y79AA1002355	12.83	12.25	28.96	22.94	22.07	21.02		
30	Y79AA1002361	2.22	2.27	3.26	2.47	4.54	1.55		
	Y79AA1002365	0.66	2.04	2.26	1.97	3.51	2.25		
	Y79AA1002373	1.17	3.93	2.42	1.59	1.97	1.43		
	Y79AA1002376	110.81	135.82	249.8	205.99	213.25	191.69		
	Y79AA1002378	1.9	4.8	4.91	2.2	3.6	3		
35	Y79AA1002381	8.65	14.11	19.19	18.84	21.52	17.97		
	Y79AA1002388	7.05	9.99	18.24	15.88	21.51	19.99		
	Y79AA1002399	1.79	4.25	3.74	4.62	4.08	3.47		
	Y79AA1002407	3.05	4.16	3.13	4.66	5.77	4.5	*	+
	Y79AA1002413	3.21	6.78	8.05	6.46	8.32	6.87		
40	Y79AA1002416	1.46	5	2.74	2.49	3.44	3.55		
	Y79AA1002429	5.5	8.15	7.27	8	11.11	8.01		
	Y79AA1002431	0.92	4.43	0.48	0.79	1.78	0.89		
	Y79AA1002433	1.27	5.9	3.24	4.8	3.84	5.58		
45	Y79AA1002445	4.01	5.34	5.76	3.1	4.89	5.41		
	Y79AA1002461	0.63	2.45	1.79	1.19	2.71	1.41		
	Y79AA1002466	39.02	70.71	94.5	91.12	82.27	94.71		
	Y79AA1002471	4.44	6.67	6.08	7.43	8.06	10.49		
	Y79AA1002472	2.41	6.16	5.99	6.8	8.39	4.06		
50	Y79AA1002474	1.93	8.27	4.31	4.89	6.52	7.13		
	Y79AA1002482	3.52	6.66	10.37	9.02	11.81	8.69		
	Y79AA1002487	1.38	4.12	2.46	1.96	3.01	2.56		
	Y79AA1002490	10.37	9.91	16.35	11.11	12.88	16.86		
	Y79AA1002493	1.96	4.07	6.14	6.5	8.9	4.1		
55	ZRV6C1006278	0.61	4.08	2.22	1.81	1.58	2.11		

Table 367

Difference in the expression level of each clone in response to TNF. stimulation or IL-1. stimulation

Before stimulation, IL1 1h, and IL1 7h represent relative levels of expression in the absence of the stimulation, 1 hour after the IL-1. stimulation, and 7 hours after the stimulation, respectively. TNF 1h, TNF 3h, and TNF 7h represent relative levels of expression 1 hour after the TNF. stimulation, 3 hours after the stimulation, and 7 hours after the stimulation, respectively. Correlation coefficients 1 and 2 indicate the correlation coefficients in the calibration curves prepared based on the data for the internal standard in reaction systems A and B, respectively.

Clone	IL1		TNF			Correlation coefficients			
	before stimulation	1h	7h	1h	3h	7h	1	2	
NT2RM1000858	5.6	7.6	3.8	4.7	2.1	1.7	0.98	0.94	
NT2RM1000462	0.9	0.9	0.5	0.7	0.1	0	1	1	
NT2RM1000855	1	1.3	1	1.1	0.4	0.4	1	1	
NT2RM1000789	1	0.9	0.4	1	0.4	0.6	0.96	0.98	
NT2RM2000306	0.7	1.1	0.3	1.1	0.3	0.1	1	0.98	
NT2RM2000514	0.2	0.2	0.6	0.2	0.1	0.2	0.98	0.96	
NT2RM2001126	0.5	0	0.4	0.3	0.3	1.2	0.99	0.99	
NT2RM2001902	1.3	1.6	0.6	1.3	0.8	0.8	1	1	
NT2RM2001738	1.6	1.8	1.5	1.7	0.8	0.9	0.98	1	
NT2RM2000582	0.2	0.1	0	0.7	0.1	0.1	0.99	0.99	
NT2RM2000773	1.1	1.2	1.4	2	1	0.8	0.95	1	
NT2RM2001626	0.4	0.2	0.6	0.7	0.1	0.7	1	1	
NT2RM2001643	1.6	3.1	1.2	2.4	0.7	0.8	1	1	
NT2RM2001792	0.2	0	0	0.3	0.1	0.1	0.98	0.97	
NT2RM2000589	0.2	0.1	0	0.1	0	0	1	0.99	
NT2RM2000588	0.6	0.7	0.1	0.8	0.2	0.2	1	1	
NT2RM2002109	0	0	0	0.2	0.1	0	0.99	0.99	
NT2RM4000284	6.5	9.1	4.8	10.1	3.4	3	1	1	
NT2RM4001735	3.8	4.6	2.1	5	1.6	1.4	1	1	
NT2RM4000100	0.5	0.6	0.2	0.5	0.3	0.3	0.95	0.95	
NT2RM4000417	0.2	0	0	0.2	0.1	0	0.99	0.98	
NT2RM4000761	3.2	3.2	2.2	2.6	0.7	0.7	0.95	1	
NT2RM4001843	1.5	1.8	1.7	2.8	1.2	0.6	0.98	1	
NT2RP1000239	2.1	3.2	1.2	2.1	0.5	0.6	1	0.99	
NT2RP1000465	0.9	0.3	0.3	0.9	0.2	0.1	0.97	0.96	
NT2RP1000679	0.3	0.3	0.4	0.9	0.2	0.3	0.97	1	
NT2RP1001031	1.4	1.4	0.4	1.2	0.1	0.3	1	0.98	
NT2RP2001200	2	1.5	0.8	2.2	0.7	0.7	0.99	1	
NT2RP2001562	2.7	2.4	0.7	3.6	0.4	1.1	1	0.94	
NT2RP2001948	1.1	1.5	0.7	1.3	0.6	0.7	0.97	0.99	
NT2RP2002015	1.3	1.7	0.7	1.8	0.6	0.5	0.99	1	
NT2RP2003390	2	1.7	1.3	2.3	0.6	0.5	0.99	0.99	
NT2RP2003664	0.4	0.1	0.1	0.8	0.1	0	0.99	0.99	
NT2RP2005597	1.2	1.4	0.5	2.7	2.2	2.2	0.96	0.99	
NT2RP2001469	1.7	1.4	1.2	2	0.6	0.6	1	1	
NT2RP2000240	0.9	0.9	0.3	1.4	0.7	0.3	1	1	
NT2RP2000610	2.4	2.2	2.1	2.7	1.5	1.6	0.93	0.96	

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	NT2RP2001276	1	0.4	0.4	0.8	0.2	0.7	0.95	1
	NT2RP2001817	1.2	0.8	0.5	1.9	0.7	0.7	1	1
5	NT2RP2004069	0.6	0.6	0.4	0.8	0.5	0.3	0.93	0.97
	NT2RP2004108	0.3	0.2	0.6	1.1	0.4	0.5	0.96	1
	NT2RP2005391	0.7	0.5	0.1	1.2	0.3	0.3	1	0.99
	NT2RP2006092	1.6	1.2	0.9	2.1	0.6	0.7	0.97	1
	NT2RP2006134	1.2	1.5	0.7	1.9	1	0	0.91	1
10	NT2RP2000818	0.9	0.3	0.3	1.6	0.3	0.3	0.95	1
	NT2RP2000092	1.8	1.8	0.8	2	1	1	0.99	0.98
	NT2RP2000092	1.1	1.1	0.5	1.4	0.6	0.6	0.99	0.97
	NT2RP2001538	2.1	1.9	1.8	2.5	0.6	0.8	0.98	1
	NT2RP2006476	2.1	2.2	1.4	3.2	1.6	2	0.97	0.98
15	NT2RP3000616	0.1	0.1	0	0	0	0	1	1
	NT2RP3000721	2.2	2.8	0.7	2.4	0.4	0.4	1	0.98
	NT2RP3001044	1.5	1.9	0.6	2	0.7	0.4	1	1
	NT2RP3001240	0.8	1	0.8	1.5	0.6	0.7	0.97	0.99
	NT2RP3001592	0.3	0.8	0.8	1.1	0	0	0.94	0.93
20	NT2RP3002448	4.6	4.2	2.5	4.5	0.8	1.2	1	0.98
	NT2RP3002721	1.3	1.6	0.5	1.4	0.3	0.3	1	0.99
	NT2RP3002738	0.1	0	0.1	1.9	0.1	0.1	0.99	1
	NT2RP3002790	1.6	2	0.6	1.7	0.6	0.5	0.98	1
	NT2RP3002836	1.7	3	0.9	2.4	1.6	0.7	1	1
25	NT2RP3003354	0.9	0.7	0.5	0.6	0.4	0.5	0.99	0.92
	NT2RP3003614	0.5	0.4	0	0.3	0.3	0.2	0.99	0.99
	NT2RP3004075	0.8	1.4	0.7	1	0.4	0.4	1	1
	NT2RP3004130	0.3	0.4	0	0.2	0.1	0	0.93	0.96
	NT2RP3004133	1.9	3.5	0.6	3.8	1	1.3	0.99	1
30	NT2RP3004321	0.2	0.2	0	1.4	0.4	0.2	1	0.99
	NT2RP3004406	1.3	0.2	0.2	0.7	0.1	0	1	1
	NT2RP3004552	0.1	0.1	0.1	0.1	0	0	1	1
	NT2RP3004557	1.3	1.1	2.2	2.6	1.5	1.4	0.98	0.94
	NT2RP3004647	1.2	2.1	0.6	1.2	1	0.5	1	1
35	NT2RP3000201	2.3	2.9	0.4	1	1.3	0.5	1	0.98
	NT2RP3000820	1.2	1.6	0.9	1.2	0.6	0.5	1	1
	NT2RP3000818	1.4	1.5	0.7	1.8	0.5	0.7	1	0.99
	NT2RP3001159	1.2	2.5	1.2	1.4	0.6	0.7	0.99	0.99
	NT2RP3002281	1.6	2	1.2	1.8	1	1.2	0.99	1
40	NT2RP3002571	3.9	1.8	1.2	5.2	1.4	0.8	0.99	0.97
	NT2RP3002983	1.4	1.7	0.5	1.4	0.4	0.3	1	1
	NT2RP3003473	0.8	0.9	1	0.7	0.4	0.5	1	0.99
	NT2RP3001976	0.6	1.1	0.1	0.7	0.4	0.1	1	0.99
	NT2RP3002286	1.4	1.8	1	1.6	0.6	0.5	1	0.99
45	NT2RP3002353	7.7	6.4	2.2	8.7	1.1	1.3	0.94	0.99
	NT2RP3004025	1.9	2	1	2.1	1	1	0.96	0.98
	NT2RP3004119	0.8	1.1	0.4	0	0	0.2	1	0.99
	NT2RP3000171	0.7	1.3	0.6	1	0.4	0.3	0.99	1
	NT2RP3000676	1.2	1.9	0.7	1.1	1.3	0.5	0.99	1
50	NT2RP3000921	0.2	0.1	0	0.2	0.1	0	1	0.99
	NT2RP3002015	0.8	0.6	0.4	0.7	0.1	0.1	0.99	0.99
	NT2RP3004294	0	0	0	0.1	0.1	0	1	1
	NT2RP3004345	0.6	0.4	0.2	0.9	0.2	0.5	1	1
55	NT2RP3000148	1.7	2.5	0.8	2	0.8	0.8	1	1

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	NT2RP3000232	0.6	0.8	0.4	0.3	0	0	1	0.99
	NT2RP3001650	2.3	1.5	1.6	1.7	1	1.3	1	1
5	NT2RP3002411	0.5	0.4	0.1	0.5	0.2	0.1	1	1
	NT2RP4001001	0.8	1.3	0.7	1	0.7	0.4	0.97	0.97
	NT2RP4001877	1.5	0.9	1.1	1.2	0.5	0.7	1	0.99
	NT2RP4002451	0.7	1	0.6	0.7	0.2	0.3	0.91	0.95
	NT2RP4000634	1	1	0.3	0.9	0.3	0.4	0.99	1
10	NT2RP4002187	0.4	0.4	0.1	0.7	0.3	0.2	1	0.99
	NT2RP4002715	1.5	1.6	0.7	1.5	0.4	0.3	1	0.99
	MAMMA1000986	3.9	4.1	1.9	4.2	1.8	1.4	0.99	1
	MAMMA1001237	0	0	1.6	0.2	0	0	0.99	0.98
	MAMMA1001978	3.5	3.4	2.3	6	3.4	2.5	0.97	0.98
15	MAMMA1002080	0.4	0	0	0.4	0.1	0	1	0.99
	MAMMA1002234	4	4.4	3	7.7	1.9	3	0.97	1
	MAMMA1000614	4.8	1	15.5	5.6	3.9	4.8	0.95	0.93
	MAMMA1000141	7.1	11.5	3.5	14.8	6.5	3.7	1	0.98
	MAMMA1000706	7.2	9.3	3.9	3.7	2.3	2.6	0.98	0.99
20	MAMMA1000788	3	3.8	2.8	8.9	4.8	4.2	0.92	0.98
	MAMMA1000994	0.3	0	0	0.4	0	0	1	1
	MAMMA1001310	4.1	6.1	3.8	8	2.5	3.6	0.99	0.95
	MAMMA1001344	2.7	4.4	2.2	3.2	2.6	2.1	1	0.99
	MAMMA1001957	2.3	2.7	1.9	1.7	1	1.8	0.99	1
25	MAMMA1002070	0.1	0.1	0	0.8	0.4	0.2	1	0.99
	MAMMA1002586	1.7	1.6	1.2	1.3	0.4	0.3	0.94	1
	MAMMA1000102	2.1	2.3	1.4	3.3	1.6	1.6	1	1
	MAMMA1001066	2.8	2.6	1.8	5.3	0.7	1.2	1	0.98
	MAMMA1001094	2.3	2.9	2	3.3	2.1	2.5	0.96	0.9
30	MAMMA1001609	2	3	1.2	2.7	1.7	2.2	0.99	0.97
	PLACE1002547	2	1.7	1.2	4.1	1.2	2	0.95	1
	PLACE1003573	0	0	0	0.1	0	0	1	0.98
	PLACE1004199	0.1	0.2	0	0	0	0	0.99	0.97
	PLACE1004305	0	0	0	0.3	0	0.2	0.96	0.99
35	PLACE1004450	0.9	0.3	0	0.1	0	0	0.98	0.98
	PLACE1005031	0.9	0	0	0.5	0	0	0.98	0.99
	PLACE1007845	0.8	1	0.4	0.4	0.1	0.1	1	0.98
	PLACE1008984	1.4	1.2	0.4	1.9	0.6	0.5	0.98	0.98
	PLACE1011116	2.6	1.5	1.6	1.6	0.3	0.4	1	1
40	PLACE1000986	0.6	0.2	0.2	0.3	0.1	0.1	1	0.98
	PLACE1004492	1.9	1.9	1.5	3.3	1	1	1	0.97
	PLACE1005569	2.6	0.4	0	1.1	0.3	0.1	0.98	0.99
	PLACE1005601	1.7	1.3	1	2.3	0.6	0.3	0.93	1
	PLACE1006079	0.6	0.3	0	0.1	0.1	0	0.98	0.99
45	PLACE1007077	1.1	0	0	0.3	0.1	0	0.97	0.98
	PLACE1008744	0.4	0.1	0.1	1.1	0.1	0	0.98	1
	PLACE1011181	0.6	0.3	0.5	1.6	0.3	0.5	0.98	0.99
	PLACE1005539	0.4	0	0.2	0.3	0.2	0	1	0.93
	PLACE1008282	1.1	0.7	0.6	1.2	0.4	0.4	0.98	1
50	PLACE1010713	0.6	0.7	0	1.4	0.5	0.4	0.99	0.95
	PLACE1010011	1.2	1.4	0.2	2.7	1.5	1.7	1	0.99
	PLACE3000213	1.9	0.2	0.1	0.8	0.1	0	0.99	1
	PLACE1002080	6.7	3.9	0.3	1.7	0.8	0.5	0.95	0.98
55	SKNMC1000082	1.3	0.1	1.1	0.7	0	0	1	1

	Y79AA1000127	1.8	1.8	1.1	2.1	0.5	0.6	1	1
	Y79AA1000226	1.4	0.8	0.6	0.9	0.3	0.4	0.99	0.99
5	Y79AA1000776	0.3	0.1	0	1.1	0.3	0.5	0.99	0.99
	Y79AA1000876	1.1	1.5	1.2	1.3	0.5	0.8	0.97	1
	Y79AA1001056	1.7	1.7	0.8	1.4	0.9	0.7	1	1
	Y79AA1000777	3.1	3.1	1.2	3.8	0.7	0.5	0.98	0.99
10	Y79AA1000030	1	1.3	0.2	1.3	0	0.6	0.98	0.96
	Y79AA1001212	1.5	1.2	1	2	0.8	0.5	1	0.99
	Y79AA1001427	2.3	3	0.6	2	0.8	0.4	1	1
	Y79AA1001530	0.9	0.9	0.5	1.1	0.4	0.4	1	1
	Y79AA1001592	0.6	0.2	0	0.7	0	0	0.97	1
15	Y79AA1001727	0.8	0.4	0.2	0.9	0.2	0.1	1	1
	Y79AA1001803	0.1	0	0	0.2	0.1	0	0.97	0.99
	Y79AA1002373	0	0	0	0	0	0	0.99	1
	Y79AA1002376	0.9	0.1	0	1.2	0.1	0.4	0.98	1
20	Y79AA1001523	0.5	0.5	0.3	0.6	0.3	0.1	1	0.98
	Y79AA1000888	1.1	1	0.7	1.4	0.7	0.5	1	1
	Y79AA1002129	0.2	0.2	0.1	0.5	0.2	0.2	0.99	1

25 [0285] The present invention has provided a total of 830 novel full length cDNA clones. As has not yet proceeded the isolation of full length cDNA within the human, the invention has a large significance. Those proteins such as secretory proteins, membrane proteins, and proteins associated with signal transduction, glycoprotein, and transcription are known to be associated with many diseases. Those genes and proteins associating with diseases are useful for developing medicines as they can be used as a diagnostic marker, or a target for gene therapy or developing medicines that is capable of regulating their expression and activity. Especially, the cDNA clones encoding a secretion protein are extremely important for medicinal industry since the protein itself is expected to be effective as a medicine, and also the gene may have potential to be associating with many diseases. Moreover, those proteins such as membrane proteins, and proteins associated with signal transduction, glycoprotein, transcription, and diseases, and the genes encoding the proteins may be used as a disease marker. These cDNA clones are also important for medicinal industry as they may be effective for treating diseases through the regulation of the expression and activity of their encoded proteins.

Table 368

40 The names of the representative sequences of the clusters (groups) and the corresponding SEQ IDs.

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	HRIFA000071a : 1574	HRIFA017921a : 1980
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	HRIFA000432a : 1581	HRIFA018287a : 1987
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	HRIFA000695a : 1587	HRIFA018794a : 1993
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	HRIFA000845a : 1591	HRIFA018904a : 1997
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55	HRIFA003340a : 1637	HRIFA021448a : 2043



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	HRIFA009414a : 1782	HRIFA026351a : 2188
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	HRIFA010085a : 1797	HRIFA026813a : 2203
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	HRIFA015246a : 1925	HRIFA030839a : 2331
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	HRIFA015547a : 1935	HRIFA031397a : 2341
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	HRIFA015802a : 1941	HRIFA031871a : 2347
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	HRIFA016070a : 1946	HRIFA032011a : 2352
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	HRIFA016214a : 1948	HRIFA032067a : 2354
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HRIFA017836a : 1978	

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Table 369

The names of the internal sequences that are used in the selection of the clones from the representative sequences, and the corresponding SEQ IDs.

AA533598 : 2384	HRIFA036799a : 2463
AI051329 : 2385	HRIFA037138a : 2464
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HRIFA000667a : 2387	HRIFA037838a : 2466
HRIFA000878a : 2388	HRIRA000001a : 2467
HRIFA001269a : 2389	HRIRA000041a : 2468
HRIFA001283a : 2390	HRIRA000058a : 2469
HRIFA002000a : 2391	HRIRA000260a : 2470
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HRIFA006468a : 2397	HRIRA000725a : 2476
HRIFA006822a : 2398	HRIRA000998a : 2477
HRIFA007048a : 2399	HRIRA001053a : 2478
HRIFA007661a : 2400	HRIRA001314a : 2479



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	HRIFA007777a : 2401	HRIRA001443a : 2480
	HRIFA007997a : 2402	HRIRA001473a : 2481
5	HRIFA008312a : 2403	HRIRA001648a : 2482
	HRIFA009250a : 2404	HRIRA001690a : 2483
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	HRIFA009607a : 2406	HRIRA001884a : 2485
	HRIFA009923a : 2407	HRIRA002098a : 2486
10	HRIFA009978a : 2408	HRIRA002100a : 2487
	HRIFA010730a : 2409	HRIRA002155a : 2488
	HRIFA011029a : 2410	HRIRA002307a : 2489
	HRIFA011416a : 2411	HRIRA002442a : 2490
	HRIFA011461a : 2412	HRIRA002446a : 2491
15	HRIFA012670a : 2413	HRIRA002479a : 2492
	HRIFA012717a : 2414	HRIRA002945a : 2493
	HRIFA012802a : 2415	HRIRA003028a : 2494
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HRIFA035542a : 2460	HRIRA020304a : 2539
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<u>HRIFA036630a : 2462</u>	

**[0286]** The internal sequences include EST, HRIFA(the representative sequence of the 5'-end), and HRIRA (the representative sequence of the 3'-end).

Table 370

5	clone	the name of full-length nucleotide sequences	SEQ ID NO of the full-length nucleotide sequences	SEQ ID NO of the deduced amino acid sequences
10	HEMBA1000006	C-HEMBA1000006	2547	2548
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	HEMBA1000128	C-HEMBA1000128	2553	2554
	HEMBA1000275	C-HEMBA1000275	2555	2556
	HEMBA1000300	C-HEMBA1000300	2557	
20	HEMBA1000349	C-HEMBA1000349	2558	2559
	HEMBA1000443	C-HEMBA1000443	2560	2561
	HEMBA1000590	C-HEMBA1000590	2562	2563
	HEMBA1000634	C-HEMBA1000634	2564	2565
25	HEMBA1000713	C-HEMBA1000713	2566	2567
	HEMBA1000745	C-HEMBA1000745	2568	2569
	HEMBA1000907	C-HEMBA1000907	2570	2571
	HEMBA1000940	C-HEMBA1000940	2572	2573
	HEMBA1000962	C-HEMBA1000962	2574	2575
30	HEMBA1001221	C-HEMBA1001221	2576	2577
	HEMBA1001228	C-HEMBA1001228	2578	2579
	HEMBA1001297	C-HEMBA1001297	2580	
	HEMBA1001390	C-HEMBA1001390	2581	2582
35	HEMBA1001563	C-HEMBA1001563	2583	
	HEMBA1001621	C-HEMBA1001621	2584	2585
	nnnnnnnnnnnn	C-nnnnnnnnnnnnn	nnnn	nnnn
	HEMBA1001878	C-HEMBA1001878	2588	2589
40	HEMBA1002131	C-HEMBA1002131	2590	2591
	HEMBA1002163	C-HEMBA1002163	2592	2593
	HEMBA1002164	C-HEMBA1002164	2594	2595
	HEMBA1002167	C-HEMBA1002167	2596	2597
45	HEMBA1002178	C-HEMBA1002178	2598	2599
	nnnnnnnnnnnn	C-nnnnnnnnnnnnn	nnnn	nnnn

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	HEMBA1002195	C-HEMBA1002195	2602	2603
	HEMBA1002227	C-HEMBA1002227	2604	2605
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5	HEMBA1002316	C-HEMBA1002316	2607	2608
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	HEMBA1002524	C-HEMBA1002524	2613	2614
10	HEMBA1002551	C-HEMBA1002551	2615	2616
	HEMBA1002767	C-HEMBA1002767	2617	2618
	HEMBA1002992	C-HEMBA1002992	2619	2620
	HEMBA1003047	C-HEMBA1003047	2621	2622
	HEMBA1003072	C-HEMBA1003072	2623	2624
15	HEMBA1003101	C-HEMBA1003101	2625	2626
	HEMBA1003230	C-HEMBA1003230	2627	2628
	HEMBA1003294	C-HEMBA1003294	2629	
	HEMBA1003315	C-HEMBA1003315	2630	2631
	HEMBA1003392	C-HEMBA1003392	2632	2633
20	HEMBA1003399	C-HEMBA1003399	2634	2635
	HEMBA1003487	C-HEMBA1003487	2636	2637
	HEMBA1003530	C-HEMBA1003530	2638	2639
	HEMBA1003602	C-HEMBA1003602	2640	2641
	HEMBA1003732	C-HEMBA1003732	2642	2643
25	HEMBA1003945	C-HEMBA1003945	2644	2645
	HEMBA1004110	C-HEMBA1004110	2646	2647
	HEMBA1004250	C-HEMBA1004250	2648	2649
	HEMBA1004391	C-HEMBA1004391	2650	2651
30	HEMBA1004444	C-HEMBA1004444	2652	2653
	HEMBA1004454	C-HEMBA1004454	2654	2655
	HEMBA1004505	C-HEMBA1004505	2656	2657
	HEMBA1004797	C-HEMBA1004797	2658	2659
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	NT2RP3001240	C-NT2RP3001240	3035	3036
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	PLACE1003598	C-PLACE1003598	3298	3299
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55	PLACE1003772	C-PLACE1003772	3303	3304
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	PLACE1006809	C-PLACE1006809	3396	3397
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	Y79AA1000030	C-Y79AA1000030	4036	4037
	Y79AA1001212	C-Y79AA1001212	4038	4039
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25	Y79AA1001793	C-Y79AA1001793	4054	4055
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50	MAMMA1002091	C-MAMMA1002091	4099	4100
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	NT2RM1000542	C-NT2RM1000542	4103	4104
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	NT2RM1000855	C-NT2RM1000855	4107	4108
55	NT2RM1000899	C-NT2RM1000899	4109	4110

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	NT2RP2003302	C-NT2RP2003302	4119	4120
	NT2RP2003950	C-NT2RP2003950	4121	4122
	NT2RP2005535	C-NT2RP2005535	4123	4124
10	NT2RP2005774	C-NT2RP2005774	4125	4126
	NT2RP3000148	C-NT2RP3000148	4127	4128
	NT2RP3000232	C-NT2RP3000232	4129	4130
	NT2RP3000427	C-NT2RP3000427	4131	
15	NT2RP3000652	C-NT2RP3000652	4132	4133
	NT2RP3001650	C-NT2RP3001650	4134	4135
	NT2RP3002409	C-NT2RP3002409	4136	
	NT2RP3002411	C-NT2RP3002411	4137	4138
20	NT2RP3003448	C-NT2RP3003448	4139	
	NT2RP4002715	C-NT2RP4002715	4140	4141
	OVARC1000307	C-OVARC1000307	4142	4143
	PLACE1000907	C-PLACE1000907	4144	4145
25	PLACE1007081	C-PLACE1007081	4146	4147
	PLACE1010011	C-PLACE1010011	4148	4149
	PLACE3000213	C-PLACE3000213	4150	4151
	PLACE4000354	C-PLACE4000354	4152	4153
30	PLACE4000455	C-PLACE4000455	4154	
	THYRO1000776	C-THYRO1000776	4155	4156
	THYRO1001593	C-THYRO1001593	4157	4158
	Y79AA1000750	C-Y79AA1000750	4159	4160
	Y79AA1000888	C-Y79AA1000888	4161	4162
35	Y79AA1002129	C-Y79AA1002129	4163	4164
	Y79AA1002334	C-Y79AA1002334	4165	4166
	MAMMA1002224	C-MAMMA1002224	4167	
40	NT2RP1000271	C-NT2RP1000271	4168	4169
	NT2RP3000481	C-NT2RP3000481	4170	4171
	NT2RP3004481	C-NT2RP3004481	4172	4173
	HEMBA1006658	C-HEMBA1006658	4174	4175
45	NT2RP2006099	C-NT2RP2006099	4176	4177
	NT2RP2006580	C-NT2RP2006580	4178	4179

Homology search result 1

**[0287]** The result of the homology search in the SwissProt using the representative sequences of the 5'-ends.

Indicated are from the top,  
the name of the representative sequence of the cluster,  
definition of the top hit data,  
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),  
the organism of which the top hit data is obtained,  
the Accession No. of the top hit data.

[0288] Homology search results of the representative sequences of the 5'-end cluster to the data in SwissProt database are shown only for the representative sequences of the cluster from which clones were selected based on the homology search results.

[0289] The P-value is the score which is determined by taking into account the statistic probability of occurrence between the two sequences, and generally low score reflects high similarity. (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272).

5  
10  
HRIFA000016a  
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).  
9.2e-05:178:32  
PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).  
P10496

15  
HRIFA000071a  
CIRCUMSPOROZOITE PROTEB PRECURSOR (CS).  
5.8e-05:194:29  
PLASMODIUM SIMIUM.  
Q03110

20  
HRIFA000116a  
HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.  
6.2e-06:83:27  
CAENORHABDITIS ELEGANS.  
25  
P34679

HRIFA000123a  
PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).  
6.2e-08:89:34  
30  
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).  
P33154

HRIFA000264a  
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.  
35  
1.4e-06:231:34  
GALLUS GALLUS (CHICKEN).  
P02457

40  
HRIFA000327a  
ATP-BINDING CASSETTE TRANSPORTER 1.  
2.0e-16:238:31  
MUS MUSCULUS (MOUSE).  
P41233

45  
HRIFA000415a  
PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
3.6e-06:120:35  
MUS MUSCULUS (MOUSE).  
P05142

50  
HRIFA000432a  
PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.  
2.2e-21:86:52  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
55  
Q09818

HRIFA000446a  
HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.

2.5e-09:138:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40085

5

HRIFA000553a

CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).

1.7e-27:117:48

GALLUS GALLUS (CHICKEN).

P05099

10

HRIFA000564a

ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).

2.9e-28:163:38

MUS MUSCULUS (MOUSE).

15

P54116

HRIFA000631a

ZINC FINGER PROTEIN 140.

8.2e-45:155:47

20

HOMO SAPIENS (HUMAN).

P52738

HRIFA000683a

FIBRILLIN 1 PRECURSOR.

25

4.8e-18:77:46

HOMO SAPIENS (HUMAN).

P35555

HRIFA000695a

30

"SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6" PEPTIDE P-H].

4.0e-06:105:33

HOMO SAPIENS (HUMAN).

P04280

35

HRIFA000776a

FIBRILLIN 2 PRECURSOR.

1.6e-42:214:44

HOMO SAPIENS (HUMAN).

40

P35556

HRIFA000814a

ZINC FINGER PROTEIN 133.

4.4e-16:49:87

45

HOMO SAPIENS (HUMAN).

P52736

HRIFA000845a

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.

50

6.0e-06:172:34

MUS MUSCULUS (MOUSE).

P11087

HRIFA001099a

55

CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-5 (FRAGMENT).

0.92:38:34

HOMO SAPIENS (HUMAN).

P18849

EP 1 130 094 A2

- 5 HRIFA001132a  
AGRIN PRECURSOR.  
1.3e-26:239:32  
GALLUS GALLUS (CHICKEN).  
P31696
- 10 HRIFA001138a  
CARTILAGE OLIGOMERIC MATRIX PROTEIN PRECURSOR (COMP).  
5.9e-114:147:83  
HOMO SAPIENS (HUMAN).  
P49747
- 15 HRIFA001200a  
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).  
0.035:119:34  
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).  
P29128
- 20 HRIFA001337a  
LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (LDL RECEPTOR).  
2.4e-17:98:42  
CRICETULUS GRISEUS (CHINESE HAMSTER).  
P35950
- 25 HRIFA001341a  
NEUROFILAMENT TRIPLET L PROTEIN (68 KD NEUROFILAMENT PROTEIN) (NF-L)  
(NF68).  
1.2e-102:248:87  
RATTUS NORVEGICUS (RAT).  
30 P19527
- 35 HRIFA001413a  
BACTENECIN 7 PRECURSOR (BAC7) (PR-59).  
0.0032:33:63  
BOS TAURUS (BOVINE).  
P19661
- 40 HRIFA001439a  
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).  
0.00031:34:61  
HOMO SAPIENS (HUMAN).  
P20931
- 45 HRIFA001489a  
PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.  
8.4e-65:105:72  
HOMO SAPIENS (HUMAN).  
P35414
- 50 HRIFA001558a  
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.  
0.0048:80:31  
PLASMODIUM LOPHURAE.  
P04929
- 55 HRIFA001712a  
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).  
2.5e-19:169:31

THERMOMONOSPORA CURVATA.  
P49695

HRIFA001720a

5 ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).  
1.4e-94:273:64  
HOMO SAPIENS (HUMAN).  
Q03923

10 HRIFA001866a

EARLY ANTIGEN PROTEIN D (EA-D).  
0.10:93:34  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03191

15 HRIFA001942a

"PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HY-  
DROXYLASE 1) (LH1)."  
4.7e-12:140:30  
20 GALLUS GALLUS (CHICKEN).  
P24802

HRIFA001971a

25 HYPOTHETICAL 46.3 KD PROTEIN IN PTA1-CDC24 INTERGENIC REGION.  
2.5e-10:86:30  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P39727

HRIFA001972a

30 LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).  
0.10:100:34  
MUS MUSCULUS (MOUSE).  
P19137

35 HRIFA001975a

ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).  
6.5e-30:243:33  
MUS MUSCULUS (MOUSE).  
P21836

40 HRIFA001984a

"PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HY-  
DROXYLASE 1) (LH1)."  
1.2e-11:140:30  
45 GALLUS GALLUS (CHICKEN).  
P24802

HRIFA002063a

50 GNS1 PROTEIN.  
1.3e-05:127:30  
SACCHAROMYCES CEREVISIAE (BAKERS YEAST).  
P25358

HRIFA002102a

55 MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).  
2.9e-07:241:30  
HOMO SAPIENS (HUMAN).  
Q02817

# EP 1 130 094 A2

HRIFA002284a

ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).

3.8e-05:104:34

RATTUS NORVEGICUS (RAT).

P04474

HRIFA002309a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

1.5e-08:110:37

THERMOMONOSPORA CURVATA.

P49695

HRIFA002384a

GAP JUNCTION ALPHA-6 PROTEIN (CONNEXIN 45) (CX45).

1.8e-31:94:42

HOMO SAPIENS (HUMAN).

P36383

HRIFA002503a

N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).

6.1e-92:246:67

MUS MUSCULUS (MOUSE).

P15535

HRIFA002689a

TRANSCRIPTION FACTOR GATA-6 (GATA BINDING FACTOR-6) (DNA BINDING PROTEIN GATA-GT2).

0.38:49:34

RATTUS NORVEGICUS (RAT).

P46153

HRIFA002694a

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

4.7e-05:93:37

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

HRIFA002743a

BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).

1.2e-23:216:31

HOMO SAPIENS (HUMAN).

P13497

HRIFA002762a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

5.1e-09:129:41

MUS MUSCULUS (MOUSE).

P05142

HRIFA002766a

FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).

1.8e-12:139:34

HOMO SAPIENS (HUMAN).

Q06828

HRIFA002787a

PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.



1.6e-10:124:37  
HOMO SAPIENS (HUMAN).  
P08123

5 HRIFA002805a  
ZINC FINGER PROTEIN 140.  
3.6e-23:43:74  
HOMO SAPIENS (HUMAN).  
P52738

10 HRIFA002891a  
"FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)."  
2.0e-41:239:39  
MUS MUSCULUS (MOUSE).  
15 Q08878

HRIFA002919a  
BEM46 PROTEIN (FRAGMENT).  
1.0e-12:171:32  
20 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
P54069

HRIFA002980a  
25 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MAC-  
ROGLOBULIN RECEPTOR) (A2MR).  
8.7e-32:202:37  
GALLUS GALLUS (CHICKEN).  
P98157

30 HRIFA003055a  
PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
3.4e-08:175:29  
MUS MUSCULUS (MOUSE).  
P05142

35 HRIFA003063a  
B-CELL LYMPHOMA 6 PROTEIN HOMOLOG.  
2.8e-15:123:34  
MUS MUSCULUS (MOUSE).  
40 P41183

HRIFA003093a  
PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
1.3e-11:142:37  
45 MUS MUSCULUS (MOUSE).  
P05142

HRIFA003340a  
50 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-  
PHA-0 PROTEIN).  
2.3e-05:200:31  
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).  
P08393

55 HRIFA003357a  
GLUCOSE REPRESSION MEDIATOR PROTEIN.  
0.0023:190:26  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P14922

HRIFA003402a

COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).

3.6e-05:194:27

BOS TAURUS (BOVINE).

P02459

HRIFA003504a

CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).

1.4e-08:150:33

DROSOPHILA MELANOGASTER (FRUIT FLY).

P33450

HRIFA003592a

CD9 ANTIGEN.

0.0053:24:70

BOS TAURUS (BOVINE).

P30932

HRIFA003635a

"MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE)."

5.3e-45:239:43

DROSOPHILA MELANOGASTER (FRUIT FLY).

P53624

HRIFA003640a

PROCYCLIC FORM SPECIFIC POLYPEPTIDE A-BETA PRECURSOR (PROCYCLIN) (PARP A-BETA).

0.00018:28:64

TRYPANOSOMA BRUCEI BRUCEI.

P09791

HRIFA003883a

TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (YIN AND YANG 1) (YY-1) (DELTA TRANSCRIPTION FACTOR) (NF-E1) (UCR-MOTIF DNA-BINDING PROTEIN).

1.0:57:35

MUS MUSCULUS (MOUSE).

Q00899

HRIFA003892a

MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).

6.5e-08:144:25

BACILLUS SUBTILIS.

P39843

HRIFA003946a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

1.4e-06:85:37

MUS MUSCULUS (MOUSE).

P05142

HRIFA004006a

ZINC FINGER PROTEIN 140.

6.2e-20:83:66

HOMO SAPIENS (HUMAN).

P52738

EP 1 130 094 A2

HRIFA004034a  
B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).  
1.4e-15:192:32  
HOMO SAPIENS (HUMAN).  
P20749

HRIFA004112a  
CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).  
7.2e-26:193:37  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P33450

HRIFA004162a  
ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).  
3.6e-10:117:29  
MUS MUSCULUS (MOUSE).  
P54116

HRIFA004401a  
LACTOSE OPERON REPRESSOR.  
1.1e-07:36:86  
ESCHERICHIA COLI.  
P03023

HRIFA004426a  
ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).  
5.1e-11:85:41  
APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).  
P15287

HRIFA004490a  
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).  
5.3e-19:101:44  
MUS MUSCULUS (MOUSE).  
P23780

HRIFA004523a  
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).  
2.6e-36:180:43  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P43636

HRIFA004663a  
T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7).  
1.2e-40:112:75  
MUS MUSCULUS (MOUSE).  
Q00417

HRIFA004696a  
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.  
1.1e-62:145:84  
CANIS FAMILIARIS (DOG).  
P38377

HRIFA004714a  
HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.  
2.3e-50:127:54  
CAENORHABDITIS ELEGANS.

Q09201

HRIFA004745a

MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.

5.0e-17:107:43

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P23500

HRIFA004780a

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

7.2e-07:142:30

ZEA MAYS (MAIZE).

P14918

HRIFA004919a

GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).

1.5e-25:156:46

PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).

P10496

HRIFA005072a

GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).

8.3e-05:24:62

LYCOPERSICON ESCULENTUM (TOMATO).

Q01157

HRIFA005102a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

2.5e-07:188:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

HRIFA005184a

CYTOCHROME B5.

3.4e-11:117:29

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40312

HRIFA005214a

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).

5.9e-05:141:33

HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).

P28284

HRIFA005231a

ORM1 PROTEIN.

1.7e-18:137:35

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53224

HRIFA005240a

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

6.3e-81:194:70

HOMO SAPIENS (HUMAN).

Q03923

HRIFA005255a

HYPOTHETICAL 57.1 KD PROTEIN IN MAP2-TEL1 INTERGENIC REGION.

1.5e-07:202:24  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P38176

5 HRIFA005271a  
MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR.  
1.2e-55:86:81  
HOMO SAPIENS (HUMAN).  
Q00325

10 HRIFA005296a  
INSULIN PROMOTER FACTOR 1 (IPF-1) (ISLET/DUODENUM HOMEBOX-1) (IDX-1) (SOMATOSTATIN  
TRANSACTIVATING FACTOR-1) (STF-1) (PANCREAS/DUODENUM HOMEBOX-1) (GLUCOSE SENSITIVE  
FACTOR) (GSF).  
15 0.82:90:34  
HOMO SAPIENS (HUMAN).  
P52945

20 HRIFA005300a  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
1.6e-07:178:30  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437

25 HRIFA005369a  
EBNA-1 NUCLEAR PROTEIN.  
2.3e-07:101:39  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03211

30 HRIFA005372a  
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-  
BOX DNA BINDING PROTEIN SUBUNIT B).  
1.1e-14:97:38  
35 PETROMYZON MARINUS (SEA LAMPREY).  
P25210

40 HRIFA005392a  
SYNDECAN-2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN)  
(HSPG) (SYND2).  
1.3e-50:126:84  
HOMO SAPIENS (HUMAN).  
P34741

45 HRIFA005409a  
HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID  
TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RET-  
ROVIRUS RECEPTOR HOMOLOG).  
7.1e-66:197:64  
50 HOMO SAPIENS (HUMAN).  
P30825

55 HRIFA005420a  
INTERFERON-RELATED PROTEIN PC4 (TPA INDUCED SEQUENCE 7) (TIS7 PROTEIN).  
1.5e-33:221:41  
MUS MUSCULUS (MOUSE).  
P19182

# EP 1 130 094 A2

HRIFA005438a  
SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR (EC 1.3.5.1) (FP)  
(FLAVOPROTEIN SUBUNIT OF COMPLEX II).

6.4e-71:175:68

HOMO SAPIENS (HUMAN).

P31040

HRIFA005462a

CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).

1.4e-19:137:37

OVIS ARIES (SHEEP).

P08060

HRIFA005500a

EBNA-1 NUCLEAR PROTEIN.

0.00042:54:50

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

HRIFA005540a

CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).

0.12:47:29

HOMO SAPIENS (HUMAN).

P18850

HRIFA005644a

VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).

1.2e-102:233:87

BOS TAURUS (BOVINE).

P40682

HRIFA005702a

CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR (MELANOMA-ASSOCIATED ANTIGEN MUC18)  
(MELANOMA-ASSOCIATED ANTIGEN A32) (S-ENDO 1 ENDOTHELIAL- ASSOCIATED ANTIGEN) (CD146 AN-  
TIGEN) (MELANOMA ADHESION MOLECULE).

8.7e-05:174:28

HOMO SAPIENS (HUMAN).

P43121

HRIFA005720a

F-SPONDIN PRECURSOR.

8.9e-12:155:31

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P35447

HRIFA005728a

SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).

1.7e-05:126:29

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P08458

HRIFA005732a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

4.4e-26:159:38

THERMOMONOSPORA CURVATA.

P49695

HRIFA005760a

# EP 1 130 094 A2

FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-ALPHA-GALACTOS-  
YLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT).

3.8e-15:53:54

HOMO SAPIENS (HUMAN).

P16442

HRIFA005781a

ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HY-  
DROXYSTEROID DEHYDROGENASE).

5.2e-47:228:47

HOMO SAPIENS (HUMAN).

P37058

HRIFA005944a

PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].

2.5e-06:142:35

MUS MUSCULUS (MOUSE).

P28481

HRIFA006183a

ZINC FINGER PROTEIN 136.

1.3e-42:129:62

HOMO SAPIENS (HUMAN).

P52737

HRIFA006250a

HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).

0.0038:75:37

DROSOPHILA MELANOGASTER (FRUIT FLY).

P25439

HRIFA006298a

EBNA-1 NUCLEAR PROTEIN.

1.4e-05:80:42

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

HRIFA006448a

SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).

8.5e-05:183:28

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P17437

HRIFA006494a

AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).

1.2e-18:201:33

HOMO SAPIENS (HUMAN).

Q02246

HRIFA006510a

CORNICHON PROTEIN.

6.0e-53:144:66

DROSOPHILA MELANOGASTER (FRUIT FLY).

P49858

HRIFA006566a

CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-

# EP 1 130 094 A2

BOX DNA BINDING PROTEIN SUBUNIT B).  
6.6e-15:97:38  
PETROMYZON MARINUS (SEA LAMPREY).  
P25210

HRIFA006572a  
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.  
7.2e-05:158:29  
MUS MUSCULUS (MOUSE).  
P11087

HRIFA006586a  
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.  
1.3e-13:219:26  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P39981

HRIFA006596a  
POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1)  
(PPSEP 1).  
7.2e-22:241:32  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
Q10071

HRIFA006609a  
PANCREATIC HORMONE PRECURSOR (PANCREATIC POLYPEPTIDE) (PP).  
0.61:28:46  
"GALLUS GALLUS (CHICKEN), AND MELEAGRIS GALLOPAVO (COMMON TURKEY)."  
P01306

HRIFA006633a  
COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.  
7.8e-07:170:34  
HOMO SAPIENS (HUMAN).  
Q07092

HRIFA006642a  
AMALGAM PROTEIN PRECURSOR.  
1.5e-09:185:28  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P15364

HRIFA006649a  
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).  
1.7e-50:166:50  
HOMO SAPIENS (HUMAN).  
Q03923

HRIFA006667a  
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).  
6.8e-45:180:43  
HOMO SAPIENS (HUMAN).  
Q03923

HRIFA006730a  
SYG1 PROTEIN.  
1.8e-14:164:35  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).



P40528

HRIFA006798a  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
0.22:149:34  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437

HRIFA006926a  
SYNAPTOTAGMIN IV.  
3.6e-19:168:38  
RATTUS NORVEGICUS (RAT).  
P50232

HRIFA007013a  
MIC1 PROTEIN.  
1.4e-13:115:38  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P53258

HRIFA007032a  
CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).  
0.00013:92:35  
CANIS FAMILIARIS (DOG).  
P39881

HRIFA007068a  
EBNA-1 NUCLEAR PROTEIN.  
7.0e-10:145:33  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03211

HRIFA007152a  
TRANSCRIPTION FACTOR SOX-4.  
0.90:47:44  
HOMO SAPIENS (HUMAN).  
Q06945

HRIFA007219a  
THROMBOSPONDIN 3 PRECURSOR.  
1.3e-105:209:88  
HOMO SAPIENS (HUMAN).  
P49746

HRIFA007228a  
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.  
2.3e-11:174:24  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P39981

HRIFA007243a  
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).  
3.0e-18:163:36  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P39986

HRIFA007244a  
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

4.2e-05:81:33  
NICOTIANA TABACUM (COMMON TOBACCO).  
P13983

5 HRIFA007256a  
DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).  
2.3e-77:186:75  
HOMO SAPIENS (HUMAN).  
P53355

10 HRIFA007262a  
PAIRED AMPHIPATHIC HELIX PROTEIN.  
1.3e-06:152:26  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
15 P22579

HRIFA007352a  
5'-TG-3'INTERACTING FACTOR (HOMEBOX PROTEIN TGIF).  
4.2e-36:146:57  
20 HOMO SAPIENS (HUMAN).  
Q15583

HRIFA007424a  
F-SPONDIN PRECURSOR.  
25 8.9e-34:84:89  
RATTUS NORVEGICUS (RAT).  
P35446

HRIFA007435a  
30 PROTEIN KINASE CEK1 (EC 2.7.1.-).  
1.0e-37:159:53  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
P38938

35 HRIFA007463a  
HST1 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 1).  
4.8e-32:85:48  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P53685

40 HRIFA007493a  
UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN  
CARRIER PROTEIN).  
1.2e-47:171:56  
45 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P33296

HRIFA007512a  
50 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).  
8.0e-07:173:28  
NICOTIANA TABACUM (COMMON TOBACCO).  
P13983

HRIFA007532a  
55 "CALPAIN P94, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEIN-  
ASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE  
SUBUNIT)."  
1.8e-10:110:37

# EP 1 130 094 A2

HOMO SAPIENS (HUMAN).  
P20807

HRIFA007547a

5 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).  
0.068:51:45  
BOVINE HERPESVIRUS TYPE 1 (STRAIN K22).  
P29836

10 HRIFA007565a

COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.  
5.1e-08:121:37  
HOMO SAPIENS (HUMAN).  
Q03692

15 HRIFA007571a

ORM1 PROTEIN.  
5.8e-17:106:36  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
20 P53224

HRIFA007659a

HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.  
2.5e-47:213:41  
25 CAENORHABDITIS ELEGANS.  
P49191

HRIFA007722a

30 HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.  
7.7e-13:146:32  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P40857

HRIFA007728a

35 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).  
9.1e-05:124:31  
NICOTIANA TABACUM (COMMON TOBACCO).  
P13983

40 HRIFA007745a

ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (ACHE).  
7.0e-15:109:36  
TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).  
P04058

45 HRIFA007829a

GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).  
0.00045:16:68  
LYCOPERSICON ESCULENTUM (TOMATO).  
50 Q01157

HRIFA007909a

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).  
6.1e-06:173:34  
55 BOS TAURUS (BOVINE).  
P02453

HRIFA007985a

# EP 1 130 094 A2

T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).

0.00079:97:37

ORYCTOLAGUS CUNICULUS (RABBIT).

P06333

5

HRIFA008000a

"DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA SUBUNITS PRECURSOR."

1.6e-37:165:42

ORYCTOLAGUS CUNICULUS (RABBIT).

10

P13806

HRIFA008174a

COLLAGEN 1(X) CHAIN PRECURSOR.

4.5e-05:215:28

15

BOS TAURUS (BOVINE).

P23206

HRIFA008186a

ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE).

20

2.1e-25:118:46

HOMO SAPIENS (HUMAN).

P37058

25

HRIFA008200a

ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

7.9e-17:139:36

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

30

P32802

HRIFA008212a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

0.035:135:28

35

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

HRIFA008252a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

40

0.00015:128:32

MUS MUSCULUS (MOUSE).

P05142

HRIFA008284a

NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1).

45

3.9e-18:153:30

HOMO SAPIENS (HUMAN).

P32004

50

HRIFA008314a

HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.

2.1e-18:99:47

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38800

55

HRIFA008362a

PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT).

9.1e-42:135:57  
GALLUS GALLUS (CHICKEN).  
P53760

5 HRIFA008426a  
HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN).  
1.3e-08:104:45  
GALLUS GALLUS (CHICKEN).  
Q90655

10 HRIFA008459a  
CARBON CATABOLITE DEREPRESSING PROTEIN KINASE (EC 2.7.1.-).  
5.5e-15:96:40  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
15 P06782

HRIFA008483a  
PROBABLE LONG-CHAIN FATTY ACID TRANSPORT PROTEIN.  
7.4e-26:154:41  
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P38225

HRIFA008547a  
ZINC FINGER PROTEIN 136.  
25 7.2e-57:228:50  
HOMO SAPIENS (HUMAN).  
P52737

HRIFA008596a  
30 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
1.6e-05:97:35  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437

35 HRIFA008611a  
NPL1 PROTEIN (SEC63 PROTEIN).  
8.1e-15:113:38  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P14906

40 HRIFA008661a  
GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).  
2.7e-16:184:29  
ESCHERICHIA COLI.  
45 P37021

HRIFA008717a  
SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).  
6.9e-32:198:41  
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P38692

HRIFA008784a  
55 HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC REGION.  
2.2e-16:93:47  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P38869

EP 1 130 094 A2

HRIFA008790a  
HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC REGION.  
4.2e-08:121:32  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P47111

HRIFA008976a  
ACROSIN PRECURSOR (EC 3.4.21.10).  
0.31:20:70  
HOMO SAPIENS (HUMAN).  
P10323

HRIFA008981a  
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).  
1.0e-84:126:74  
HOMO SAPIENS (HUMAN).  
Q03923

HRIFA008989a  
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).  
1.2e-05:134:33  
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).  
P08393

HRIFA009071 a  
CELLULAR TUMOR ANTIGEN P53 (PHOSPHOPROTEIN P53).  
0.14:104:31  
HOMO SAPIENS (HUMAN).  
P04637

HRIFA009101a  
ZINC FINGER PROTEIN 136.  
6.5e-47:126:67  
HOMO SAPIENS (HUMAN).  
P52737

HRIFA009123a  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
0.010:127:35  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437

HRIFA009136a  
REGULATORY PROTEIN E2.  
0.032:100:37  
HUMAN PAPILLOMAVIRUS TYPE 25.  
P36787

HRIFA009171a  
BUTYROPHILIN PRECURSOR (BT).  
1.6e-15:168:31  
BOS TAURUS (BOVINE).  
P18892

HRIFA009220a  
HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I.  
2.2e-48:268:41

# EP 1 130 094 A2

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
Q09895

HRIFA009339a  
PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.  
0.63:57:35  
MUS MUSCULUS (MOUSE).  
Q01149

HRIFA009451a  
METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID POTENTIATING ACTIVITY) (EPA)  
(TISSUE INHIBITOR OF METALLOPROTEINASES) (FIBROBLAST COLLAGENASE INHIBITOR) (COLLA-  
GENASE INHIBITOR).  
1.7e-57:163:73  
HOMO SAPIENS (HUMAN).  
P01033

HRIFA009482a  
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).  
7.7e-25:86:59  
MUS MUSCULUS (MOUSE).  
P23780

HRIFA009578a  
HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.  
8.8e-10:199:26  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P40857

HRIFA009762a  
CCAAT DISPLACEMENT PROTEIN (CDP) (CDP2) (FRAGMENT).  
0.17:116:32  
RATTUS NORVEGICUS (RAT).  
P53565

HRIFA009783a  
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.  
6.2e-48:231:48  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
Q09782

HRIFA009825a  
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.  
4.0e-06:70:38  
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).  
P40602

HRIFA009852a  
"NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM  
140]."  
4.0e-07:198:27  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P16170

HRIFA009881a  
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).  
1.5e-11:106:35  
SORGHUM VULGARE (SORGHUM).

P24152

HRIFA009983a

G-BOX BINDING FACTOR (GBF).

3.8e-10:156:30

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P36417

HRIFA010005a

"M PROTEIN, SEROTYPE 49 PRECURSOR."

1.6e-05:183:27

STREPTOCOCCUS PYOGENES.

P16947

HRIFA010078a

HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.

4.7e-05:194:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53214

HRIFA010085a

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

2.9e-92:243:69

HOMO SAPIENS (HUMAN).

Q03923

HRIFA010090a

N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).

6.7e-16:78:51

HOMO SAPIENS (HUMAN).

P15586

HRIFA010130a

DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).

5.6e-13:99:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P46971

HRIFA010152a

"ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE)."

2.3e-05:73:43

CANIS FAMILIARIS (DOG).

P30803

HRIFA010176a

HEPATOCTE NUCLEAR FACTOR 3-BETA (HNF-3B).

0.066:105:31

MUS MUSCULUS (MOUSE).

P35583

HRIFA010301a

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

1.1e-09:120:34

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602



# EP 1 130 094 A2

- HRIFA010319a  
DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE)  
(DBH).  
4.8e-23:185:32  
5 RATTUS NORVEGICUS (RAT).  
Q05754
- HRIFA010361a  
10 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
2.6e-08:136:32  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437
- HRIFA010394a  
15 HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.  
3.3e-36:144:47  
CAENORHABDITIS ELEGANS.  
P49191
- HRIFA010425a  
20 A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.  
1.9e-09:199:29  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P32323
- HRIFA010460a  
25 TRANSCRIPTIONAL ACTIVATOR FE65.  
2.3e-27:101:54  
RATTUS NORVEGICUS (RAT).  
30 P46933
- HRIFA010466a  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
5.3e-07:123:34  
35 XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437
- HRIFA010490a  
40 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (EARLY PROTEIN 0) (EP0).  
0.0031:118:30  
PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).  
P29129
- HRIFA010736a  
45 PROTEIN Q300.  
0.018:14:85  
MUS MUSCULUS (MOUSE).  
Q02722
- HRIFA010790a  
50 RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANS-  
PORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RE-  
NAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).  
1.6e-82:197:72  
55 HOMO SAPIENS (HUMAN).  
Q06495
- HRIFA010799a

EP 1 130 094 A2

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.

1.7e-05:220:30

GALLUS GALLUS (CHICKEN).

P02457

HRIFA010859a

ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1 ADRENOCEPTOR) (SUBTYPE C4).

0.063:134:33

HOMO SAPIENS (HUMAN).

P18825

HRIFA010891a

HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION.

0.044:28:64

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P36015

HRIFA010975a

TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).

8.5e-113:144:86

HOMO SAPIENS (HUMAN).

P43405

HRIFA010988a

GASTRIN PRECURSOR.

0.084:59:37

HOMO SAPIENS (HUMAN).

P01350

HRIFA011016a

PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) (CALCIUM-BINDING PROTEIN 2) (CABP2).

3.1e-15:127:37

RATTUS NORVEGICUS (RAT).

P38659

HRIFA011105a

SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.

0.97:41:43

DROSOPHILA MELANOGASTER (FRUIT FLY).

P02841

HRIFA011128a

GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).

0.0046:30:63

LYCOPERSICON ESCULENTUM (TOMATO).

Q01157

HRIFA011179a

PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-).

1.1e-20:127:42

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P34244

HRIFA011197a

DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM).

5.8e-26:169:40

MUS MUSCULUS (MOUSE).

P28843

HRIFA011449a

GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE P58/GTA (EC 2.7.1.-).

1.9e-26:109:53

MUS MUSCULUS (MOUSE).

P24788

HRIFA011484a

D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).

0.00055:115:33

HOMO SAPIENS (HUMAN).

P21917

HRIFA011512a

POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2 (SNF2-ALPHA).

0.00024:139:25

HOMO SAPIENS (HUMAN).

P51531

HRIFA011580a

VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI) PHOSVITIN (PV)  
LIPOVITELLIN II (LVII) YGP40].

4.0e-08:182:32

GALLUS GALLUS (CHICKEN).

P02845

HRIFA011659a

VON WILLEBRAND FACTOR PRECURSOR.

9.8e-17:210:25

HOMO SAPIENS (HUMAN).

P04275

HRIFA011820a

ZINC FINGER PROTEIN 136.

1.9e-10:42:73

HOMO SAPIENS (HUMAN).

P52737

HRIFA011926a

TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).

1.0:149:22

PSEUDOMONAS AERUGINOSA.

P15276

HRIFA011947a

ZINC FINGER PROTEIN 136.

1.3e-80:180:72

HOMO SAPIENS (HUMAN).

P52737

HRIFA012069a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

0.0027:205:28

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

HRIFA012151a

EP 1 130 094 A2

NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.  
0.00028:72:37  
RATTUS NORVEGICUS (RAT).  
Q07008

5

HRIFA012167a  
HYPOTHETICAL SYMPORTER IN GLTS-SELC INTERGENIC REGION.  
6.4e-09:145:28  
ESCHERICHIA COLI.  
P31435

10

HRIFA012278a  
ZINC FINGER PROTEIN 140.  
3.1e-14:88:52  
HOMO SAPIENS (HUMAN).  
P52738

15

HRIFA012354a  
"SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT."  
2.1e-05:120:32  
RATTUS NORVEGICUS (RAT).  
P04775

20

HRIFA012427a  
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.  
6.3e-08:250:28  
MUS MUSCULUS (MOUSE).  
P11087

25

HRIFA012436a  
INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).  
4.7e-09:95:31  
HOMO SAPIENS (HUMAN).  
Q04941

30

HRIFA012515a  
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).  
3.5e-06:181:27  
ORYCTOLAGUS CUNICULUS (RABBIT).  
P11170

35

HRIFA012584a  
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).  
4.9e-14:136:29  
NEUROSPORA CRASSA.  
P23231

45

HRIFA012625a  
"HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT)."  
9.6e-12:103:40  
RATTUS NORVEGICUS (RAT).  
P13386

55

HRIFA012692a

BLOOM'S SYNDROME PROTEIN.

6.3e-26:203:34

HOMO SAPIENS (HUMAN).

P54132

5

HRIFA012702a

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

1.9e-07:153:30

ZEA MAYS (MAIZE).

10

P14918

HRIFA012737a

LEUCOCYTE ANTIGEN CD97 PRECURSOR.

1.6e-09:170:24

15

HOMO SAPIENS (HUMAN).

P48960

HRIFA012795a

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DRK1).

20

3.0e-34:189:39

RATTUS NORVEGICUS (RAT).

P15387

HRIFA012885a

25

HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECURSOR.

2.9e-21:159:40

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P47032

30

HRIFA012914a

ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70 TRANSMEMBRANE PROTEIN P20E].

3.4e-29:134:47

BABOON ENDOGENOUS VIRUS (STRAIN M7).

35

P10269

HRIFA012969a

ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

40

1.2e-30:228:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32802

HRIFA012990a

45

PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).

7.4e-20:181:33

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P39986

50

HRIFA013092a

OUTER MEMBRANE PROTEIN H.8 PRECURSOR.

0.0039:51:39

NEISSERIA GONORRHOEAE.

P11910

55

HRIFA013103a

N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANS-

FERASE) (GT).

0.25:50:34

MUS MUSCULUS (MOUSE).

P15535

5

HRIFA013135a

CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (SLAYER PROTEIN 1).

1.6e-05:214:28

CLOSTRIDIUM THERMOCELLUM.

10

Q06852

HRIFA013235a

PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.

1.9e-05:113:40

15

HOMO SAPIENS (HUMAN).

P02461

HRIFA013254a

COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN].

20

3.8e-13:123:41

MUS MUSCULUS (MOUSE).

P01029

HRIFA013265a

25

CATHEPSIN L PRECURSOR (EC 3.4.22.15) (MAJOR EXCRETED PROTEIN) (MEP).

7.0e-107:225:86

HOMO SAPIENS (HUMAN).

P07711

30

HRIFA013276a

5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).

2.2e-117:270:85

HOMO SAPIENS (HUMAN).

P21589

35

HRIFA013279a

CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).

4.9e-05:127:37

PLASMODIUM VIVAX.

40

P08677

HRIFA013376a

MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).

45

8.0e-23:230:31

NEUROSPORA CRASSA.

P23231

50

HRIFA013477a

OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).

5.8e-87:197:87

HOMO SAPIENS (HUMAN).

P41217

55

HRIFA013586a

ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

3.8e-31:93:64  
BOS TAURUS (BOVINE).  
P07106

5 HRIFA013589a  
T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN).  
5.0e-06:95:35  
HOMO SAPIENS (HUMAN).  
P40200

10 HRIFA013620a  
"HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT)."  
7.1e-08:95:37  
15 MUS MUSCULUS (MOUSE).  
P20490

HRIFA013726a  
SERINE/THREONINE-PROTEIN KINASE STE20 (EC 2.7.1.-).  
20 1.5e-33:99:50  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
Q03497

HRIFA013744a  
25 ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).  
7.5e-15:105:38  
BOS TAURUS (BOVINE).  
P07106

30 HRIFA013911a  
BIOTINIDASE PRECURSOR (EC 3.5.1.12).  
7.8e-37:104:46  
HOMO SAPIENS (HUMAN).  
35 P43251

HRIFA013919a  
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).  
1.2e-10:170:32  
40 HOMO SAPIENS (HUMAN).  
Q02817

HRIFA013932a  
45 "SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6" PEPTIDE P-H].  
2.6e-05:168:34  
HOMO SAPIENS (HUMAN).  
P04280

50 HRIFA013980a  
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4).  
0.00036:157:27  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
55 P18480

HRIFA014006a  
T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).

EP 1 130 094 A2

9.4e-16:185:28  
MUS MUSCULUS (MOUSE).  
P20937

5 HRIFA014024a  
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).  
0.0013:102:44  
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).  
P29128

10 HRIFA014056a  
PROTEIN Q300.  
5.1e-05:24:70  
MUS MUSCULUS (MOUSE).  
15 Q02722

HRIFA014111a  
TOLL PROTEIN PRECURSOR.  
5.5e-08:203:27  
20 DROSOPHILA MELANOGASTER (FRUIT FLY).  
P08953

HRIFA014133a  
PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
25 1.6e-06:143:33  
MUS MUSCULUS (MOUSE).  
P05142

HRIFA014185a  
30 LEUCOCYTE ANTIGEN CD97 PRECURSOR.  
6.0e-14:192:30  
HOMO SAPIENS (HUMAN).  
P48960

35 HRIFA014336a  
"GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (FRAGMENT)."  
2.8e-70:198:58  
SUS SCROFA (PIG).  
P20305

40 HRIFA014396a  
CREB-BINDING PROTEIN.  
2.6e-07:101:34  
MUS MUSCULUS (MOUSE).  
45 P45481

HRIFA014397a  
GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1.  
5.2e-05:147:30  
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P25655

HRIFA014465a  
55 HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.  
2.8e-11:166:30  
CAENORHABDITIS ELEGANS.  
P30638



# EP 1 130 094 A2

- 5 HRIFA014500a  
HYPOTHETICAL 71.4 KD PROTEIN IN NMD3-ENO2 INTERGENIC REGION.  
1.0e-14:149:35  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P38862
- 10 HRIFA014561a  
PROBABLE G PROTEIN-COUPLED RECEPTOR GPR1.  
4.1e-70:156:89  
HOMO SAPIENS (HUMAN).  
P46091
- 15 HRIFA014568a  
AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE).  
2.4e-40:196:44  
RATTUS NORVEGICUS (RAT).  
P15684
- 20 HRIFA014590a  
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).  
0.18:26:30  
GALLUS GALLUS (CHICKEN).  
P14093
- 25 HRIFA014598a  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
4.9e-05:124:29  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437
- 30 HRIFA014620a  
ENL PROTEIN.  
0.58:170:30  
HOMO SAPIENS (HUMAN).  
35 Q03111
- 40 HRIFA014621a  
PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR.  
2.7e-50:150:74  
HOMO SAPIENS (HUMAN).  
P11462
- 45 HRIFA014688a  
INTEGRIN BETA-6 SUBUNIT PRECURSOR.  
6.9e-31:189:39  
HOMO SAPIENS (HUMAN).  
P18564
- 50 HRIFA014702a  
PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
6.4e-05:89:40  
MUS MUSCULUS (MOUSE).  
P05142
- 55 HRIFA014819a  
MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.  
7.8e-26:117:46  
HOMO SAPIENS (HUMAN).

P55083

HRIFA014868a  
SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.  
8.9e-08:195:29  
DROSOPHILA ERECTA (FRUIT FLY).  
P13730

HRIFA014951a  
PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).  
4.1e-23:132:39  
EQUUS CABALLUS (HORSE).  
P80010

HRIFA014967a  
CHLORINE CHANNEL PROTEIN P64.  
2.0e-52:142:76  
BOS TAURUS (BOVINE).  
P35526

HRIFA015063a  
ZINC FINGER PROTEIN 136.  
6.6e-53:229:48  
HOMO SAPIENS (HUMAN).  
P52737

HRIFA015070a  
SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).  
9.3e-24:143:41  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P38692

HRIFA015122a  
REGULATORY PROTEIN E2.  
0.45:129:30  
HUMAN PAPILLOMAVIRUS TYPE 5.  
P06921

HRIFA015219a  
FIBRILLIN 1 PRECURSOR (MP340).  
9.9e-09:132:32  
BOS TAURUS (BOVINE).  
P98133

HRIFA015246a  
PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 4 PRECURSOR (PSBG-4).  
2.4e-33:184:46  
HOMO SAPIENS (HUMAN).  
Q00888

HRIFA015351a  
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).  
0.0021:122:30  
RATTUS NORVEGICUS (RAT).  
P03994

HRIFA015423a  
B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).

1.2e-11:148:35

HOMO SAPIENS (HUMAN).

P20749

5

HRIFA015453a

RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).

6.8e-11:91:37

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P54644

10

HRIFA015486a

BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR).

2.0e-22:208:27

15

MUS MUSCULUS (MOUSE).

Q01339

HRIFA015506a

COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).

20

1.3e-12:73:50

HOMO SAPIENS (HUMAN).

P23508

HRIFA015536a

25

CHLORINE CHANNEL PROTEIN P64.

1.2e-49:115:79

BOS TAURUS (BOVINE).

P35526

30

HRIFA015547a

BEM46 PROTEIN (FRAGMENT).

1.4e-33:137:49

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

P54069

35

HRIFA015568a

HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.

2.4e-16:152:34

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

40

Q09875

HRIFA015756a

EBNA-2 NUCLEAR PROTEIN.

2.9e-15:28:75

45

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P12978

HRIFA015802a

PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).

50

0.0035:122:30

RATTUS NORVEGICUS (RAT).

P03994

HRIFA015811a

55

GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).

6.2e-39:171:43

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P43636

- 5 HRIFA015902a  
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.  
0.0075:161:29  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P32323
- 10 HRIFA015947a  
ZINC FINGER Y-CHROMOSOMAL PROTEIN 1.  
0.035:98:28  
MUS MUSCULUS (MOUSE).  
P10925
- 15 HRIFA015995a  
PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.  
6.2e-08:221:37  
HOMO SAPIENS (HUMAN).  
P02461
- 20 HRIFA016070a  
"COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR."  
1.0e-18:179:35  
HOMO SAPIENS (HUMAN).  
P02745
- 25 HRIFA016214a  
PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
4.0e-05:96:42  
MUS MUSCULUS (MOUSE).  
P05142
- 30 HRIFA016240a  
HYPOTHETICAL 65.3 KD PROTEIN IN PRE3-SAG1 INTERGENIC REGION.  
8.5e-05:103:33  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
35 P47082
- 40 HRIFA016255a  
EBNA-1 NUCLEAR PROTEIN.  
4.5e-09:219:33  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03211
- 45 HRIFA016290a  
COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).  
6.7e-21:182:41  
HOMO SAPIENS (HUMAN).  
P12259
- 50 HRIFA016430a  
ER LUMEN PROTEIN RETAINING RECEPTOR 1 (KDEL RECEPTOR 1).  
7.1e-50:120:86  
HOMO SAPIENS (HUMAN).  
P24390
- 55 HRIFA016599a  
MEIOTIC RECOMBINATION PROTEIN REC104.  
0.57:73:31  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P33323

HRIFA016639a

"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."

8.0e-06:206:23

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P08640

HRIFA016654a

HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).

1.1e-78:181:86

ORYCTOLAGUS CUNICULUS (RABBIT).

P33279

HRIFA016669a

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

1.4e-08:87:36

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

HRIFA016758a

GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).

9.5e-17:158:40

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P43636

HRIFA016963a

FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR.

6.2e-08:131:32

LYMNAEA STAGNALIS (GREAT POND SNAIL).

P42565

HRIFA017031a

MYOSIN HEAVY CHAIN KINASE A (EC 2.7.1.129) (MHCK A).

2.6e-11:152:34

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P42527

HRIFA017146a

D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).

0.0014:78:37

HOMO SAPIENS (HUMAN).

P21917

HRIFA017190a

FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).

0.0026:89:30

HOMO SAPIENS (HUMAN).

Q01543

HRIFA017257a

"GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL)."

2.5e-79:261:57

HOMO SAPIENS (HUMAN).

P06396

HRIFA017295a

# EP 1 130 094 A2

"ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II)."

3.4e-20:66:78

HOMO SAPIENS (HUMAN).

Q10469

HRIFA017312a

C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN) (PRP).

2.7e-19:221:33

HOMO SAPIENS (HUMAN).

P04003

HRIFA017456a

LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).

0.11:94:35

MUS MUSCULUS (MOUSE).

P19137

HRIFA017457a

SYNAPTOTAGMIN II.

7.2e-07:98:35

MUS MUSCULUS (MOUSE).

P46097

HRIFA017643a

NOV PROTEIN HOMOLOG PRECURSOR (NOVH).

2.2e-07:81:41

HOMO SAPIENS (HUMAN).

P48745

HRIFA017670a

TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.

4.9e-06:172:27

RATTUS NORVEGICUS (RAT).

P19814

HRIFA017703a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

1.9e-16:129:34

THERMOMONOSPORA CURVATA.

P49695

HRIFA017791a

MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).

0.012:71:38

HOMO SAPIENS (HUMAN).

Q02817

HRIFA017801a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

4.5e-07:86:39

MUS MUSCULUS (MOUSE).

P05142

HRIFA017818a

ATP SYNTHASE C CHAIN (EC 3.6.1.34) (LIPID-BINDING PROTEIN).

1.0:32:40

STREPTOMYCES LIVIDANS.  
P50014

HRIFA017836a

5 "TETRACYCLINE RESISTANCE PROTEIN, CLASS H (TETA(H))."

1.3e-08:113:31

PASTEURELLA MULTOCIDA.

P51564

10 HRIFA017855a

ORM1 PROTEIN.

1.7e-18:137:35

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53224

15 HRIFA017921a

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).

2.0e-09:182:35

20 HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).

P08393

HRIFA018092a

25 "DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2-DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT)."

2.1e-20:119:42

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P17898

30 HRIFA018131a

ORM1 PROTEIN.

2.6e-20:137:37

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53224

35 HRIFA018134a

SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37).

1.1e-11:147:32

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

40 Q05609

HRIFA018238a

NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (MOTCH PROTEIN).

8.6e-06:74:44

45 MUS MUSCULUS (MOUSE).

Q01705

HRIFA018262a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

6.4e-10:71:38

THERMOMONOSPORA CURVATA.

P49695

55 HRIFA018287a

HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.

1.5e-06:214:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53214

# EP 1 130 094 A2

HRIFA018447a  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
0.00065:133:33  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437

HRIFA018580a  
COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).  
2.1e-18:109:41  
CRICETULUS GRISEUS (CHINESE HAMSTER).  
P49020

HRIFA018666a  
PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE  
PHOSPHOHYDROLASE).  
1.7e-06:191:28  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P16621

HRIFA018688a  
PHLB PROTEIN PRECURSOR.  
1.9e-06:110:35  
SERRATIA LIQUEFACIENS.  
P18954

HRIFA018754a  
"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-  
GLUCAN GLUCOHYDROLASE)."  
1.8e-06:195:27  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P08640

HRIFA018794a  
MSP1 PROTEIN HOMOLOG.  
3.2e-06:93:25  
CAENORHABDITIS ELEGANS.  
P54815

HRIFA018827a  
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.  
3.1e-17:180:28  
CAENORHABDITIS ELEGANS.  
P30638

HRIFA018870a  
HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.  
4.7e-09:70:37  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P47088

HRIFA018904a  
MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DYSTROPHY PROTEIN KINASE) (MDPK) (DM-KI-  
NASE) (DMK) (DMPK) (MT-PK).  
5.5e-12:142:32  
HOMO SAPIENS (HUMAN).  
Q09013

HRIFA018931a



ZINC FINGER PROTEIN 140.  
2.9e-10:47:74  
HOMO SAPIENS (HUMAN).  
P52738

5

HRIFA018993a  
HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.  
1.2e-13:117:34  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P53073

10

HRIFA019105a  
DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR (EC 3.4.24.-).  
7.5e-22:203:32  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P25723

15

HRIFA019136a  
"MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, LIGHT CHAIN) (PKCSL) (80K-L PROTEIN)."  
1.0e-25:74:81  
HOMO SAPIENS (HUMAN).  
P29966

20

HRIFA019175a  
PROTEIN KINASE WIS1 (EC 2.7.1.-).  
1.3e-14:84:39  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
P33886

25

HRIFA019262a  
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).  
2.5e-55:188:50  
HOMO SAPIENS (HUMAN).  
Q03923

30

HRIFA019412a  
CATHEPSIN E PRECURSOR (EC 3.4.23.34).  
1.4e-09:121:33  
CAVIA PORCELLUS (GUINEA PIG).  
P25796

40

HRIFA019437a  
REGULATORY PROTEIN E2.  
0.26:77:37  
HUMAN PAPILLOMAVIRUS TYPE 14.  
P36783

45

HRIFA019466a  
EBNA-1 NUCLEAR PROTEIN.  
2.7e-19:130:43  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03211

50

HRIFA019490a  
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TFE4).  
1.1e-09:132:34

55

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P18480

HRIFA019498a

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAL (SHAL2).

5.6e-05:87:36

DROSOPHILA MELANOGASTER (FRUIT FLY).

P17971

HRIFA019532a

EBNA-1 NUCLEAR PROTEIN.

1.8e-05:67:49

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

HRIFA019651a

ACIDIC PHOSPHOPROTEIN PRECURSOR (50 KD ANTIGEN).

6.1e-05:31:64

PLASMODIUM CHABAUDI.

Q02752

HRIFA019867a

RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).

8.2e-34:103:71

RATTUS NORVEGICUS (RAT).

Q06496

HRIFA019869a

SERINE/THREONINE-PROTEIN KINASE FUSED (EC 2.7.1.-).

7.2e-29:83:49

DROSOPHILA MELANOGASTER (FRUIT FLY).

P23647

HRIFA019958a

REPRESSOR PROTEIN CI (FRAGMENT).

0.99:45:37

BACTERIOPHAGE 434.

P16117

HRIFA020144a

SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).

2.8e-06:176:30

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P17437

HRIFA020184a

NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).

1.9e-10:102:37

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P18160

HRIFA020272a

MUSCARINIC ACETYLCHOLINE RECEPTOR M3.

5.5e-91:211:85

HOMO SAPIENS (HUMAN).

P20309

# EP 1 130 094 A2

- 5 HRIFA020335a  
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).  
5.0e-104:275:72  
HOMO SAPIENS (HUMAN).  
P27448
- 10 HRIFA020349a  
BRITTLE-1 PROTEIN PRECURSOR.  
6.0e-30:214:35  
ZEA MAYS (MAIZE).  
P29518
- 15 HRIFA020453a  
PROTEIN TRANSPORT PROTEIN SEC22 (PROTEIN SLY2).  
2.5e-08:132:28  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P22214
- 20 HRIFA020693a  
TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).  
3.9e-09:96:35  
HOMO SAPIENS (HUMAN).  
P43146
- 25 HRIFA020707a  
PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-SA-1).  
3.4e-09:95:33  
TRYPANOSOMA BRUCEI BRUCEI.  
30 Q06084
- 35 HRIFA020748a  
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).  
3.2e-09:210:28  
NICOTIANA TABACUM (COMMON TOBACCO).  
P13983
- 40 HRIFA020862a  
MODIFIER 3 PROTEIN (M33).  
5.6e-26:76:61  
MUS MUSCULUS (MOUSE).  
P30658
- 45 HRIFA020883a  
PROTEIN Q300.  
0.00054:21:66  
MUS MUSCULUS (MOUSE).  
Q02722
- 50 HRIFA021007a  
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).  
0.092:73:36  
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).  
55 P08393
- HRIFA021040a  
TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).

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0.98:63:39  
HOMO SAPIENS (HUMAN).  
P43694

5 HRIFA021061a  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
2.8e-09:162:31  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437

10 HRIFA021213a  
OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.  
2.0e-38:96:72  
CAENORHABDITIS ELEGANS.  
P46975

15 HRIFA021224a  
RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).  
2.8e-06:55:52  
20 RATTUS NORVEGICUS (RAT).  
Q02975

HRIFA021398a  
COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).  
25 2.5e-17:78:51  
ORYCTOLAGUS CUNICULUS (RABBIT).  
P98139

HRIFA021445a  
30 PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-1 (HOMEBOX PROTEIN PBX1) (HOMEBOX PROTEIN PRL).  
0.38:146:31  
HOMO SAPIENS (HUMAN).  
P40424

35 HRIFA021494a  
EBNA-1 NUCLEAR PROTEIN.  
6.8e-07:116:41  
40 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03211

HRIFA021499a  
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).  
7.1e-34:159:50  
45 GALLUS GALLUS (CHICKEN).  
P05099

HRIFA021543a  
50 ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).  
0.0087:50:40  
GALLUS GALLUS (CHICKEN).  
Q03352

55 HRIFA021620a  
PLATELET FACTOR 4 (PF-4).  
0.019:65:27  
SUS SCROFA (PIG).  
P30034

- 5  
HRIFA021637a  
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).  
6.0e-37:147:53  
GALLUS GALLUS (CHICKEN).  
P05099
- 10  
HRIFA021651a  
CARG-BINDING FACTOR-A (CBF-A).  
2.6e-11:170:30  
MUS MUSCULUS (MOUSE).  
Q99020
- 15  
HRIFA021754a  
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).  
1.2e-37:137:51  
GALLUS GALLUS (CHICKEN).  
P05099
- 20  
HRIFA021781a  
DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COM-  
PLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2).  
7.1e-19:199:31  
HOMO SAPIENS (HUMAN).  
P18074
- 25  
HRIFA021787a  
PROTEIN Q300.  
0.051:13:84  
MUS MUSCULUS (MOUSE).  
Q02722
- 30  
HRIFA021794a  
RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).  
1.6e-07:90:32  
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).  
P54644
- 35  
HRIFA021855a  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
8.6e-06:163:30  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437
- 40  
HRIFA021906a  
S-ANTIGEN PROTEIN PRECURSOR.  
2.1e-09:226:28  
PLASMODIUM FALCIPARUM (ISOLATE V1).  
P09593
- 45  
HRIFA022055a  
BETA-LYTIC METALLOENDOPEPTIDASE PRECURSOR (EC 3.4.24.32) (BETA-LYTIC PROTEASE).  
0.63:118:31  
ACHROMOBACTER LYTICUS.  
P27458
- 50  
HRIFA022065a  
BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR.  
9.7e-24:235:34
- 55

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HOMO SAPIENS (HUMAN).  
P16279

HRIFA022139a  
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.  
2.1e-57:232:52  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
Q09782

HRIFA022156a  
"GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR."  
1.4e-07:133:35  
TRITICUM AESTIVUM (WHEAT).  
P08489

HRIFA022166a  
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).  
3.5e-28:194:35  
HOMO SAPIENS (HUMAN).  
Q03468

HRIFA022177a  
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).  
2.2e-12:137:32  
THERMOMONOSPORA CURVATA.  
P49695

HRIFA022182a  
SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-ASSOCIATED KINASE).  
1.2e-47:121:79  
RATTUS NORVEGICUS (RAT).  
P20793

HRIFA022203a  
COLLAGEN ALPHA 1 (III) CHAIN.  
1.1e-05:211:33  
BOS TAURUS (BOVINE).  
P04258

HRIFA022227a  
POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1)  
(PPSEP 1).  
3.2e-31:229:36  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
Q10071

HRIFA022234a  
CARBOXYPEPTIDASE KEX1 PRECURSOR (EC 3.4.16.6) (CARBOXYPEPTIDASE D).  
1.8e-08:110:30  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P09620

HRIFA022249a  
ZINC FINGER PROTEIN 133.  
1.1e-34:84:48  
HOMO SAPIENS (HUMAN).  
P52736

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- HRIFA022265a  
CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN (EC 2.7.1.123) (CAM KINASE-GR) (CAMK IV) [CONTAINS: CALSPERMIN].  
5.1e-26:188:40  
5 RATTUS NORVEGICUS (RAT).  
P13234
- HRIFA022328a  
SCO1 PROTEIN PRECURSOR.  
10 5.4e-25:84:45  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P23833
- HRIFA022335a  
15 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).  
0.21:121:29  
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).  
P08393  
20
- HRIFA022348a  
AGAMOUS PROTEIN.  
1.0:40:42  
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).  
25 P17839
- HRIFA022411a  
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).  
30 0.00059:111:35  
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).  
P08393
- HRIFA022423a  
35 HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.  
2.5e-15:106:42  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P40857
- HRIFA022462a  
40 RETINOIC ACID RECEPTOR RXR-BETA.  
0.0010:124:33  
HOMO SAPIENS (HUMAN).  
P28702  
45
- HRIFA022493a  
ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR).  
0.0018:130:34  
MUS MUSCULUS (MOUSE).  
50 Q01338
- HRIFA022528a  
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).  
3.2e-23:230:28  
55 ZEA MAYS (MAIZE).  
P14918
- HRIFA022546a

NINAC SHORT PROTEIN (EC 2.7.1.-).  
8.5e-42:209:43  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P10677

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HRIFA022564a  
ZINC FINGER PROTEIN 140.  
7.9e-23:116:51  
HOMO SAPIENS (HUMAN).  
P52738

10

HRIFA022616a  
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91).  
7.4e-36:172:43  
HOMO SAPIENS (HUMAN).  
Q07954

15

HRIFA022671a  
PAIRED AMPHIPATHIC HELIX PROTEIN.  
2.0e-26:186:36  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P22579

20

HRIFA022691a  
FIBRINOGEN-LIKE PROTEIN A PRECURSOR (FREPI-A).  
1.4e-44:229:41  
PARASTICHOPUS PARVIMENSIS (SEA CUCUMBER).  
P19477

25

30

HRIFA022702a  
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.  
1.1e-08:146:38  
GALLUS GALLUS (CHICKEN).  
P02457

35

HRIFA022707a  
GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9) (TCF-9).  
7.0e-40:229:37  
HOMO SAPIENS (HUMAN).  
P16383

40

HRIFA022714a  
"AMELOGENIN, CLASS I PRECURSOR."  
0.62:96:31  
BOS TAURUS (BOVINE).  
P02817

45

HRIFA022728a  
ACROSIN PRECURSOR (EC 3.4.21.10) (53 KD FUCOSE-BINDING PROTEIN).  
1.7e-06:28:64  
SUS SCROFA (PIG).  
P08001

50

HRIFA022729a  
"ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II)."

55



7.7e-29:69:84

HOMO SAPIENS (HUMAN).

Q10469

- 5 HRIFA022737a  
TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225).  
6.7e-19:170:37  
GALLUS GALLUS (CHICKEN).  
10 P10039
- HRIFA022776a  
PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).  
4.0e-20:199:31  
15 MEDICAGO SATIVA (ALFALFA).  
P38661
- HRIFA022782a  
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).  
20 3.7e-09:184:36  
PLASMODIUM CYNOMOLGI (STRAIN BEROK).  
P08672
- HRIFA022865a  
25 COLLAGEN ALPHA 1(III) CHAIN.  
2.5e-09:169:33  
BOS TAURUS (BOVINE).  
P04258
- HRIFA022875a  
30 BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).  
9.1e-14:115:33  
BOS TAURUS (BOVINE).  
P21793
- HRIFA022890a  
35 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
1.8e-10:237:30  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
40 P17437
- HRIFA022895a  
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).  
2.4e-106:283:67  
45 HOMO SAPIENS (HUMAN).  
Q03923
- HRIFA022985a  
50 PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-SA-1).  
3.0e-10:33:72  
TRYPANOSOMA BRUCEI BRUCEI.  
Q06084
- HRIFA023007a  
55 MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).  
1.1e-27:66:54  
HOMO SAPIENS (HUMAN).

# EP 1 130 094 A2

P22670

HRIFA023048a

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).

2.2e-07:221:33

RATTUS NORVEGICUS (RAT).

P02454

HRIFA023069a

BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).

3.4e-08:149:31

HOMO SAPIENS (HUMAN).

P98160

HRIFA023129a

HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.

4.2e-06:37:51

PLASMODIUM LOPHURAE.

P04929

HRIFA023154a

GLYCOPROTEIN X PRECURSOR.

8.2e-05:140:27

EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).

P28968

HRIFA023212a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

8.3e-10:249:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

HRIFA023227a

GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).

9.2e-15:180:30

ESCHERICHIA COLI.

P37021

HRIFA023257a

PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.

2.4e-118:229:88

RATTUS NORVEGICUS (RAT).

P38378

HRIFA023304a

PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETICULUM CA2+-ATPASE).

1.3e-23:222:29

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P39524

HRIFA023434a

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (RCK2) (KV2).

0.00018:157:30

RATTUS NORVEGICUS (RAT).

P17659

- 5 HRIFA023464a  
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.  
1.0e-11:75:46  
ORYZA SATIVA (RICE).  
P29834
- 10 HRIFA023489a  
HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.  
4.4e-09:230:23  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
Q10297
- 15 HRIFA023634a  
EBNA-1 NUCLEAR PROTEIN.  
1.8e-08:113:45  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03211
- 20 HRIFA023767a  
CYTOCHROME B5.  
1.1e-12:92:38  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P40312
- 25 HRIFA023894a  
PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
3.6e-05:80:40  
MUS MUSCULUS (MOUSE).  
P05142
- 30 HRIFA023923a  
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).  
4.2e-76:128:85  
HOMO SAPIENS (HUMAN).  
35 P00395
- 40 HRIFA024088a  
NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).  
1.1e-05:118:32  
MUS MUSCULUS (MOUSE).  
P98084
- 45 HRIFA024132a  
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.9.  
6.5e-40:136:61  
HOMO SAPIENS (HUMAN).  
P51787
- 50 HRIFA024185a  
ETS-DOMAIN TRANSCRIPTION FACTOR ERF.  
0.55:128:29  
HOMO SAPIENS (HUMAN).  
P50548
- 55 HRIFA024197a  
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEM-  
BRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP (CARRIER) (TRANSLOCASE  
OF OUTER MEMBRANE TOM70).

7.5e-09:93:34  
NEUROSPORA CRASSA.  
P23231

5 HRIFA024218a  
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.  
6.7e-06:180:36  
HOMO SAPIENS (HUMAN).  
P02452

10 HRIFA024255a  
HYPOTHETICAL 116.3 KD PROTEIN C26F1.09 IN CHROMOSOME I.  
4.8e-23:172:33  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
15 Q10496

HRIFA024305a  
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).  
0.047:47:29  
20 HOMO SAPIENS (HUMAN).  
P18850

HRIFA024392a  
TRANSMEMBRANE PROTEIN SEX PRECURSOR.  
25 6.7e-24:119:43  
HOMO SAPIENS (HUMAN).  
P51805

HRIFA024423a  
30 COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).  
2.1e-18:109:41  
CRICETULUS GRISEUS (CHINESE HAMSTER).  
P49020

35 HRIFA024473a  
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).  
3.3e-05:106:41  
BOS TAURUS (BOVINE).  
P02453

40 HRIFA024482a  
PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).  
1.2e-07:99:31  
NICOTIANA TABACUM (COMMON TOBACCO).  
45 Q03211

HRIFA024504a  
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HY-  
50 DROXYSTEROID DEHYDROGENASE).  
2.6e-43:205:49  
HOMO SAPIENS (HUMAN).  
P37058

55 HRIFA024543a  
GLYCOPROTEIN X PRECURSOR.  
1.5e-06:257:28  
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).  
P28968

- 5 HRIFA024718a  
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).  
5.3e-45:168:52  
MUS MUSCULUS (MOUSE).  
P23780
- 10 HRIFA024767a  
SODIUM CHANNEL PROTEIN (NA<sup>+</sup> CHANNEL).  
7.4e-30:221:31  
ELECTROPHORUS ELECTRICUS (ELECTRIC EEL).  
P02719
- 15 HRIFA024884a  
HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.  
0.0089:23:65  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P53245
- 20 HRIFA024893a  
REGULATORY PROTEIN E2.  
0.0021:167:31  
HUMAN PAPILLOMAVIRUS TYPE 8.  
P06422
- 25 HRIFA024937a  
GNS1 PROTEIN.  
1.0e-15:173:33  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P25358
- 30 HRIFA024978a  
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).  
0.00019:150:32  
HOMO SAPIENS (HUMAN).  
35 Q02817
- 40 HRIFA024994a  
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).  
5.3e-22:145:46  
NICOTIANA TABACUM (COMMON TOBACCO).  
P13983
- 45 HRIFA025033a  
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).  
0.50:215:29  
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).  
P28284
- 50 HRIFA025046a  
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).  
1.7e-41:104:48  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P39986
- 55 HRIFA025250a  
"PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR))."  
7.4e-17:126:34  
DROSOPHILA MELANOGASTER (FRUIT FLY).

P05130

HRIFA025261a  
MYOSIN I ALPHA (MMI-ALPHA).  
2.3e-64:141:84  
MUS MUSCULUS (MOUSE).  
P46735

HRIFA025290a  
EBNA-1 NUCLEAR PROTEIN.  
0.016:79:40  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03211

HRIFA025327a  
PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
2.3e-06:104:37  
MUS MUSCULUS (MOUSE).  
P05142

HRIFA025353a  
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.  
1.0e-11:75:46  
ORYZA SATIVA (RICE).  
P29834

HRIFA025479a  
PROTEASE DEGS PRECURSOR (EC 3.4.21.-).  
3.0e-05:112:33  
ESCHERICHIA COLI.  
P31137

HRIFA025488a  
PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR (FRAGMENTS).  
9.5e-05:104:40  
MUS MUSCULUS (MOUSE).  
P08121

HRIFA025492a  
SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK).  
1.8e-53:159:69  
HOMO SAPIENS (HUMAN).  
Q13627

HRIFA025636a  
MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 (EC 3.4.24.-) (TAT-BIND-  
ING HOMOLOG 12).  
4.7e-32:81:66  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P40341

HRIFA025695a  
PEREGRIN (BR140 PROTEIN).  
3.1e-40:227:43  
HOMO SAPIENS (HUMAN).  
P55201

HRIFA025703a

# EP 1 130 094 A2

CELL SURFACE ANTIGEN 114/A10 PRECURSOR.

1.8e-08:71:42

MUS MUSCULUS (MOUSE).

P19467

5

HRIFA025706a

GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).

1.2e-28:111:44

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

10

P43636

HRIFA025766a

CYTOCHROME B5.

4.2e-13:133:33

ORYCTOLAGUS CUNICULUS (RABBIT).

15

P00169

HRIFA025771a

HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.

20

6.7e-10:129:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53288

HRIFA025778a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

25

1.5e-05:212:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

HRIFA025800a

HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.

30

3.7e-18:165:33

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40544

35

HRIFA025904a

COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).

2.6e-05:211:28

HOMO SAPIENS (HUMAN).

40

P17927

HRIFA025907a

INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN PRECURSOR (IGUPI-5111).

2.1e-38:176:38

HOMO SAPIENS (HUMAN).

45

Q06323

HRIFA025913a

DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).

50

2.5e-32:185:37

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P46971

HRIFA025936a

TRANSCRIPTIONAL ACTIVATOR FE65.

55

3.4e-09:43:46

RATTUS NORVEGICUS (RAT).

P46933

5 HRIFA025966a  
 SYNAPTOTAGMIN III.  
 4.5e-05:93:33  
 RATTUS NORVEGICUS (RAT).  
 P40748

10 HRIFA025978a  
 "GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DX5 PRECURSOR."  
 3.5e-06:224:28  
 TRITICUM AESTIVUM (WHEAT).  
 P10388

15 HRIFA026089a  
 BUTYROPHILIN PRECURSOR (BT).  
 1.1e-12:146:29  
 BOS TAURUS (BOVINE).  
 P18892

20 HRIFA026121a  
 FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).  
 9.7e-06:72:43  
 HOMO SAPIENS (HUMAN).  
 P48023

25 HRIFA026242a  
 HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.  
 7.4e-09:188:26  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
 P48566

30 HRIFA026265a  
 DNA BINDING PROTEIN S1FA.  
 0.67:43:37  
 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).  
 P42551

35 HRIFA026303a  
 SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).  
 0.014:88:32  
 40 HOMO SAPIENS (HUMAN).  
 P10163

45 HRIFA026316a  
 EBNA-2 NUCLEAR PROTEIN.  
 1.5e-07:82:35  
 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
 P12978

50 HRIFA026351a  
 FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).  
 0.019:89:31  
 HOMO SAPIENS (HUMAN).  
 Q01543

55 HRIFA026364a  
 PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.  
 8.3e-40:167:49  
 RATTUS NORVEGICUS (RAT).



P48303

HRIFA026382a

T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).

6.2e-10:135:38

ORYCTOLAGUS CUNICULUS (RABBIT).

P06333

HRIFA026465a

COLLAGEN ALPHA 1(IX) CHAIN PRECURSOR (FRAGMENTS).

8.6e-07:158:35

GALLUS GALLUS (CHICKEN).

P12106

HRIFA026496a

ZINC FINGER PROTEIN 140.

5.9e-24:122:52

HOMO SAPIENS (HUMAN).

P52738

HRIFA026519a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

1.3e-08:130:36

MUS MUSCULUS (MOUSE).

P05142

HRIFA026564a

GLYCOPROTEIN X PRECURSOR

1.8e-10:225:25

EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).

P28968

HRIFA026576a

"ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (AD-ENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)."

1.7e-09:116:34

HOMO SAPIENS (HUMAN).

P12235

HRIFA026615a

REGULATORY PROTEIN E2.

0.0024:132:31

HUMAN PAPILLOMAVIRUS TYPE 9.

P36780

HRIFA026618a

PROTEIN Q300.

1.2e-05:27:66

MUS MUSCULUS (MOUSE).

Q02722

HRIFA026659a

SERINE/THREONINE-PROTEIN KINASE SGK (EC 2.7.1.-) (SERUM/GLUCOCORTICOID-REGULATED KINASE).

2.0e-10:81:45

RATTUS NORVEGICUS (RAT).

Q06226

# EP 1 130 094 A2

- HRIFA026764a  
MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1) (CD48).  
3.4e-05:162:25  
RATTUS NORVEGICUS (RAT).  
P10252
- HRIFA026789a  
PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.  
8.1e-22:175:38  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
Q09818
- HRIFA026813a  
"PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU)."  
7.1e-89:256:67  
HOMO SAPIENS (HUMAN).  
Q15139
- HRIFA026860a  
MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).  
2.6e-19:103:43  
MESOCRICETUS AURATUS (GOLDEN HAMSTER).  
P53988
- HRIFA026923a  
CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).  
0.18:119:36  
CANIS FAMILIARIS (DOG).  
P39881
- HRIFA027012a  
"MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSI-  
DASE) (ALPHA-MANNOSIDASE 1A)."  
1.8e-44:234:41  
MUS MUSCULUS (MOUSE).  
P45700
- HRIFA027045a  
HYPOTHETICAL PROTEIN HI0519.  
2.7e-27:181:38  
HAEMOPHILUS INFLUENZAE.  
P44742
- HRIFA027125a  
ZINC FINGER PROTEIN 133.  
3.9e-33:70:61  
HOMO SAPIENS (HUMAN).  
P52736
- HRIFA027173a  
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).  
0.15:137:27  
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).  
P28284
- HRIFA027179a  
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).  
3.6e-30:90:77

HOMO SAPIENS (HUMAN).  
Q03468

5 HRIFA027187a  
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).  
4.7e-11:44:61  
HOMO SAPIENS (HUMAN).  
P20931

10 HRIFA027327a  
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.  
3.8e-07:184:35  
HOMO SAPIENS (HUMAN).  
Q03692

15 HRIFA027329a  
SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.  
9.1e-08:195:29  
DROSOPHILA ERECTA (FRUIT FLY).  
20 P13730

HRIFA027355a  
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).  
1.9e-06:33:72  
25 HOMO SAPIENS (HUMAN).  
P20931

HRIFA027485a  
COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR.  
30 0.00099:174:36  
HOMO SAPIENS (HUMAN).  
P12107

HRIFA027536a  
35 VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).  
0.0042:104:35  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P13238

40 HRIFA027549a  
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).  
0.00023:101:44  
HOMO SAPIENS (HUMAN).  
45 P21917

HRIFA027622a  
GUANOSINE-DIPHOSPHATASE (EC 3.6.1.42) (GDPASE).  
2.2e-23:146:45  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
50 P32621

HRIFA027625a  
CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).  
1.1e-57:220:54  
55 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P13586

HRIFA027644a

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).  
7.5e-05:72:40  
RATTUS NORVEGICUS (RAT).  
P02454

5

HRIFA027656a  
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).  
1.6e-13:149:34  
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).  
P18160

10

HRIFA027673a  
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.  
6.4e-06:47:57  
HOMO SAPIENS (HUMAN).  
P29279

15

HRIFA027681a  
SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).  
1.1e-13:158:31  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P08458

20

HRIFA027714a  
HYPOTHETICAL 146.8 KD PROTEIN C34E10.5 IN CHROMOSOME III.  
7.2e-06:146:30  
CAENORHABDITIS ELEGANS.  
P46580

25

HRIFA027722a  
SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).  
2.7e-105:242:85  
CANIS FAMILIARIS (DOG).  
Q00004

30

HRIFA027860a  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
8.3e-08:168:32  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437

35

HRIFA027867a  
STANNIOCALCIN PRECURSOR (STC) (CORPUSCLES OF STANNIUS PROTEIN) (CS) (HYPOCALCIN) (TEL-  
EOCALCIN).  
1.0:100:27  
ANGUILLA AUSTRALIS (AUSTRALIAN EEL).  
P18301

45

HRIFA027940a  
INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).  
8.7e-15:149:38  
HOMO SAPIENS (HUMAN).  
P55103

50

HRIFA028061a  
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).  
9.7e-07:157:26  
THERMOMONOSPORA CURVATA.

55

P49695

HRIFA028157a

HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).

2.8e-71:201:68

HOMO SAPIENS (HUMAN).

P30825

HRIFA028187a

EBNA-1 NUCLEAR PROTEIN.

1.5e-09:131:38

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

HRIFA028262a

CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).

7.2e-09:99:33

MUS MUSCULUS (MOUSE).

P53996

HRIFA028371a

PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).

1.0e-08:103:33

RATTUS NORVEGICUS (RAT).

Q01177

HRIFA028402a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

3.2e-33:204:39

THERMOMONOSPORA CURVATA.

P49695

HRIFA028440a

COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.

1.9e-07:192:36

HOMO SAPIENS (HUMAN).

P53420

HRIFA028468a

CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN (EC 2.7.1.123) (CAM KINASE-GR) (CAMK IV) [CONTAINS: CALSPERMIN].

5.8e-32:178:44

RATTUS NORVEGICUS (RAT).

P13234

HRIFA028501a

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (RCK2) (KV2).

6.3e-05:161:31

RATTUS NORVEGICUS (RAT).

P17659

HRIFA028511a

ANKYRIN HOMOLOG PRECURSOR.

3.0e-19:176:34

CHROMATIUM VINOSUM.

Q06527

- 5 HRIFA028576a  
ACROSIN PRECURSOR (EC 3.4.21.10).  
4.8e-08:78:46  
ORYCTOLAGUS CUNICULUS (RABBIT).  
P48038
- 10 HRIFA028614a  
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.  
1.0e-08:82:39  
PLASMODIUM LOPHURAE.  
P04929
- 15 HRIFA028651a  
BAND 3 ANION TRANSPORT PROTEIN.  
1.3e-18:156:32  
GALLUS GALLUS (CHICKEN).  
P15575
- 20 HRIFA028790a  
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).  
5.0e-18:212:29  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P39986
- 25 HRIFA028804a  
CCAAT-BINDING FACTOR (CBF).  
0.98:232:23  
MUS MUSCULUS (MOUSE).  
P53569
- 30 HRIFA028867a  
REGULATORY PROTEIN E2.  
0.0057:124:31  
HUMAN PAPILLOMAVIRUS TYPE 25.  
P36787
- 35 HRIFA028911a  
HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.  
1.2e-09:206:33  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P47179
- 45 HRIFA028983a  
HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).  
0.0051:115:33  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P25439
- 50 HRIFA029002a  
FIBRINOGEN BETA CHAIN.  
3.2e-25:121:45  
BOS TAURUS (BOVINE).  
P02676
- 55 HRIFA029050a  
RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD).  
1.2e-10:134:32  
GALLUS GALLUS (CHICKEN).

P24503

HRIFA029208a

RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).

1.4e-14:64:59

RATTUS NORVEGICUS (RAT).

Q02975

HRIFA029209a

"ALPHA-MANNOSIDASE II (EC 3.2.1.114) (MANNOsyl-OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSIDASE) (MAN II) (GOLGI ALPHA-MANNOSIDASE II)."

2.3e-12:114:37

MUS MUSCULUS (MOUSE).

P27046

HRIFA029256a

GAP JUNCTION BETA-2 PROTEIN (CONNEXIN 26) (CX26).

1.8e-35:89:75

HOMO SAPIENS (HUMAN).

P29033

HRIFA029263a

SARCALUMENIN PRECURSOR.

2.1e-16:161:31

ORYCTOLAGUS CUNICULUS (RABBIT).

P13666

HRIFA029278a

"SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6" PEPTIDE P-H].

3.5e-10:204:32

HOMO SAPIENS (HUMAN).

P04280

HRIFA029285a

GLYCOPROTEIN 25L PRECURSOR (GP25L).

4.9e-58:197:55

CANIS FAMILIARIS (DOG).

P27869

HRIFA029317a

HIGH AFFINITY SULPHATE TRANSPORTER 2.

2.3e-25:83:50

STYLOSANTHES HAMATA.

P53392

HRIFA029327a

MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN (OGCP).

9.1e-34:227:37

BOS TAURUS (BOVINE).

P22292

HRIFA029349a

CUTICLE COLLAGEN 12 PRECURSOR.

5.1e-09:190:33

CAENORHABDITIS ELEGANS.

P20630

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- 5 HRIFA029393a  
PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.  
9.7e-69:165:84  
HOMO SAPIENS (HUMAN).  
P35414
- 10 HRIFA029398a  
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).  
0.011:170:34  
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).  
P29128
- 15 HRIFA029425a  
ALPHA CRYSTALLIN B CHAIN (ALPHA(B)-CRYSTALLIN).  
2.0e-08:99:32  
BOS TAURUS (BOVINE).  
P02510
- 20 HRIFA029434a  
"SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CPS) [CONTAINS: BASIC PEP-  
TIDE IB-6" PEPTIDE P-H].  
2.6e-05:232:32  
HOMO SAPIENS (HUMAN).  
P04280
- 25 HRIFA029440a  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
0.00046:131:33  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
30 P17437
- 35 HRIFA029460a  
SYNAPTOTAGMIN III.  
1.5e-08:102:35  
RATTUS NORVEGICUS (RAT).  
P40748
- 40 HRIFA029467a  
GLYCOPROTEIN X PRECURSOR.  
5.2e-07:182:31  
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).  
P28968
- 45 HRIFA029508a  
PROPERDIN PRECURSOR.  
1.9e-06:218:32  
HOMO SAPIENS (HUMAN).  
P27918
- 50 HRIFA029511a  
POTASSIUM CHANNEL PROTEIN EAG.  
2.3e-66:139:61  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
Q02280
- 55 HRIFA029602a  
SEX-DETERMINING REGION Y PROTEIN (TESTIS-DETERMINING FACTOR).  
1.0:37:37



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SUS SCROFA (PIG).  
P36393

HRIFA029649a

5 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).  
0.30:99:34

HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).  
P28284

10 HRIFA029715a

GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 (DNA-DAMAGE INDUCIBLE TRANSCRIPT 3) (DDIT3) (C/EBP-HOMOLOGOUS PROTEIN) (CHOP).  
0.54:95:30

HOMO SAPIENS (HUMAN).  
15 P35638

HRIFA029730a

HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.  
3.8e-05:131:29

20 PLASMODIUM LOPHURAE.  
P04929

HRIFA029792a

25 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).  
9.0e-09:178:30

THERMOMONOSPORA CURVATA.  
P49695

HRIFA029802a

30 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN).  
7.2e-73:204:69  
CANIS FAMILIARIS (DOG).  
Q01685

35 HRIFA029866a

PROTEIN KINASE BYR2 (EC 2.7.1.-) (PROTEIN KINASE STE8) (MAPK KINASE KINASE) (MAPKKK).  
1.2e-27:144:45  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
40 P28829

HRIFA029932a

F-SPONDIN PRECURSOR.  
9.1e-24:191:37

45 XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P35447

HRIFA030025a

50 ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).  
1.0e-11:138:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P32802

HRIFA030045a

55 SARCALUMENIN PRECURSOR.  
2.4e-20:151:32

ORYCTOLAGUS CUNICULUS (RABBIT).  
P13666

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HRIFA030103a  
HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.  
2.1e-05:215:29  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P53214

HRIFA030106a  
SCO-SPONDIN (FRAGMENT).  
0.53:60:36  
BOS TAURUS (BOVINE).  
P98167

HRIFA030147a  
PUTATIVE MITOCHONDRIAL CARRIER YGR096W.  
1.8e-10:93:34  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P53257

HRIFA030250a  
ENAMELIN (TUFTELIN).  
3.7e-108:250:86  
BOS TAURUS (BOVINE).  
P27628

HRIFA030264a  
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).  
3.3e-09:119:27  
ORYCTOLAGUS CUNICULUS (RABBIT).  
P11170

HRIFA030342a  
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE).  
1.5e-42:203:49  
HOMO SAPIENS (HUMAN).  
P37058

HRIFA030370a  
HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.  
8.0e-12:88:48  
MYCOBACTERIUM TUBERCULOSIS.  
Q10555

HRIFA030371a  
"PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU)."  
1.6e-68:228:59  
HOMO SAPIENS (HUMAN).  
Q15139

HRIFA030381a  
COLLAGEN 1(X) CHAIN PRECURSOR.  
3.0e-05:204:30  
GALLUS GALLUS (CHICKEN).  
P08125

HRIFA030385a  
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.

0.029:162:31

HOMO SAPIENS (HUMAN).

Q03692

5 HRIFA030411a  
SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2).

1.2e-27:115:53

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

10 Q09925

HRIFA030448a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).

2.5e-92:225:77

15 HOMO SAPIENS (HUMAN).

P27448

HRIFA030456a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

20 9.3e-08:127:35

MUS MUSCULUS (MOUSE).

P05142

HRIFA030461a

25 CUTICLE COLLAGEN 12 PRECURSOR.

0.046:140:31

CAENORHABDITIS ELEGANS.

P20630

30 HRIFA030472a

NUC-1 NEGATIVE REGULATORY PROTEIN PREG.

0.0030:98:31

NEUROSPORA CRASSA.

35 Q06712

HRIFA030509a

"INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE (EC 2.7.1.-) (INTERFERON-INDUCIBLE RNA-DEPENDENT PROTEIN KINASE) (P68 KINASE) (P1/EIF-2A PROTEIN KINASE)."

2.5e-09:65:43

40 HOMO SAPIENS (HUMAN).

P19525

HRIFA030511a

T-LYMPHOCYTE MATURATION-ASSOCIATED PROTEIN.

45 0.00010:99:33

HOMO SAPIENS (HUMAN).

P21145

HRIFA030545a

50 PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).

7.6e-21:165:35

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53974

55 HRIFA030566a

"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."

2.7e-07:221:30

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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P08640

HRIFA030599a  
GLYCOPROTEIN X PRECURSOR.  
2.8e-05:236:27  
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).  
P28968

HRIFA030629a  
PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLASE BETA SUB-  
UNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55).  
3.5e-16:115:38  
BOS TAURUS (BOVINE).  
P05307

HRIFA030642a  
SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).  
2.5e-12:93:47  
VOLVOX CARTERI.  
P21997

HRIFA030662a  
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).  
9.1e-120:279:83  
HOMO SAPIENS (HUMAN).  
P03886

HRIFA030839a  
HYPOTHETICAL GENE 51 MEMBRANE PROTEIN.  
1.0:66:27  
ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV).  
Q00135

HRIFA031091a  
PROTEIN Q300.  
0.0042:27:62  
MUS MUSCULUS (MOUSE).  
Q02722

HRIFA031126a  
P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (RB INTRON ENCODED G-PROTEIN COUPLED  
RECEPTOR).  
1.3e-06:70:34  
HOMO SAPIENS (HUMAN).  
P43657

HRIFA031249a  
ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).  
5.9e-05:166:31  
RATTUS NORVEGICUS (RAT).  
P04474

HRIFA031336a  
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-  
BOX DNA BINDING PROTEIN SUBUNIT B).  
6.6e-15:97:38  
PETROMYZON MARINUS (SEA LAMPREY).

P25210

HRIFA031395a

COLD SHOCK PROTEIN CSPB (FRAGMENT).

0.95:32:40

BACILLUS GLOBISPORUS.

P41018

HRIFA031397a

REGULATORY PROTEIN E2.

0.0077:145:35

HUMAN PAPILLOMAVIRUS TYPE 47.

P22420

HRIFA031438a

GLUCOSE REPRESSION MEDIATOR PROTEIN.

1.3e-06:176:26

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P14922

HRIFA031869a

TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY-LIKE) (RHL).

1.7e-18:163:41

RATTUS NORVEGICUS (RAT).

Q04666

HRIFA031935a

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

1.8e-06:192:32

ZEA MAYS (MAIZE).

P14918

HRIFA031986a

SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21-ACTIVATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2).

2.4e-49:222:47

RATTUS NORVEGICUS (RAT).

P35465

HRIFA032009a

PROBABLE G PROTEIN-COUPLED RECEPTOR FROM T-CELLS PRECURSOR (GLUCOCORTICOID-INDUCED RECEPTOR).

1.0e-17:118:36

MUS MUSCULUS (MOUSE).

P30731

HRIFA032011a

MUSCARINIC ACETYLCHOLINE RECEPTOR M4.

7.8e-35:184:32

HOMO SAPIENS (HUMAN).

P08173

HRIFA032070a

MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.

2.1e-18:107:44

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P23500

HRIFA032073a  
SECRETOTRANIN III PRECURSOR (SGIII).  
9.7e-69:182:76  
MUS MUSCULUS (MOUSE).  
P47867

5

HRIFA032079a  
HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I.  
3.5e-12:96:39  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
Q09906

10

HRIFA032097a  
GLYCOPROTEIN J.  
0.023:61:32  
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).  
P06480

15

HRIFA032161a  
CCAAT/ENHANCER BINDING PROTEIN DELTA (C/EBP DELTA) (NUCLEAR FACTOR NF-IL6-BETA) (NF-IL6-BETA).  
0.22:56:42  
HOMO SAPIENS (HUMAN).  
P49716

20

HRIFA032186a  
D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN) (TAXREB302).  
0.86:50:38  
HOMO SAPIENS (HUMAN).  
Q10586

25

HRIFA032224a  
HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.  
2.6e-43:196:45  
CAENORHABDITIS ELEGANS.  
Q03567

35

HRIFA032257a  
GLUCOSE REPRESSION MEDIATOR PROTEIN.  
4.7e-07:204:25  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P14922

40

HRIFA032274a  
ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).  
7.8e-60:163:74  
MUS MUSCULUS (MOUSE).  
Q07231

45

HRIFA032275a  
CELL DIVISION CONTROL PROTEIN 28 (EC 2.7.1.-).  
7.2e-41:179:38  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P00546

50

HRIFA032360a  
HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.  
3.0e-05:198:28

55

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CAENORHABDITIS ELEGANS.  
Q09625

5 HRIFA032389a  
EBNA-1 NUCLEAR PROTEIN.  
1.3e-05:86:39  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). P03211

10 HRIFA032433a  
GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R).  
3.1e-14:54:53  
RATTUS NORVEGICUS (RAT).  
P30969

15 HRIFA032453a  
BUTYROPHILIN PRECURSOR (BT).  
5.9e-13:162:32  
BOS TAURUS (BOVINE).  
P18892

20 HRIFA032478a  
GLYCOPROTEIN X PRECURSOR.  
3.8e-06:253:28  
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).  
25 P28968

HRIFA032506a  
COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR.  
1.2e-06:226:34  
30 HOMO SAPIENS (HUMAN).  
P12111

HRIFA032511a  
COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.  
35 8.7e-09:229:34  
HOMO SAPIENS (HUMAN).  
Q07092

HRIFA032530a  
40 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
9.0e-05:159:33  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437

45 HRIFA032587a  
SYNAPTOTAGMIN (P65).  
3.2e-08:72:52  
APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).  
P41823

50 HRIFA032605a  
ANTIGEN PEPTIDE TRANSPORTER 1 (APT1) (PEPTIDE TRANSPORTER TAP1) (PEPTIDE TRANSPORTER  
PSF1) (PEPTIDE SUPPLY FACTOR 1) (PSF-1) (PEPTIDE TRANSPORTER INVOLVED IN ANTIGEN PROCESS-  
ING 1).  
55 8.4e-37:192:41  
HOMO SAPIENS (HUMAN).  
Q03518

HRIFA032642a  
 PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
 5.0e-05:127:33  
 MUS MUSCULUS (MOUSE).  
 P05142

HRIFA032696a  
 COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).  
 1.4e-13:200:38  
 BOS TAURUS (BOVINE).  
 P02459

HRIFA032730a  
 K-GLYPICAN PRECURSOR.  
 4.8e-67:180:68  
 MUS MUSCULUS (MOUSE).  
 P51655

HRIFA032820a  
 GLUTAMIC ACID-RICH PROTEIN PRECURSOR.  
 7.5e-05:192:23  
 PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).  
 P13816

## Homology search result 2

**[0290]** Homology of representative sequences of the 5'-end cluster to the data in Swiss-Prot database

**[0291]** Representative sequence of the 5'-end cluster exhibiting relatively high homology (304 cluster: "exhibiting relatively high homology" means that the P value is  $10^{-10}$  or less)

HRIFA000327a, HRIFA000432a, HRIFA000553a, HRIFA000564a, HRIFA000631a, HRIFA000683a, HRIFA000776a,  
 HRIFA000814a, HRIFA001132a, HRIFA001138a, HRIFA001337a, HRIFA001341a, HRIFA001489a, HRIFA001712a,  
 HRIFA001720a, HRIFA001942a, HRIFA001975a, HRIFA001984a, HRIFA002384a, HRIFA002503a, HRIFA002743a,  
 HRIFA002766a, HRIFA002805a, HRIFA002891a, HRIFA002919a, HRIFA002980a, HRIFA003063a, HRIFA003093a,  
 HRIFA003635a, HRIFA004006a, HRIFA004034a, HRIFA004112a, HRIFA004426a, HRIFA004490a, HRIFA004523a,  
 HRIFA004663a, HRIFA004696a, HRIFA004714a, HRIFA004745a, HRIFA004919a, HRIFA005184a, HRIFA005231a,  
 HRIFA005240a, HRIFA005271a, HRIFA005372a, HRIFA005392a, HRIFA005409a, HRIFA005420a, HRIFA005438a,  
 HRIFA005462a, HRIFA005644a, HRIFA005720a, HRIFA005732a, HRIFA005760a, HRIFA005781a, HRIFA006183a,  
 HRIFA006494a, HRIFA006510a, HRIFA006566a, HRIFA006586a, HRIFA006596a, HRIFA006649a, HRIFA006667a,  
 HRIFA006730a, HRIFA006926a, HRIFA007013a, HRIFA007219a, HRIFA007228a, HRIFA007243a, HRIFA007352a,  
 HRIFA007424a, HRIFA007435a, HRIFA007463a, HRIFA007493a, HRIFA007571a, HRIFA007659a, HRIFA007722a,  
 HRIFA007745a, HRIFA008000a, HRIFA008200a, HRIFA008284a, HRIFA008314a, HRIFA008362a, HRIFA008459a,  
 HRIFA008483a, HRIFA008547a, HRIFA008611a, HRIFA008661a, HRIFA008717a, HRIFA008784a, HRIFA008981a,  
 HRIFA009101a, HRIFA009171a, HRIFA009220a, HRIFA009451a, HRIFA009482a, HRIFA009783a, HRIFA009881a,  
 HRIFA010085a, HRIFA010090a,  
 HRIFA010130a, HRIFA010319a, HRIFA010394a, HRIFA010460a, HRIFA010790a, HRIFA010975a, HRIFA011016a,  
 HRIFA011179a, HRIFA011197a, HRIFA011449a, HRIFA011659a, HRIFA011947a, HRIFA012278a, HRIFA012584a,  
 HRIFA012625a, HRIFA012692a, HRIFA012795a, HRIFA012885a, HRIFA012914a, HRIFA012969a, HRIFA012990a,  
 HRIFA013254a, HRIFA013265a, HRIFA013276a, HRIFA013376a, HRIFA013477a, HRIFA013586a, HRIFA013726a,  
 HRIFA013744a, HRIFA013911a, HRIFA014006a, HRIFA014185a, HRIFA014336a, HRIFA014465a, HRIFA014500a,  
 HRIFA014561a, HRIFA014568a, HRIFA014621a, HRIFA014688a, HRIFA014819a, HRIFA014951a, HRIFA014967a,  
 HRIFA015063a, HRIFA015070a, HRIFA015246a, HRIFA015423a, HRIFA015453a, HRIFA015486a, HRIFA015506a,  
 HRIFA015536a, HRIFA015547a, HRIFA015568a, HRIFA015756a, HRIFA015811a, HRIFA016070a, HRIFA016290a,  
 HRIFA016430a, HRIFA016654a, HRIFA016758a, HRIFA017031a, HRIFA017257a, HRIFA017295a, HRIFA017312a,  
 HRIFA017703a, HRIFA017855a, HRIFA018092a, HRIFA018131a, HRIFA018134a, HRIFA018580a, HRIFA018827a,  
 HRIFA018904a, HRIFA018993a, HRIFA019105a, HRIFA019136a, HRIFA019175a, HRIFA019262a, HRIFA019466a,  
 HRIFA019867a, HRIFA019869a, HRIFA020272a, HRIFA020335a, HRIFA020349a, HRIFA020862a, HRIFA021213a,  
 HRIFA021398a, HRIFA021499a, HRIFA021637a, HRIFA021651a, HRIFA021754a, HRIFA021781a, HRIFA022065a,  
 HRIFA022139a, HRIFA022166a, HRIFA022177a, HRIFA022182a, HRIFA022227a, HRIFA022249a, HRIFA022265a,



HRIFA022328a, HRIFA022423a, HRIFA022528a, HRIFA022546a, HRIFA022564a, HRIFA022616a, HRIFA022671a, HRIFA022691a, HRIFA022707a, HRIFA022729a, HRIFA022737a, HRIFA022776a, HRIFA022875a, HRIFA022895a, HRIFA023007a, HRIFA023227a, HRIFA023257a, HRIFA023304a, HRIFA023464a, HRIFA023767a, HRIFA023923a, HRIFA024132a, HRIFA024255a, HRIFA024392a, HRIFA024423a, HRIFA024504a, HRIFA024718a, HRIFA024767a, 5 HRIFA024937a, HRIFA024994a, HRIFA025046a, HRIFA025250a, HRIFA025261a, HRIFA025353a, HRIFA025492a, HRIFA025636a, HRIFA025695a, HRIFA025706a, HRIFA025766a, HRIFA025800a, HRIFA025907a, HRIFA025913a, HRIFA026089a, HRIFA026364a, HRIFA026496a, HRIFA026789a, HRIFA026813a, HRIFA026860a, HRIFA027012a, HRIFA027045a, HRIFA027125a, HRIFA027179a, HRIFA027187a, HRIFA027622a, HRIFA027625a, HRIFA027656a, HRIFA027681a, HRIFA027722a, HRIFA027940a, HRIFA028157a, HRIFA028402a, HRIFA028468a, HRIFA028511a, 10 HRIFA028651a, HRIFA028790a, HRIFA029002a, HRIFA029208a, HRIFA029209a, HRIFA029256a, HRIFA029263a, HRIFA029285a, HRIFA029317a, HRIFA029327a, HRIFA029393a, HRIFA029511a, HRIFA029802a, HRIFA029866a, HRIFA029932a, HRIFA030025a, HRIFA030045a, HRIFA030250a, HRIFA030342a, HRIFA030370a, HRIFA030371a, HRIFA030411a, HRIFA030448a, HRIFA030545a, HRIFA030629a, HRIFA030642a, HRIFA030662a, HRIFA031336a, HRIFA031869a, HRIFA031986a, HRIFA032009a, HRIFA032011a, HRIFA032070a, HRIFA032073a, HRIFA032079a, 15 HRIFA032224a, HRIFA032274a, HRIFA032275a, HRIFA032433a, HRIFA032453a, HRIFA032605a, HRIFA032696a, HRIFA032730a,

## Homology search result 3

20 **[0292]** Representative sequence of the 5'-end cluster exhibiting relatively low homology (221 cluster: "exhibiting relatively low homology" means that the P value is higher than  $10^{-10}$  and  $10^{-4}$  or less)  
 HRIFA000016a, HRIFA000071a, HRIFA000116a, HRIFA000123a, HRIFA000264a, HRIFA000415a, HRIFA000446a, HRIFA000695a, HRIFA000845a, HRIFA001971a, HRIFA002063a, HRIFA002102a, HRIFA002284a, HRIFA002309a, HRIFA002694a, HRIFA002762a, HRIFA002787a, HRIFA003055a, HRIFA003340a, HRIFA003402a, HRIFA003504a, 25 HRIFA003892a, HRIFA003946a, HRIFA004162a, HRIFA004401a, HRIFA004780a, HRIFA005072a, HRIFA005102a, HRIFA005214a, HRIFA005255a, HRIFA005300a, HRIFA005369a, HRIFA005702a, HRIFA005728a, HRIFA005944a, HRIFA006298a, HRIFA006448a, HRIFA006572a, HRIFA006633a, HRIFA006642a, HRIFA007068a, HRIFA007244a, HRIFA007262a, HRIFA007512a, HRIFA007532a, HRIFA007565a, HRIFA007728a, HRIFA007909a, HRIFA008174a, HRIFA008426a, HRIFA008596a, HRIFA008790a, HRIFA008989a, HRIFA009578a, HRIFA009825a, HRIFA009852a, 30 HRIFA009983a, HRIFA010005a, HRIFA010078a, HRIFA010152a, HRIFA010301a, HRIFA010361a, HRIFA010425a, HRIFA010466a, HRIFA010799a, HRIFA011580a, HRIFA011820a, HRIFA012167a, HRIFA012354a, HRIFA012427a, HRIFA012436a, HRIFA012515a, HRIFA012702a, HRIFA012737a, HRIFA013135a, HRIFA013235a, HRIFA013279a, HRIFA013589a, HRIFA013620a, HRIFA013919a, HRIFA013932a, HRIFA014056a, HRIFA014111a, HRIFA014133a, HRIFA014396a, HRIFA014397a, HRIFA014598a, HRIFA014702a, HRIFA014868a, HRIFA015219a, HRIFA015995a, 35 HRIFA016214a, HRIFA016240a, HRIFA016255a, HRIFA016639a, HRIFA016669a, HRIFA016963a, HRIFA017457a, HRIFA017643a, HRIFA017670a, HRIFA017801a, HRIFA017836a, HRIFA017921a, HRIFA018238a, HRIFA018262a, HRIFA018287a, HRIFA018666a, HRIFA018688a, HRIFA018754a, HRIFA018794a, HRIFA018870a, HRIFA018931a, HRIFA019412a, HRIFA019490a, HRIFA019498a, HRIFA019532a, HRIFA019651a, HRIFA0201440, HRIFA020184a, HRIFA020453a, HRIFA020693a, 40 HRIFA020707a, HRIFA020748a, HRIFA021061a, HRIFA021224a, HRIFA021494a, HRIFA021794a, HRIFA021855a, HRIFA021906a, HRIFA022156a, HRIFA022203a, HRIFA022234a, HRIFA022702a, HRIFA022728a, HRIFA022782a, HRIFA022865a, HRIFA022890a, HRIFA022985a, HRIFA023048a, HRIFA023069a, HRIFA023129a, HRIFA023154a, HRIFA023212a, HRIFA023489a, HRIFA023634a, HRIFA023894a, HRIFA024088a, HRIFA024197a, HRIFA024218a, HRIFA024473a, HRIFA024482a, HRIFA024543a, HRIFA025327a, HRIFA025479a, HRIFA025488a, HRIFA025703a, 45 HRIFA025771a, HRIFA025778a, HRIFA025904a, HRIFA025966a, HRIFA025978a, HRIFA026121a, HRIFA026242a, HRIFA026316a, HRIFA026382a, HRIFA026465a, HRIFA026519a, HRIFA026564a, HRIFA026576a, HRIFA026618a, HRIFA026659a, HRIFA026764a, HRIFA027327a, HRIFA027329a, HRIFA027355a, HRIFA027644a, HRIFA027673a, HRIFA027714a, HRIFA027860a, HRIFA028061a, HRIFA028187a, HRIFA028262a, HRIFA028371a, HRIFA028440a, HRIFA028501a, HRIFA028576a, HRIFA028614a, HRIFA028911a, HRIFA029050a, HRIFA029278a, HRIFA029349a, 50 HRIFA029425a, HRIFA029434a, HRIFA029460a, HRIFA029467a, HRIFA029508a, HRIFA029730a, HRIFA029792a, HRIFA030103a, HRIFA030147a, HRIFA030264a, HRIFA030381a, HRIFA030456a, HRIFA030509a, HRIFA030511a, HRIFA030566a, HRIFA030599a, HRIFA031126a, HRIFA031249a, HRIFA031438a, HRIFA031935a, HRIFA032257a, HRIFA032360a, HRIFA032389a, HRIFA032478a, HRIFA032506a, HRIFA032511a, HRIFA032530a, HRIFA032587a, HRIFA032642a, HRIFA032820a, 55

## Homology search result 4

**[0293]** Representative sequence of the 5'-end cluster exhibiting low homology (115 cluster: "exhibiting low homology"

means that the P value is higher than  $10^{-4}$  and 1 or less)

HRIFA001099a, HRIFA001200a, HRIFA001413a, HRIFA001439a, HRIFA001558a, HRIFA001866a, HRIFA001972a,  
 HRIFA002689a, HRIFA003357a, HRIFA003592a, HRIFA003640a, HRIFA003883a, HRIFA005296a, HRIFA005500a,  
 HRIFA005540a, HRIFA006250a, HRIFA006609a, HRIFA006798a, HRIFA007032a, HRIFA007152a, HRIFA007547a,  
 5 HRIFA007829a, HRIFA007985a, HRIFA008212a, HRIFA008252a, HRIFA008976a, HRIFA009071a, HRIFA009123a,  
 HRIFA009136a, HRIFA009339a, HRIFA009762a, HRIFA010176a, HRIFA010490a, HRIFA010736a, HRIFA010859a,  
 HRIFA010891a, HRIFA010988a, HRIFA011105a, HRIFA011128a, HRIFA011484a, HRIFA011512a, HRIFA011926a,  
 HRIFA012069a, HRIFA012151a, HRIFA013092a, HRIFA013103a, HRIFA013980a, HRIFA014024a, HRIFA014590a,  
 HRIFA014620a, HRIFA015122a, HRIFA015351a, HRIFA015802a, HRIFA015902a, HRIFA015947a, HRIFA016599a,  
 10 HRIFA017146a, HRIFA017190a, HRIFA017456a, HRIFA017791a, HRIFA017818a, HRIFA018447a, HRIFA019437a,  
 HRIFA019958a, HRIFA020883a, HRIFA021007a, HRIFA021040a, HRIFA021445a, HRIFA021543a, HRIFA021620a,  
 HRIFA021787a, HRIFA022055a, HRIFA022335a, HRIFA022348a, HRIFA022411a, HRIFA022462a, HRIFA022493a,  
 HRIFA022714a, HRIFA023434a, HRIFA024185a, HRIFA024305a, HRIFA024884a, HRIFA024893a, HRIFA024978a,  
 HRIFA025033a, HRIFA025290a, HRIFA026265a, HRIFA026303a, HRIFA026351a, HRIFA026615a, HRIFA026923a,  
 15 HRIFA027173a, HRIFA027485a, HRIFA027536a, HRIFA027549a, HRIFA027867a, HRIFA028804a, HRIFA028867a,  
 HRIFA028983a, HRIFA029398a,  
 HRIFA029440a, HRIFA029602a, HRIFA029649a, HRIFA029715a, HRIFA030106a, HRIFA030385a, HRIFA030461a,  
 HRIFA030472a, HRIFA030839a, HRIFA031091a, HRIFA031395a, HRIFA031397a, HRIFA032097a, HRIFA032161a,  
 HRIFA032186a,

Homology search result 5

[0294] The result of the homology search in the SwissProt using the clone sequences of the 5'-ends.

Indicated are from the top,  
 the name of the clone sequence,  
 definition of the top hit data,  
 the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),  
 the organism of which the top hit data is obtained,  
 30 the Accession No. of the top hit data.

[0295] Data were not shown for the clones in which the P-value was higher than 1.

F-BNGH41000020  
 35 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).  
 1.2e-119:279:83  
 HOMO SAPIENS (HUMAN).  
 P03886

40 F-BNGH41000087  
 PROPERDIN PRECURSOR.  
 2.5e-06:218:32  
 HOMO SAPIENS (HUMAN).  
 P27918

45 F-BNGH41000091  
 POTASSIUM CHANNEL PROTEIN EAG.  
 3.1e-66:139:61  
 DROSOPHILA MELANOGASTER (FRUIT FLY).  
 50 Q02280

F-HEMBA1000006  
 S-ANTIGEN PROTEIN PRECURSOR.  
 3.0e-05:164:31  
 55 PLASMODIUM FALCIPARUM (ISOLATE V1).  
 P09593

F-HEMBA1000121

# EP 1 130 094 A2

HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.

8.2e-06:83:27

CAENORHABDITIS ELEGANS.

P34679

5

F-HEMBA1000128

PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).

8.2e-08:89:34

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

10

P33154

F-HEMBA1000275

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.

1.9e-06:231:34

15

GALLUS GALLUS (CHICKEN).

P02457

F-HEMBA1000300

!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!

20

1.4e-13:73:56

HOMO SAPIENS (HUMAN).

P39195

F-HEMBA1000349

ATP-BINDING CASSETTE TRANSPORTER 1.

2.6e-16:238:31

25

MUS MUSCULUS (MOUSE).

P41233

F-HEMBA1000443

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

4.8e-06:120:35

30

MUS MUSCULUS (MOUSE).

P05142

35

F-HEMBA1000462

PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.

2.9e-21:86:52

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

40

Q09818

F-HEMBA1000477

HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.

3.3e-09:138:34

45

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40085

F-HEMBA1000590

CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).

2.2e-27:117:48

50

GALLUS GALLUS (CHICKEN).

P05099

F-HEMBA1000634

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).

0.00027:85:43

55

HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).

P08393

F-HEMBA1000671  
ZINC FINGER PROTEIN 140.  
1.1e-44:155:47  
HOMO SAPIENS (HUMAN).  
P52738

F-HEMBA1000713  
BLADDER CANCER 10 KD PROTEIN.  
1.5e-42:81:97  
HOMO SAPIENS (HUMAN).  
060629

F-HEMBA1000732  
FIBRILLIN 1 PRECURSOR.  
6.3e-18:77:46  
HOMO SAPIENS (HUMAN).  
P35555

F-HEMBA1000745  
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-  
TIDE IB-6; PEPTIDE P-H].  
5.2e-06:105:33  
HOMO SAPIENS (HUMAN).  
P04280

F-HEMBA1000835  
FIBRILLIN 2 PRECURSOR.  
2.1e-42:214:44  
HOMO SAPIENS (HUMAN).  
P35556

F-HEMBA1000875  
ZINC FINGER PROTEIN 133.  
5.8e-16:49:87  
HOMO SAPIENS (HUMAN).  
P52736

F-HEMBA1000907  
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.  
2.2e-05:172:34  
MUS MUSCULUS (MOUSE).  
P11087

F-HEMBA1000940  
GAP JUNCTION CX43.4 PROTEIN (CONNEXIN 43.4) (CX43.4).  
1.4e-20:90:42  
BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).  
Q92052

F-HEMBA1000962  
WATER-STRESS INDUCIBLE PROTEIN RAB21.  
0.089:122:25  
ORYZA SATIVA (RICE).  
P12253

F-HEMBA1001184

# EP 1 130 094 A2

SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP).

4.9e-33:100:60

HOMO SAPIENS (HUMAN).

P55822

5

F-HEMBA1001221

AGRIN PRECURSOR.

1.7e-26:239:32

GALLUS GALLUS (CHICKEN).

10

P31696

F-HEMBA1001228

CARTILAGE OLIGOMERIC MATRIX PROTEIN PRECURSOR (COMP).

7.7e-114:147:83

15

HOMO SAPIENS (HUMAN).

P49747

F-HEMBA1001272

SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).

5.8e-06:129:33

20

HOMO SAPIENS (HUMAN).

Q15427

F-HEMBA1001296

TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).

0.0019:115:36

25

GALLUS GALLUS (CHICKEN).

Q98937

F-HEMBA1001297

50S RIBOSOMAL PROTEIN L37E (L35E).

0.65:40:40

30

HALOARCUA MARISMORTUI (HALOBACTERIUM MARISMORTUI).

P32410

35

F-HEMBA1001390

SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).

0.00050:89:33

NEPHILA CLAVIPES (ORB SPIDER).

40

P46804

F-HEMBA1001563

B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).

0.00041:34:61

45

HOMO SAPIENS (HUMAN).

P20931

F-HEMBA1001621

PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.

1.1e-64:105:72

50

HOMO SAPIENS (HUMAN).

P35414

F-HEMBA1001878

VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.

1.3e-24:170:35

55

PODOSPORA ANSERINA.

Q00808

# EP 1 130 094 A2

- 5 F-HEMBA1001886  
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).  
1.8e-94:273:64  
HOMO SAPIENS (HUMAN).  
Q03923
- 10 F-HEMBA1002048  
EARLY ANTIGEN PROTEIN D (EA-D).  
0.13:93:34  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03191
- 15 F-HEMBA1002131  
PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HY-  
DROXYLASE 1) (LH1).  
6.3e-12:140:30  
GALLUS GALLUS (CHICKEN).  
P24802
- 20 F-HEMBA1002163  
HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION.  
2.1e-10:204:27  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
Q04651
- 25 F-HEMBA1002164  
BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (EC 6.4.1.2) (BC-  
CP).  
0.022:62:32  
30 GLYCINE MAX (SOYBEAN).  
Q42783
- 35 F-HEMBA1002167  
ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).  
5.2e-31:247:31  
BUNGARUS FASCIATUS (BANDED KRAIT).  
Q92035
- 40 F-HEMBA1002178  
PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HY-  
DROXYLASE 1) (LH1).  
1.5e-11:140:30  
GALLUS GALLUS (CHICKEN).  
P24802
- 45 F-HEMBA1002195  
VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.  
5.0e-07:52:36  
50 PODOSPORA ANSERINA.  
Q00808
- 55 F-HEMBA1002227  
MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (ACAMP-81).  
0.00063:21:100  
BOS TAURUS (BOVINE).  
P12624
- F-HEMBA1002239

!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!

1.5e-33:101:70

HOMO SAPIENS (HUMAN).

P39192

F-HEMBA1002316

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

4.6e-08:186:32

SORGHUM VULGARE (SORGHUM).

P24152

F-HEMBA1002420

WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).

0.0078:19:68

MUS MUSCULUS (MOUSE).

P70315

F-HEMBA1002421

SYNDECAN-2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2).

1.1e-52:107:97

HOMO SAPIENS (HUMAN).

P34741

F-HEMBA1002524

ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).

5.0e-05:104:34

RATTUS NORVEGICUS (RAT).

P04474

F-HEMBA1002551

HYPOTHETICAL WD-REPEAT PROTEIN SLR0143.

9.9e-09:128:29

SYNECHOCYSTIS SP. (STRAIN PCC 6803).

P74442

F-HEMBA1002767

N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).

8.0e-92:246:67

MUS MUSCULUS (MOUSE).

P15535

F-HEMBA1002985

TRANSCRIPTION FACTOR GATA-6 (GATA BINDING FACTOR-6).

0.060:49:34

MUS MUSCULUS (MOUSE).

Q61169

F-HEMBA1002992

HOLOTRICIN 3 PRECURSOR.

0.0035:64:37

HOLOTRICHIA DIOMPHALIA.

Q25055

F-HEMBA1003047

BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).

1.5e-23:216:31  
HOMO SAPIENS (HUMAN).  
P13497

5 F-HEMBA1003072  
PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
6.8e-09:129:41  
MUS MUSCULUS (MOUSE).  
P05142

10 F-HEMBA1003101  
PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.  
2.2e-10:124:37  
HOMO SAPIENS (HUMAN).  
15 P08123

F-HEMBA1003120  
ZINC FINGER PROTEIN 140.  
4.8e-23:43:74  
20 HOMO SAPIENS (HUMAN).  
P52738

F-HEMBA1003230  
FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90).  
25 2.7e-41:239:39  
MUS MUSCULUS (MOUSE).  
Q08878

F-HEMBA1003294  
30 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!  
7.0e-34:84:69  
HOMO SAPIENS (HUMAN).  
P39194

35 F-HEMBA1003315  
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).  
0.00012:178:32  
PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).  
P10496

40 F-HEMBA1003392  
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MAC-  
ROGLOBULIN RECEPTOR) (A2MR).  
1.1e-31:202:37  
45 GALLUS GALLUS (CHICKEN).  
P98157

F-HEMBA1003399  
MVP1 PROTEIN.  
50 5.6e-12:67:38  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P40959

F-HEMBA1003487  
55 PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
4.5e-08:175:29  
MUS MUSCULUS (MOUSE).  
P05142



- 5 F-HEMBA1003497  
ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1)  
(ZINC FINGER PROTEIN Z13).  
9.3e-18:171:33  
MUS MUSCULUS (MOUSE).  
Q60821
- 10 F-HEMBA1003530  
SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).  
9.9e-12:122:35  
HOMO SAPIENS (HUMAN).  
P81489
- 15 F-HEMBA1003602  
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).  
0.98:114:33  
MUS MUSCULUS (MOUSE).  
P05143
- 20 F-HEMBA1003732  
TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).  
0.35:225:28  
PSEUDOMONAS AERUGINOSA.  
P15276
- 25 F-HEMBA1003945  
HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I.  
2.9e-48:268:41  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
30 Q09895
- F-HEMBA1004007  
THYROID TRANSCRIPTION FACTOR 1 (THYROID NUCLEAR FACTOR 1) (TTF-1) (FRAGMENT).  
0.90:60:30  
35 CAVIA PORCELLUS (GUINEA PIG).  
P97273
- F-HEMBA1004067  
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-  
40 PHA-0 PROTEIN).  
3.0e-05:200:31  
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).  
P08393
- 45 F-HEMBA1004085  
GLUCOSE REPRESSION MEDIATOR PROTEIN.  
0.0030:190:26  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P14922
- 50 F-HEMBA1004110  
EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15).  
1.2e-14:102:36  
MUS MUSCULUS (MOUSE).  
55 P42567
- F-HEMBA1004250  
CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).

1.8e-08:150:33  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P33450

5 F-HEMBA1004391  
TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.  
4.5e-09:96:35  
MUS MUSCULUS (MOUSE).  
P70211

10 F-HEMBA1004444  
GLYCOPROTEIN 25L PRECURSOR (GP25L).  
4.6e-41:148:52  
CANIS FAMILIARIS (DOG).  
15 P27869

F-HEMBA1004454  
CD9 ANTIGEN.  
0.0070:24:70  
20 BOS TAURUS (BOVINE).  
P30932

F-HEMBA1004505  
25 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE).  
7.0e-45:239:43  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P53624

30 F-HEMBA1004785  
MODIFIER 3 PROTEIN (M33).  
7.4e-26:76:61  
MUS MUSCULUS (MOUSE).  
P30658

35 F-HEMBA1004797  
PROTEIN Q300.  
0.00071:21:66  
MUS MUSCULUS (MOUSE).  
40 Q02722

F-HEMBA1004952  
EBNA-1 NUCLEAR PROTEIN.  
2.4e-05:67:49  
45 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03211

F-HEMBA1004971

50 F-HEMBA1004982  
MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).  
8.6e-08:144:25  
BACILLUS SUBTILIS.  
P39843

55 F-HEMBA1005070  
HYPOTHETICAL PROTEIN KIAA0310.  
1.0e-38:140:68

HOMO SAPIENS (HUMAN).  
O15027

F-HEMBA1005084

NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).  
2.5e-10:102:37  
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).  
P18160

F-HEMBA1005145

PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
1.8e-06:85:37  
MUS MUSCULUS (MOUSE).  
P05142

F-HEMBA1005230

ZINC FINGER PROTEIN 140.  
8.2e-20:83:66  
HOMO SAPIENS (HUMAN).  
P52738

F-HEMBA1005246

TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TFE4).  
1.5e-09:132:34  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P18480

F-HEMBA1005267

B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).  
1.9e-15:192:32  
HOMO SAPIENS (HUMAN).  
P20749

F-HEMBA1005337

ACIDIC PHOSPHOPROTEIN PRECURSOR (50 KD ANTIGEN).  
8.0e-05:31:64  
PLASMODIUM CHABAUDI.  
Q02752

F-HEMBA1005430

MALE SPECIFIC SPERM PROTEIN MST84DB.  
0.34:42:42  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
Q01643

F-HEMBA1005449

PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-SA-1).  
4.5e-09:95:33  
TRYPANOSOMA BRUCEI BRUCEI.  
Q06084

F-HEMBA1005489

CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110).  
7.2e-05:90:36  
HOMO SAPIENS (HUMAN).  
Q15700

- 5 F-HEMBA1005522  
COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).  
3.3e-17:78:51  
ORYCTOLAGUS CUNICULUS (RABBIT).  
P98139
- 10 F-HEMBA1005545  
MUSCARINIC ACETYLCHOLINE RECEPTOR M3.  
7.2e-91:211:85  
HOMO SAPIENS (HUMAN).  
P20309
- 15 F-HEMBA1005698  
PROTEIN TRANSPORT PROTEIN SEC22 (PROTEIN SLY2).  
3.3e-08:132:28  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P22214
- 20 F-HEMBA1005913  
HYPOTHETICAL 5.8 KD PROTEIN.  
0.97:43:30  
CLOVER YELLOW MOSAIC VIRUS (CYMV).  
P16485
- 25 F-HEMBA1005929  
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).  
6.6e-104:275:72  
HOMO SAPIENS (HUMAN).  
P27448
- 30 F-HEMBA1005945  
BRITTLE-1 PROTEIN PRECURSOR.  
7.8e-30:214:35  
ZEA MAYS (MAIZE).  
P29518
- 35 F-HEMBA1006016  
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!  
1.9e-07:34:76  
HOMO SAPIENS (HUMAN).  
P39188
- 40 F-HEMBA1006171  
PROBABLE E5 PROTEIN.  
0.98:66:31  
HUMAN PAPILLOMAVIRUS TYPE 33.  
P06426
- 45 F-HEMBA1006276  
ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).  
4.1e-07:56:57  
MUS MUSCULUS (MOUSE).  
Q61967
- 50 F-HEMBA1006299  
BASIC PROLINE-RICH PEPTIDE P-E (IB-9).  
0.11:38:28  
HOMO SAPIENS (HUMAN).

P02811

F-HEMBA1006311

ZINC FINGER PROTEIN 23 (ZINC FINGER PROTEIN KOX16) (FRAGMENT).

0.91:22:45

HOMO SAPIENS (HUMAN).

P17027

F-HEMBA1006335

PERIPHERAL MYELIN PROTEIN 22 (PMP-22) (GROWTH-ARREST-SPECIFIC PROTEIN 3) (GAS3).

0.017:125:27

MUS MUSCULUS (MOUSE).

P16646

F-HEMBA1006357

SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.

5.2e-40:136:52

HOMO SAPIENS (HUMAN).

O15127

F-HEMBA1006430

OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.

2.7e-38:96:72

CAENORHABDITIS ELEGANS.

P46975

F-HEMBA1006482

SCO1 PROTEIN PRECURSOR.

7.1e-25:84:45

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P23833

F-HEMBA1006517

HYPOTHETICAL 93.4 KD PROTEIN IN STE3-GIN10 INTERGENIC REGION.

0.48:145:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P34239

F-HEMBA1006544

TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).

7.0e-11:210:37

HOMO SAPIENS (HUMAN).

000268

F-HEMBA1006572

ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).

0.011:50:40

GALLUS GALLUS (CHICKEN).

Q03352

F-HEMBA1006658

SERINE/THREONINE-PROTEIN KINASE MIG-15 (EC 2.7.1.-).

4.6e-44:234:45

CAENORHABDITIS ELEGANS.

Q23356

F-HEMBA1006707

CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).

9.3e-34:159:50  
GALLUS GALLUS (CHICKEN).  
P05099

5 F-HEMBA1006724  
PLATELET FACTOR 4 (PF-4).  
0.025:65:27  
SUS SCROFA (PIG).  
P30034

10 F-HEMBA1006749  
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).  
7.9e-37:147:53  
GALLUS GALLUS (CHICKEN).  
15 P05099

F-HEMBA1006770  
FLOWERING TIME CONTROL PROTEIN FCA.  
3.4e-27:139:39  
20 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).  
004425

F-HEMBA1006902  
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).  
25 1.5e-37:137:51  
GALLUS GALLUS (CHICKEN).  
P05099

F-HEMBA1006912  
30 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).  
0.27:121:29  
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).  
P08393

35 F-HEMBA1006916  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
1.1e-05:163:30  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
40 P17437

F-HEMBA1006960  
SMALL PROLINE-RICH PROTEIN 2-1.  
1.0:34:35  
45 HOMO SAPIENS (HUMAN).  
P35326

F-HEMBA1007013  
S-ANTIGEN PROTEIN PRECURSOR.  
50 2.8e-09:226:28  
PLASMODIUM FALCIPARUM (ISOLATE V1).  
P09593

F-HEMBA1007057  
55 PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-SA-1).  
4.0e-10:33:72  
TRYPANOSOMA BRUCEI BRUCEI.

Q06084

F-HEMBA1007063  
AGAMOUS PROTEIN.

5 1.0:40:42  
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).  
P17839

F-HEMBA1007226  
PUTATIVE CUTICLE COLLAGEN C09G5.5.  
0.10:105:38  
CAENORHABDITIS ELEGANS.  
Q09456

15 F-HEMBA1007241  
HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.  
3.3e-15:106:42  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P40857

20 F-HEMBA1007291  
RETINOIC ACID RECEPTOR RXR-BETA.  
0.0013:124:33  
HOMO SAPIENS (HUMAN).  
25 P28702

F-HEMBA1007332  
ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR).  
0.0024:130:34  
30 MUS MUSCULUS (MOUSE).  
Q01338

F-HEMBB1000106  
CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).  
35 9.5e-09:99:33  
MUS MUSCULUS (MOUSE).  
P53996

F-HEMBB1000276

40 F-HEMBB1000309

F-HEMBB1000407  
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).  
45 0.38:99:34  
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).  
P28284

F-HEMBB1000447  
50 HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.  
0.0076:80:31  
PLASMODIUM LOPHURAE.  
P04929

55 F-HEMBB1000542  
BETA-2 BUNGAROTOXIN B CHAIN PRECURSOR (BUNGAROTOXIN, B2 CHAIN).  
0.017:53:33  
BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).

P00989

F-HEMBB1000567

HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.

5.0e-05:131:29

PLASMODIUM LOPHURAE.

P04929

F-HEMBB1000642

BASIC PROLINE-RICH PEPTIDE IB-1.

0.0074:66:31

HOMO SAPIENS (HUMAN).

P04281

F-HEMBB1000668

VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.

7.3e-10:184:32

PODOSPORA ANSERINA.

Q00808

F-HEMBB1000679

TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN).

9.5e-73:204:69

CANIS FAMILIARIS (DOG).

Q01685

F-HEMBB1000881

F-SPONDIN PRECURSOR.

1.2e-23:191:37

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P35447

F-HEMBB1000905

TRANSCRIPTIONAL REPRESSOR RCO-1.

0.068:105:34

NEUROSPORA CRASSA.

P78706

F-HEMBB1001026

ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

1.3e-11:138:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32802

F-HEMBB1001048

SARCALUMENIN PRECURSOR.

3.1e-20:151:32

ORYCTOLAGUS CUNICULUS (RABBIT).

P13666

F-HEMBB1001200

HYPOTHETICAL GENE 51 MEMBRANE PROTEIN.

1.0:66:27

ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV).

Q00135

F-HEMBB1001407



!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!

2.0e-24:58:60

HOMO SAPIENS (HUMAN).

P39194

5

F-HEMBB1001530

SLS1 PROTEIN PRECURSOR.

0.0012:37:51

YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).

10

Q99158

F-HEMBB1001547

HYPOTHETICAL 71.7 KD PROTEIN F52H3.2 IN CHROMOSOME II.

4.1e-49:200:55

15

CAENORHABDITIS ELEGANS.

Q20680

F-HEMBB1001573

PROTEIN Q300.

20

0.0055:27:62

MUS MUSCULUS (MOUSE).

Q02722

F-HEMBB1001847

25

ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).

7.8e-05:166:31

RATTUS NORVEGICUS (RAT).

P04474

30

F-HEMBB1001959

CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).

8.8e-15:97:38

PETROMYZON MARINUS (SEA LAMPREY).

35

P25210

F-HEMBB1001978

MICROCIN B17 PROCESSING PROTEIN MCBC.

0.049:100:31

40

ESCHERICHIA COLI.

P23185

F-HEMBB1002039

COLD SHOCK PROTEIN CSPB (FRAGMENT).

45

0.98:32:40

BACILLUS GLOBISPORUS.

P41018

F-HEMBB1002041

50

REGULATORY PROTEIN E2.

0.010:145:35

HUMAN PAPILLOMAVIRUS TYPE 47.

P22420

55

F-HEMBB1002051

FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).

0.0056:89:31

HOMO SAPIENS (HUMAN).

Q01543

F-HEMBB1002120

UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT  
(EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).

1.4e-08:154:30

RATTUS NORVEGICUS (RAT).

P56558

F-HEMBB1002162

IMMEDIATE-EARLY PROTEIN IE180.

0.86:130:31

PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).

P11675

F-HEMBB1002228

PTB-ASSOCIATED SPLICING FACTOR (PSF).

0.00092:97:34

HOMO SAPIENS (HUMAN).

P23246

F-HEMBB1002245

PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN).

2.5e-55:128:88

RATTUS NORVEGICUS (RAT).

Q62786

F-HEMBB1002302

REGULATORY PROTEIN E2.

0.042:100:37

HUMAN PAPILLOMAVIRUS TYPE 25.

P36787

F-HEMBB1002427

FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-ALPHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT).

5.0e-15:53:54

HOMO SAPIENS (HUMAN).

P16442

F-HEMBB1002465

ACYL-COA DEHYDROGENASE (EC 1.3.99.-).

8.2e-35:162:50

BACILLUS SUBTILIS.

P45857

F-HEMBB1002661

TRANSCRIPTION FACTOR HES-1 (C-HAIRY1).

2.2e-18:159:40

GALLUS GALLUS (CHICKEN).

057337

F-HEMBB1002663

F-HEMBB1002693

GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN

# EP 1 130 094 A2

P30; NUCLEOPROTEIN P10].  
0.83:74:28  
DUPLAN MURINE LEUKEMIA VIRUS.  
P23090

5

F-MAMMA1000046  
!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!  
2.3e-24:98:67  
HOMO SAPIENS (HUMAN).  
P39191

10

F-MAMMA1000102  
APOLIPOPROTEIN L PRECURSOR (APO-L).  
4.3e-22:213:34  
HOMO SAPIENS (HUMAN).  
O14791

15

F-MAMMA1000106  
PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).  
1.6e-07:99:31  
NICOTIANA TABACUM (COMMON TOBACCO).  
Q03211

20

F-MAMMA1000118  
HYPOTHETICAL 29.3 KD PROTEIN (ORF92).  
0.00059:155:30  
ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV). O10341

25

F-MAMMA1000141  
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!  
0.00011:39:66  
HOMO SAPIENS (HUMAN).  
P39195

30

F-MAMMA1000204  
SYNAPTOTAGMIN III (SYTIII).  
5.9e-05:93:33  
MUS MUSCULUS (MOUSE).  
O35681

35

F-MAMMA1000226  
GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DX5 PRECURSOR.  
4.6e-06:224:28  
TRITICUM AESTIVUM (WHEAT).  
P10388

40

F-MAMMA1000403  
COLLAGEN ALPHA 1(IX) CHAIN PRECURSOR (FRAGMENTS).  
1.1e-06:158:35  
GALLUS GALLUS (CHICKEN).  
P12106

50

F-MAMMA1000449  
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).  
6.3e-05:137:32  
HOMO SAPIENS (HUMAN).  
P17600

55

F-MAMMA1000457  
 NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2).  
 7.6e-48:151:62  
 BOS TAURUS (BOVINE).  
 5 P07514

F-MAMMA1000473  
 SPERM PROTAMINE P1.  
 0.024:29:44  
 10 DROMICIOPS AUSTRALIS (MONITO DEL MONTE) (DROMICIOPS GLIROIDES). P42132

F-MAMMA1000496  
 HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.  
 9.8e-09:188:26  
 15 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
 P48566

F-MAMMA1000528  
 DNA BINDING PROTEIN S1FA.  
 20 0.77:43:37  
 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).  
 P42551

F-MAMMA1000591  
 25 SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).  
 0.018:88:32  
 HOMO SAPIENS (HUMAN).  
 P10163

F-MAMMA1000614  
 30 HYPOTHETICAL 29.3 KD PROTEIN (ORF92).  
 7.5e-08:148:36  
 ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV). O10341

F-MAMMA1000652  
 35 !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!  
 5.3e-36:56:85  
 HOMO SAPIENS (HUMAN).  
 P39189

F-MAMMA1000681  
 40 PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.  
 7.5e-41:167:51  
 MUS MUSCULUS (MOUSE).  
 45 008530

F-MAMMA1000706  
 T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).  
 8.1e-10:135:38  
 50 ORYCTOLAGUS CUNICULUS (RABBIT).  
 P06333

F-MAMMA1000788  
 55 HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.  
 2.0e-06:214:32  
 SACCHAROMYCES CEREVISIAE (BAKERS YEAST).  
 P53214

5 F-MAMMA1000810  
REGULATORY PROTEIN E2.  
0.0031:132:31  
HUMAN PAPILLOMAVIRUS TYPE 9.  
P36780

10 F-MAMMA1000814  
PROTEIN Q300.  
1.6e-05:27:66  
MUS MUSCULUS (MOUSE).  
Q02722

15 F-MAMMA1000881  
SERINE/THREONINE-PROTEIN KINASE SGK (EC 2.7.1.-) (SERUM/GLUCOCORTICOID-REGULATED KI-  
NASE).  
2.7e-10:81:45  
RATTUS NORVEGICUS (RAT).  
Q06226

20 F-MAMMA1000986  
INVOLUCRIN.  
0.95:125:24  
SUS SCROFA (PIG).  
P18175

25 F-MAMMA1000994  
CUTICLE COLLAGEN 2C (FRAGMENT).  
0.00062:97:34  
HAEMONCHUS CONTORTUS.  
30 P16252

35 F-MAMMA1001043  
MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1) (CD48).  
4.5e-05:162:25  
RATTUS NORVEGICUS (RAT).  
P10252

40 F-MAMMA1001066  
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).  
2.6e-06:33:72  
HOMO SAPIENS (HUMAN).  
P20931

45 F-MAMMA1001094  
PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.  
1.1e-21:175:38  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
Q09818

50 F-MAMMA1001141  
PTB-ASSOCIATED SPLICING FACTOR (PSF).  
0.13:196:27  
HOMO SAPIENS (HUMAN).  
P23246

55 F-MAMMA1001150  
PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).  
9.4e-89:256:67

HOMO SAPIENS (HUMAN).  
Q15139

5 F-MAMMA1001237  
MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).  
3.5e-19:103:43  
MESOCRICETUS AURATUS (GOLDEN HAMSTER).  
P53988

10 F-MAMMA1001284  
AUTOIMMUNE REGULATOR (APECED PROTEIN).  
0.027:178:30  
HOMO SAPIENS (HUMAN).  
043918

15 F-MAMMA1001310  
HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-REC114 INTERGENIC RE-  
GION.  
1.9e-14:151:31  
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
Q04225

F-MAMMA1001344  
MALE SPECIFIC SPERM PROTEIN MST84DC.  
25 0.16:35:42  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
Q01644

30 F-MAMMA1001418  
HYPOTHETICAL PROTEIN HI0519.  
3.5e-27:181:38  
HAEMOPHILUS INFLUENZAE.  
P44742

35 F-MAMMA1001532  
ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).  
1.1e-34:78:58  
MUS MUSCULUS (MOUSE).  
Q61967

40 F-MAMMA1001609  
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).  
0.20:137:27  
45 HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).  
P28284

F-MAMMA1001615  
5E5 ANTIGEN.  
2.3e-07:205:34  
50 RATTUS NORVEGICUS (RAT).  
Q63003

F-MAMMA1001623  
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).  
55 4.8e-30:90:77  
HOMO SAPIENS (HUMAN).  
Q03468

F-MAMMA1001634

B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).

6.1e-11:44:61

HOMO SAPIENS (HUMAN).

P20931

F-MAMMA1001893

COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR.

0.0013:174:36

HOMO SAPIENS (HUMAN).

P12107

F-MAMMA1001901

!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!

1.3e-21:65:66

HOMO SAPIENS (HUMAN).

P39195

F-MAMMA1001957

VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).

0.0055:104:35

DROSOPHILA MELANOGASTER (FRUIT FLY).

P13238

F-MAMMA1001978

D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).

0.00030:101:44

HOMO SAPIENS (HUMAN).

P21917

F-MAMMA1002070

PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).

1.4e-08:103:33

RATTUS NORVEGICUS (RAT).

Q01177

F-MAMMA1002080

FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR.

8.2e-08:131:32

LYMNAEA STAGNALIS (GREAT POND SNAIL).

P42565

F-MAMMA1002087

MALE SPECIFIC SPERM PROTEIN MST84DD.

0.65:24:45

DROSOPHILA MELANOGASTER (FRUIT FLY).

Q01645

F-MAMMA1002091

APYRASE PRECURSOR (EC 3.6.1.5) (ATP-DIPHOSPHATASE) (ADENOSINE DIPHOSPHATASE) (ADPASE) (ATP-DIPHOSPHOHYDROLASE).

2.6e-24:155:43

SOLANUM TUBEROSUM (POTATO).

P80595

F-MAMMA1002095

CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE).

2.3e-58:213:56

YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).  
043108

5 F-MAMMA1002128  
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).  
9.9e-05:72:40  
RATTUS NORVEGICUS (RAT).  
P02454

10 F-MAMMA1002142  
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).  
2.1e-13:149:34  
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).  
P18160

15 F-MAMMA1002165  
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.  
8.4e-06:47:57  
HOMO SAPIENS (HUMAN).  
20 P29279

F-MAMMA1002205  
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!  
5.9e-26:56:78  
25 HOMO SAPIENS (HUMAN).  
P39188

F-MAMMA1002224  
!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!  
30 3.7e-16:62:67  
HOMO SAPIENS (HUMAN).  
P39194

F-MAMMA1002234  
35 SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).  
3.5e-105:242:85  
CANIS FAMILIARIS (DOG).  
Q00004

40 F-MAMMA1002586  
MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSI-  
DASE) (ALPHA-MANNOSIDASE 1A).  
4.7e-24:203:35  
MUS MUSCULUS (MOUSE).  
45 P45700

F-MAMMA1002633  
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!  
7.3e-27:49:73  
50 HOMO SAPIENS (HUMAN).  
P39188

F-MAMMA1003126  
55 SARCALUMENIN PRECURSOR.  
7.9e-30:156:35  
ORYCTOLAGUS CUNICULUS (RABBIT).  
P13666



EP 1 130 094 A2

- 5 F-NT2RM1000407  
LACTOSE OPERON REPRESSOR.  
1.4e-07:36:86  
ESCHERICHIA COLI.  
P03023
- 10 F-NT2RM1000462  
ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).  
6.7e-11:85:41  
APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).  
P15287
- 15 F-NT2RM1000542  
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).  
3.5e-19:104:48  
FELIS SILVESTRIUS CATUS (CAT).  
O19015
- 20 F-NT2RM1000580  
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).  
3.4e-36:180:43  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P43636
- 25 F-NT2RM1000789  
T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7).  
1.5e-40:112:75  
MUS MUSCULUS (MOUSE).  
Q00417
- 30 F-NT2RM1000855  
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.  
2.5e-81:152:94  
CANIS FAMILIARIS (DOG).  
P38377
- 35 F-NT2RM1000858  
HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.  
3.1e-50:127:54  
CAENORHABDITIS ELEGANS.  
Q09201
- 40 F-NT2RM1000899  
MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.  
6.6e-17:107:43  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P23500
- 50 F-NT2RM2000241  
DOUBLESEX PROTEIN, MALE-SPECIFIC.  
0.0021:64:32  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P23023
- 55 F-NT2RM2000306  
PUTATIVE GTP-BINDING PROTEIN W08E3.3.  
1.1e-69:198:69  
CAENORHABDITIS ELEGANS.

P91917

F-NT2RM2000410

BETA-LYTIC METALLOENDOPEPTIDASE PRECURSOR (EC 3.4.24.32) (BETA-LYTIC PROTEASE).

0.73:118:31

ACHROMOBACTER LYTICUS.

P27458

F-NT2RM2000423

BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR.

1.3e-23:235:34

HOMO SAPIENS (HUMAN).

P16279

F-NT2RM2000497

DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2).

9.4e-19:199:31

CRICETULUS GRISEUS (CHINESE HAMSTER).

Q60452

F-NT2RM2000514

HYPOTHETICAL PROTEIN HI1558.

7.7e-06:82:34

HAEMOPHILUS INFLUENZAE.

P45252

F-NT2RM2000565

HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.

2.8e-57:232:52

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q09782

F-NT2RM2000582

PROTEIN Q300.

0.066:13:84

MUS MUSCULUS (MOUSE).

Q02722

F-NT2RM2000589

RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).

2.1e-07:90:32

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P54644

F-NT2RM2000622

GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.

1.9e-07:133:35

TRITICUM AESTIVUM (WHEAT).

P08489

F-NT2RM2000632

EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).

4.6e-28:194:35

HOMO SAPIENS (HUMAN).

Q03468

F-NT2RM2000773

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MYC-ASSOCIATED ZINC FINGER PROTEIN (MAZI) (PUR-1) (ZF87).

3.4e-24:156:47

HOMO SAPIENS (HUMAN).

P56270

F-NT2RM2001126

NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).

1.5e-05:118:32

MUS MUSCULUS (MOUSE).

P98084

F-NT2RM2001558

MAJOR FIBROUS SHEATH PROTEIN PRECURSOR (FSC1) (P82).

1.9e-24:164:40

MUS MUSCULUS (MOUSE).

Q60662

F-NT2RM2001626

HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.

1.6e-09:206:33

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P47179

F-NT2RM2001643

HYPOTHETICAL PROTEIN MJ1025.

0.21:203:22

METHANOCOCCUS JANNASCHII.

Q58431

F-NT2RM2001738

REGULATORY PROTEIN E2.

0.0076:124:31

HUMAN PAPILLOMAVIRUS TYPE 25.

P36787

F-NT2RM2001767

HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).

0.0068:115:33

DROSOPHILA MELANOGASTER (FRUIT FLY).

P25439

F-NT2RM2001792

FIBRINOGEN BETA CHAIN.

4.3e-25:121:45

BOS TAURUS (BOVINE).

P02676

F-NT2RM2001818

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

2.4e-06:192:32

ZEA MAYS (MAIZE).

P14918

F-NT2RM2001902

SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTIVATED KINASE 3) (P65-PAK).

2.3e-52:250:45

RATTUS NORVEGICUS (RAT).

Q62829

F-NT2RM2001939

PROBABLE G PROTEIN-COUPLEID RECEPTOR GPR19 (GPR-NGA).

4.0e-97:204:92

HOMO SAPIENS (HUMAN).

Q15760

F-NT2RM2001941

MUSCARINIC ACETYLCHOLINE RECEPTOR M4.

1.0e-34:184:32

HOMO SAPIENS (HUMAN).

P08173

F-NT2RM4000100

EBNA-1 NUCLEAR PROTEIN.

1.7e-05:86:39

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

F-NT2RM4000115

DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RNA POLYMERASE II SUBUNIT 1).

9.5e-05:116:35

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

P36594

F-NT2RM4000198

BUTYROPHILIN PRECURSOR (BT).

8.6e-14:162:33

MUS MUSCULUS (MOUSE).

Q62556

F-NT2RM4000284

COLLAGEN ALPHA 2(VI) CHAIN (FRAGMENT).

0.86:95:37

HOMO SAPIENS (HUMAN).

P12110

F-NT2RM4000295

COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.

1.1e-08:229:34

HOMO SAPIENS (HUMAN).

Q07092

F-NT2RM4000326

SH3 DOMAIN-BINDING PROTEIN 3BP-2.

6.1e-05:187:31

HOMO SAPIENS (HUMAN).

P78314

F-NT2RM4000417

SYNAPTOTAGMIN (P65).

4.2e-08:72:52

APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).

P41823

F-NT2RM4000444

ANTIGEN PEPTIDE TRANSPORTER 1 (APT1) (PEPTIDE TRANSPORTER TAP1) (PEPTIDE TRANSPORTER

# EP 1 130 094 A2

PSF1) (PEPTIDE SUPPLY FACTOR 1) (PSF-1) (PEPTIDE TRANSPORTER INVOLVED IN ANTIGEN PROCESS-  
ING 1).

1.1e-36:192:41

HOMO SAPIENS (HUMAN).

Q03518

F-NT2RM4000587

COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).

1.8e-13:200:38

BOS TAURUS (BOVINE).

P02459

F-NT2RM4000593

F-NT2RM4000648

K-GLYPICAN PRECURSOR.

6.4e-67:180:68

MUS MUSCULUS (MOUSE).

P51655

F-NT2RM4000761

CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).

2.3e-53:107:81

RATTUS NORVEGICUS (RAT).

P05503

F-NT2RM4000965

PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).

4.9e-14:188:34

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

060100

F-NT2RM4000997

HISTONE H1C (CLONE XLHW2).

0.88:73:26

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P15866

F-NT2RM4001321

HOMEODOMAIN PROTEIN HOX-A2.

0.27:77:37

GALLUS GALLUS (CHICKEN).

Q08727

F-NT2RM4001325

CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST).

3.8e-30:184:39

GALLUS GALLUS (CHICKEN).

Q92179

F-NT2RM4001377

HYPOTHETICAL BHLF1 PROTEIN.

5.9e-06:216:33

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03181

F-NT2RM4001735

GNS 1 PROTEIN.

0.0028:114:29  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P25358

5 F-NT2RM4001768  
PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).  
8.6e-24:205:36  
STREPTOMYCES ANTIBIOTICUS.  
Q03326

10 F-NT2RM4001843  
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).  
4.6e-33:258:37  
XANTHOMONAS MANIHOTIS.  
15 P48982

F-NT2RM4002352  
BASEMENT MEMBRANE PROTEOGLYCAN PRECURSOR (PERLECAN HOMOLOG).  
1.0e-15:85:45  
20 CAENORHABDITIS ELEGANS.  
Q06561

F-NT2RP1000002  
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).  
25 0.00011:24:62  
LYCOPERSICON ESCULENTUM (TOMATO).  
Q01157

F-NT2RP1000050  
30 A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.  
2.5e-07:198:33  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P32323

35 F-NT2RP1000181  
CYTOCHROME B5.  
4.4e-11:117:29  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
40 P40312

F-NT2RP1000239  
TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).  
7.8e-05:141:33  
45 HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).  
P28284

F-NT2RP1000261  
ORM1 PROTEIN.  
2.2e-18:137:35  
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P53224

F-NT2RP1000271  
55 ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).  
8.3e-81:194:70  
HOMO SAPIENS (HUMAN).  
Q03923

# EP 1 130 094 A2

F-NT2RP1000300  
HYPOTHETICAL 57.1 KD PROTEIN IN MAP2-TEL1 INTERGENIC REGION.  
2.0e-07:202:24  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P38176

F-NT2RP1000325  
MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR.  
1.6e-55:86:81  
HOMO SAPIENS (HUMAN).  
Q00325

F-NT2RP1000448  
PROLINE-RICH PEPTIDE P-B.  
0.094:32:43  
HOMO SAPIENS (HUMAN).  
P02814

F-NT2RP1000465  
EBNA-1 NUCLEAR PROTEIN.  
3.1e-07:101:39  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03211

F-NT2RP1000468  
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DIVA BINDING PROTEIN SUBUNIT B).  
1.4e-14:97:38  
PETROMYZON MARINUS (SEA LAMPREY).  
P25210

F-NT2RP1000551  
INTERFERON-RELATED PROTEIN PC4 (TPA INDUCED SEQUENCE 7) (TIS7 PROTEIN).  
1.9e-33:221:41  
MUS MUSCULUS (MOUSE).  
P19182

F-NT2RP1000579  
SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR (EC 1.3.5.1) (FP) (FLAVOPROTEIN SUBUNIT OF COMPLEX II).  
3.4e-68:247:62  
HOMO SAPIENS (HUMAN).  
P31040

F-NT2RP1000613  
CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).  
1.9e-19:137:37  
OVIS ARIES (SHEEP).  
P08060

F-NT2RP1000679  
EBNA-1 NUCLEAR PROTEIN.  
0.00055:54:50  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03211

F-NT2RP1000740  
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).

0.071:71:45  
HOMO SAPIENS (HUMAN).  
000268

5 F-NT2RP1000903  
SPORE COAT PROTEIN SP96.  
0.016:124:26  
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).  
P14328

10 F-NT2RP1000981  
CELL SURFACE A33 ANTIGEN PRECURSOR.  
1.1e-08:196:28  
HOMO SAPIENS (HUMAN).  
15 Q99795

F-NT2RP1001004  
F-SPONDIN PRECURSOR.  
1.2e-11:155:31  
20 XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P35447

F-NT2RP1001020  
SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).  
25 2.2e-05:126:29  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P08458

F-NT2RP1001031  
30 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).  
5.8e-26:159:38  
THERMOMONOSPORA CURVATA.  
P49695

35 F-NT2RP1001563  
METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).  
0.00036:42:40  
BOS TAURUS (BOVINE).  
P37359

40 F-NT2RP2000092  
ZINC FINGER PROTEIN 136.  
2.9e-44:129:62  
HOMO SAPIENS (HUMAN).  
45 P52737

F-NT2RP2000178  
HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).  
0.0050:75:37  
50 DROSOPHILA MELANOGASTER (FRUIT FLY).  
P25439

F-NT2RP2000240  
PUTATIVE CUTICLE COLLAGEN C09G5.5.  
55 9.2e-08:137:34  
CAENORHABDITIS ELEGANS.  
Q09456



# EP 1 130 094 A2

F-NT2RP2000394  
 PROCYCLIC FORM SPECIFIC POLYPEPTIDE A-BETA PRECURSOR (PROCYCLIN) (PARP A-BETA).  
 0.00019:28:64  
 TRYPANOSOMA BRUCEI BRUCEI.  
 P09791

F-NT2RP2000447  
 GOLGIN-95.  
 6.4e-25:55:67  
 HOMO SAPIENS (HUMAN).  
 Q08379

F-NT2RP2000479  
 PROBABLE E5B PROTEIN.  
 1.0:32:37  
 HUMAN PAPILLOMAVIRUS TYPE 6B.  
 P06461

F-NT2RP2000514  
 AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).  
 1.5e-18:201:33  
 HOMO SAPIENS (HUMAN).  
 Q02246

F-NT2RP2000533  
 CORNICHON PROTEIN.  
 5.6e-52:144:65  
 DROSOPHILA MELANOGASTER (FRUIT FLY).  
 P49858

F-NT2RP2000610  
 CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-  
 BOX DNA BINDING PROTEIN SUBUNIT B).  
 8.7e-15:97:38  
 PETROMYZON MARINUS (SEA LAMPREY).  
 P25210

F-NT2RP2000616  
 PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.  
 0.028:163:30  
 MUS MUSCULUS (MOUSE).  
 P11087

F-NT2RP2000649  
 POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1)  
 (PPSEP 1).  
 9.5e-22:241:32  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
 Q10071

F-NT2RP2000663  
 PANCREATIC HORMONE PRECURSOR (PANCREATIC POLYPEPTIDE) (PP).  
 0.71:28:46  
 GALLUS GALLUS (CHICKEN), AND MELEAGRIS GALLOPAVO (COMMON TURKEY).  
 P01306

F-NT2RP2000694  
 WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).

8.8e-10:90:42  
MUS MUSCULUS (MOUSE).  
P70315

5 F-NT2RP2000712  
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).  
2.3e-50:166:50  
HOMO SAPIENS (HUMAN).  
Q03923

10 F-NT2RP2000739  
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).  
8.9e-45:180:43  
HOMO SAPIENS (HUMAN).  
15 Q03923

F-NT2RP2000818  
SYG1 PROTEIN.  
2.4e-14:164:35  
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P40528

F-NT2RP2000903  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
25 0.28:149:34  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437

F-NT2RP2001200  
30 MIC1 PROTEIN.  
1.8e-13:115:38  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P53258

35 F-NT2RP2001223  
CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).  
0.00017:92:35  
CANIS FAMILIARIS (DOG).  
P39881

40 F-NT2RP2001276  
NPDC-1 PROTEIN PRECURSOR.  
4.9e-35:96:71  
MUS MUSCULUS (MOUSE).  
45 Q64322

F-NT2RP2001388  
CECROPIN B PRECURSOR.  
0.98:31:51  
50 DROSOPHILA MELANOGASTER (FRUIT FLY).  
P14956

F-NT2RP2001469  
VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.  
55 6.0e-07:146:22  
PODOSPORA ANSERINA.  
Q00808

F-NT2RP2001480  
THROMBOSPONDIN 3 PRECURSOR.  
2.1e-100:209:88  
HOMO SAPIENS (HUMAN).  
P49746

F-NT2RP2001495  
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.  
3.1e-11:174:24  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P39981

F-NT2RP2001514  
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).  
4.0e-18:163:36  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P39986

F-NT2RP2001529  
DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).  
4.4e-83:186:78  
HOMO SAPIENS (HUMAN).  
P53355

F-NT2RP2001538  
PAIRED AMPHIPATHIC HELIX PROTEIN.  
1.7e-06:152:26  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P22579

F-NT2RP2001562  
CLATHRIN LIGHT CHAIN B (BRAIN AND LYMPHOCYTE LCB).  
0.0093:124:27  
HOMO SAPIENS (HUMAN).  
P09497

F-NT2RP2001662  
5'-TG-3'INTERACTING FACTOR (HOMEBOX PROTEIN TGIF).  
5.6e-36:146:57  
HOMO SAPIENS (HUMAN).  
Q15583

F-NT2RP2001755  
F-SPONDIN PRECURSOR.  
1.2e-33:84:89  
RATTUS NORVEGICUS (RAT).  
P35446

F-NT2RP2001769  
PROTEIN KINASE CEK1 (EC 2.7.1.-).  
1.3e-37:159:53  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
P38938

F-NT2RP2001817  
HST1 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 1).  
6.4e-32:85:48  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53685

F-NT2RP2001878

EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

5 1.1e-06:173:28

NICOTIANA TABACUM (COMMON TOBACCO).

P13983

F-NT2RP2001903

10 CALPAIN P94, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEIN-ASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE SUBUNIT).

2.4e-10:110:37

HOMO SAPIENS (HUMAN).

15 P20807

F-NT2RP2001915

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).

0.0069:74:39

20 HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).

P28284

F-NT2RP2001921

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).

25 0.016:51:45

BOVINE HERPESVIRUS TYPE 1 (STRAIN K22).

P29836

F-NT2RP2001948

30 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.

6.7e-08:121:37

HOMO SAPIENS (HUMAN).

Q03692

F-NT2RP2001956

ORM1 PROTEIN.

7.6e-17:106:36

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53224

40

F-NT2RP2002015

HOMEBOX PROTEIN HOX-A2.

0.12:77:37

GALLUS GALLUS (CHICKEN).

45 Q08727

F-NT2RP2002063

HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.

3.2e-47:213:41

50 CAENORHABDITIS ELEGANS.

P49191

F-NT2RP2002188

ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (ACHE).

55 9.2e-15:109:36

TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).

P04058

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F-NT2RP2002232  
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.  
2.0e-12:92:50  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
Q09782

F-NT2RP2002304  
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).  
0.00059:16:68  
LYCOPERSICON ESCULENTUM (TOMATO).  
Q01157

F-NT2RP2002409  
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).  
0.00039:184:33  
BOS TAURUS (BOVINE).  
P02453

F-NT2RP2002510  
T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).  
0.0010:97:37  
ORYCTOLAGUS CUNICULUS (RABBIT).  
P06333

F-NT2RP2002527  
CYTOCHROME B5.  
1.3e-11:77:38  
SACCHAROMYCES CEREVISIAE (BAKERS YEAST).  
P40312

F-NT2RP2002533  
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA SUBUNITS PRECURSOR.  
2.0e-37:165:42  
ORYCTOLAGUS CUNICULUS (RABBIT).  
P13806

F-NT2RP2002564  
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).  
4.7e-06:81:35  
NICOTIANA TABACUM (COMMON TOBACCO).  
P13983

F-NT2RP2002674  
SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CYTOSOLIC EPOXIDE HY-  
DROLASE) (CEH).  
2.4e-25:147:41  
HOMO SAPIENS (HUMAN).  
P34913

F-NT2RP2002721  
GLUCOSE 6-PHOSPHATE TRANSLOCASE.  
0.0073:88:26  
HOMO SAPIENS (HUMAN).  
043826

F-NT2RP2002824  
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-  
FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

1.0e-16:139:36  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P32802

5 F-NT2RP2002942  
NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1).  
5.1e-18:153:30  
HOMO SAPIENS (HUMAN).  
P32004

10 F-NT2RP2002974  
HOMEODOMAIN PROTEIN SIX5 (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HOMOLOG) (FRAGMENT).  
3.6e-80:187:84  
15 MUS MUSCULUS (MOUSE).  
P70178

F-NT2RP2002976  
20 HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.  
2.8e-18:99:47  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P38800

25 F-NT2RP2003042  
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT).  
1.2e-41:135:57  
GALLUS GALLUS (CHICKEN).  
P53760

30 F-NT2RP2003138  
5'-TG-3'INTERACTING FACTOR (HOMEODOMAIN PROTEIN TGIF).  
3.3e-09:104:45  
MUS MUSCULUS (MOUSE).  
35 P70284

F-NT2RP2003179  
40 CARBON CATABOLITE DEREPRESSING PROTEIN KINASE (EC 2.7.1.-).  
7.2e-15:96:40  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P06782

F-NT2RP2003210  
45 LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP).  
6.2e-69:235:57  
MUS MUSCULUS (MOUSE).  
Q60714

50 F-NT2RP2003302  
ZINC FINGER PROTEIN 136.  
9.7e-52:140:52  
HOMO SAPIENS (HUMAN).  
P52737

55 F-NT2RP2003369  
SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).  
0.00020:87:32  
HOMO SAPIENS (HUMAN).

P10161

F-NT2RP2003383

LONG NEUROTOXIN 2 (TOXINS I AND V).

0.86:38:39

DENDROASPIS VIRIDIS (WESTERN GREEN MAMBA).

P01395

F-NT2RP2003390

NPL1 PROTEIN (SEC63 PROTEIN).

1.1e-14:113:38

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P14906

F-NT2RP2003469

MYO-INOSITOL TRANSPORTER 2.

1.7e-09:148:28

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P30606

F-NT2RP2003545

SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).

9.2e-32:198:41

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38692

F-NT2RP2003593

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

0.00019:128:32

MUS MUSCULUS (MOUSE).

P05142

F-NT2RP2003599

ATP-DEPENDENT BILE ACID PERMEASE.

0.88:69:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32386

F-NT2RP2003655

HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC REGION.

2.9e-16:93:47

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38869

F-NT2RP2003664

HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC REGION.

5.6e-08:121:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P47111

F-NT2RP2003931

ACROSIN PRECURSOR (EC 3.4.21.10).

0.38:20:70

HOMO SAPIENS (HUMAN).

P10323

F-NT2RP2003940

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

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1.3e-84:126:74  
HOMO SAPIENS (HUMAN).  
Q03923

5 F-NT2RP2003950  
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-  
PHA-0 PROTEIN).  
1.5e-05:134:33  
10 HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).  
P08393

F-NT2RP2004069  
HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.  
4.3e-13:68:54  
15 CAENORHABDITIS ELEGANS.  
Q09297

F-NT2RP2004108  
ZINC FINGER PROTEIN 136.  
20 8.6e-47:126:67  
HOMO SAPIENS (HUMAN).  
P52737

F-NT2RP2004141  
25 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
0.013:127:35  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437

30 F-NT2RP2004179  
GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (GLYCEROPHOSPHODIESTER  
PHOSPHODIESTERASE).  
5.9e-10:110:36  
35 ESCHERICHIA COLI.  
P10908

F-NT2RP2004205  
MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.  
4.6e-10:99:34  
40 HOMO SAPIENS (HUMAN).  
Q16653

F-NT2RP2004447  
45 PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.  
0.86:48:37  
MUS MUSCULUS (MOUSE).  
Q01149

F-NT2RP2004495  
50 HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.  
0.031:135:31  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P39981

55 F-NT2RP2004524  
HYPOTHETICAL 18.7 KD PROTEIN IN HMS1-ABF2 INTERGENIC REGION.  
0.042:96:23  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).



Q04767

F-NT2RP2004556

SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).

0.0082:87:35

HOMO SAPIENS (HUMAN).

P81489

F-NT2RP2004606

METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID POTENTIATING ACTIVITY) (EPA) (TISSUE INHIBITOR OF METALLOPROTEINASES) (FIBROBLAST COLLAGENASE INHIBITOR) (COLLAGENASE INHIBITOR).

2.2e-57:163:73

HOMO SAPIENS (HUMAN).

P01033

F-NT2RP2004648

BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).

3.2e-25:90:62

FELIS SILVESTRIUS CATUS (CAT).

O19015

F-NT2RP2004670

CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).

6.6e-14:108:34

RATTUS NORVEGICUS (RAT).

Q63450

F-NT2RP2004794

HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.

5.7e-11:140:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40857

F-NT2RP2004837

F-NT2RP2004847

ADULT ENHANCER FACTOR 1 (AEF-1).

7.9e-09:81:37

DROSOPHILA MELANOGASTER (FRUIT FLY).

P39413

F-NT2RP2005027

GLUCOSE TRANSPORTER TYPE 3, BRAIN.

3.6e-64:130:96

HOMO SAPIENS (HUMAN).

P11169

F-NT2RP2005069

CCAAT DISPLACEMENT PROTEIN (CDP) (CDP2) (FRAGMENT).

0.22:116:32

RATTUS NORVEGICUS (RAT).

P53565

F-NT2RP2005163

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

5.3e-06:70:38

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

F-NT2RP2005181

HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).

4.2e-54:153:69

HOMO SAPIENS (HUMAN).

P30825

F-NT2RP2005247

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

2.0e-11:106:35

SORGHUM VULGARE (SORGHUM).

P24152

F-NT2RP2005378

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

0.11:97:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

F-NT2RP2005391

G-BOX BINDING FACTOR (GBF).

5.1e-10:156:30

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P36417

F-NT2RP2005425

M PROTEIN, SEROTYPE 49 PRECURSOR.

2.1e-05:183:27

STREPTOCOCCUS PYOGENES.

P16947

F-NT2RP2005463

OVOMUCOID (FRAGMENT).

1.0:21:52

BAMBUSICOLA THORACICA (CHINESE BAMBOO-PARTRIDGE).

P52259

F-NT2RP2005514

MOBC PROTEIN.

1.0:26:53

THIOBACILLUS FERROOXIDANS.

P22899

F-NT2RP2005535

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

3.8e-92:243:69

HOMO SAPIENS (HUMAN).

Q03923

F-NT2RP2005541

N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).

8.8e-16:78:51

HOMO SAPIENS (HUMAN).

P15586

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F-NT2RP2005597  
DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC  
2.4.1.109).  
7.4e-13:99:34  
5 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P46971

F-NT2RP2005632  
10 ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENY-  
LYL CYCLASE).  
3.0e-05:73:43  
CANIS FAMILIARIS (DOG).  
P30803

15 F-NT2RP2005666  
HEPATOCTE NUCLEAR FACTOR 3-BETA (HNF-3B).  
0.086:105:31  
MUS MUSCULUS (MOUSE).  
P35583

20 F-NT2RP2005774  
ZINC FINGER PROTEIN 136.  
7.8e-33:128:57  
HOMO SAPIENS (HUMAN).  
25 P52737

F-NT2RP2005878  
30 PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).  
6.8e-23:96:48  
MUS MUSCULUS (MOUSE).  
070503

F-NT2RP2005883  
35 DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE)  
(DBH).  
6.4e-23:185:32  
RATTUS NORVEGICUS (RAT).  
Q05754

40 F-NT2RP2005887  
DNA-DIRECTED RNA POLYMERASE SUBUNIT K (EC 2.7.7.6).  
1.0:40:30  
METHANOCOCCUS JANNASCHII.  
Q57650

45 F-NT2RP2005941  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
3.5e-08:136:32  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
50 P17437

F-NT2RP2005994  
55 HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.  
4.4e-36:144:47  
CAENORHABDITIS ELEGANS.  
P49191

F-NT2RP2006004

EP 1 130 094 A2

BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG).

0.030:28:50

RATTUS NORVEGICUS (RAT).

Q01129

F-NT2RP2006042

HYPOTHETICAL PROTEIN KIAA0144.

1.2e-22:228:39

HOMO SAPIENS (HUMAN).

Q14157

F-NT2RP2006092

TRANSCRIPTIONAL ACTIVATOR FE65.

3.1e-27:101:54

RATTUS NORVEGICUS (RAT).

P46933

F-NT2RP2006099

SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).

7.0e-07:123:34

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P17437

F-NT2RP2006134

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (EARLY PROTEIN 0) (EP0).

0.0041:118:30

PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).

P29129

F-NT2RP2006269

DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).

6.3e-17:119:36

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P46971

F-NT2RP2006512

GNS1 PROTEIN.

8.6e-14:186:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P25358

F-NT2RP3000011

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

2.9e-12:137:32

THERMOMONOSPORA CURVATA.

P49695

F-NT2RP3000022

SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-ASSOCIATED KINASE).

1.6e-47:121:79

RATTUS NORVEGICUS (RAT).

P20793

F-NT2RP3000059

COLLAGEN ALPHA 1(III) CHAIN.

1.5e-05:211:33

BOS TAURUS (BOVINE).

P04258

F-NT2RP3000063

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

4.2e-23:230:28

ZEA MAYS (MAIZE).

P14918

F-NT2RP3000125

CARBOXYPEPTIDASE KEX1 PRECURSOR (EC 3.4.16.6) (CARBOXYPEPTIDASE D).

2.3e-08:110:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P09620

F-NT2RP3000148

ZINC FINGER PROTEIN 133.

1.4e-34:84:48

HOMO SAPIENS (HUMAN).

P52736

F-NT2RP3000169

SMALL PROLINE-RICH PROTEIN 2-1.

0.00092:14:57

HOMO SAPIENS (HUMAN).

P35326

F-NT2RP3000171

24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION.

4.6e-10:134:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P28707

F-NT2RP3000172

CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).

1.8e-33:161:42

RATTUS NORVEGICUS (RAT).

Q63450

F-NT2RP3000201

SERINE/THREONINE-PROTEIN KINASE MIG-15 (EC 2.7.1.-).

4.1e-79:254:64

CAENORHABDITIS ELEGANS.

Q23356

F-NT2RP3000232

ZINC FINGER PROTEIN 184 (FRAGMENT).

8.5e-23:119:45

HOMO SAPIENS (HUMAN).

Q99676

F-NT2RP3000304

LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91).

9.8e-36:172:43

HOMO SAPIENS (HUMAN).

Q07954

F-NT2RP3000378

# EP 1 130 094 A2

PAIRED AMPHIPATHIC HELIX PROTEIN.  
2.7e-26:186:36  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P22579

5

F-NT2RP3000427  
5E5 ANTIGEN.  
0.086:204:31  
RATTUS NORVEGICUS (RAT).  
Q63003

10

F-NT2RP3000436  
PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).  
1.3e-23:106:33  
CAENORHABDITIS ELEGANS.  
Q11067

15

F-NT2RP3000444  
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).  
0.00052:166:36  
HOMO SAPIENS (HUMAN).  
000268

20

F-NT2RP3000460  
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.  
1.0e-98:194:100  
RATTUS NORVEGICUS (RAT).  
P38378

25

F-NT2RP3000481  
NONSENSE-MEDIATED MRNA DECAY PROTEIN 5.  
7.4e-19:217:29  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P46970

30

F-NT2RP3000616  
BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).  
1.2e-13:115:33  
BOS TAURUS (BOVINE).  
P21793

35

F-NT2RP3000645  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
2.3e-10:237:30  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437

45

F-NT2RP3000652  
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).  
3.1e-106:283:67  
HOMO SAPIENS (HUMAN).  
Q03923

50

F-NT2RP3000676  
ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (AD-  
ENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).  
7.4e-07:102:32  
HOMO SAPIENS (HUMAN).

55

P12235

F-NT2RP3000677

MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).

1.5e-27:66:54

HOMO SAPIENS (HUMAN).

P22670

F-NT2RP3000721

HYPOTHETICAL 62.5 KD PROTEIN IN SEC53-ACT1 INTERGENIC REGION.

1.6e-22:208:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P43560

F-NT2RP3000789

ONCONEURAL VENTRAL ANTIGEN-1 (NOVA-1) (PARANEOPLASTIC RI ANTIGEN) (VENTRAL NEURON-SPECIFIC PROTEIN 1).

1.0e-07:190:26

HOMO SAPIENS (HUMAN).

P51513

F-NT2RP3000818

HYPOTHETICAL 67.5 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION.

5.9e-05:100:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P34248

F-NT2RP3000820

BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).

0.92:97:26

SYNECHOCYSTIS SP. (STRAIN PCC 6803).

P73538

F-NT2RP3000838

SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).

6.4e-07:231:31

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P17437

F-NT2RP3000871

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).

2.8e-07:221:33

RATTUS NORVEGICUS (RAT).

P02454

F-NT2RP3000907

PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).

2.2e-41:104:48

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P39986

F-NT2RP3000921

BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).

4.5e-08:149:31

HOMO SAPIENS (HUMAN).

P98160

EP 1 130 094 A2

F-NT2RP3001012  
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.  
5.5e-06:37:51  
PLASMODIUM LOPHURAE.  
P04929

F-NT2RP3001044  
RNA POLYMERASE PRINCIPAL SIGMA FACTOR HRDA.  
0.10:61:31  
STREPTOMYCES COELICOLOR.  
P18182

F-NT2RP3001061  
GLYCOPROTEIN X PRECURSOR.  
0.00011:140:27  
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).  
P28968

F-NT2RP3001159  
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.  
1.1e-09:249:32  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P32323

F-NT2RP3001170  
POU DOMAIN PROTEIN 1 (DJPOU1).  
0.020:173:29  
DUGESIA JAPONICA (PLANARIAN).  
P31370

F-NT2RP3001195  
GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).  
1.2e-14:180:30  
ESCHERICHIA COLI.  
P37021

F-NT2RP3001240  
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.  
3.1e-118:229:88  
RATTUS NORVEGICUS (RAT).  
P38378

F-NT2RP3001271  
EBNA-1 NUCLEAR PROTEIN.  
2.3e-08:113:45  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03211

F-NT2RP3001322  
PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETICULUM CA<sub>2</sub><sup>+</sup>-AT-  
PASE).  
1.7e-23:222:29  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P39524

F-NT2RP3001388  
SYNAPTOTAGMIN IV.  
4.8e-19:168:38



RATTUS NORVEGICUS (RAT).  
P50232

5 F-NT2RP3001542  
TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).  
2.7e-12:132:37  
HOMO SAPIENS (HUMAN).  
Q13829

10 F-NT2RP3001560  
SYNAPSINS IA AND IB.  
0.59:104:35  
BOS TAURUS (BOVINE).  
P17599

15 F-NT2RP3001592  
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.  
1.3e-11:75:46  
20 ORYZA SATIVA (RICE).  
P29834

F-NT2RP3001650  
CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).  
0.23:119:36  
25 CANIS FAMILIARIS (DOG).  
P39881

F-NT2RP3001685  
HYPOTHETICAL PROTEIN IN MMSB 3'REGION (ORF1) (FRAGMENT).  
30 2.2e-48:207:48  
PSEUDOMONAS AERUGINOSA.  
P28812

35 F-NT2RP3001738  
CYTOCHROME B5.  
9.5e-13:133:33  
ORYCTOLAGUS CUNICULUS (RABBIT).  
P00169

40 F-NT2RP3001754  
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).  
7.9e-05:117:29  
HOMO SAPIENS (HUMAN).  
P17600

45 F-NT2RP3001858  
CUTICLE COLLAGEN 2.  
0.030:118:35  
50 CAENORHABDITIS ELEGANS.  
P17656

F-NT2RP3001976  
ZINC FINGER PROTEIN 140.  
7.8e-24:122:52  
55 HOMO SAPIENS (HUMAN).  
P52738

F-NT2RP3002015

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.  
0.018:224:30  
GALLUS GALLUS (CHICKEN).  
P02457

5

F-NT2RP3002160  
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
0.0058:206:29  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437

10

F-NT2RP3002281  
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).  
1.3e-14:86:40  
HOMO SAPIENS (HUMAN).  
P52597

15

F-NT2RP3002286  
ETS-DOMAIN TRANSCRIPTION FACTOR ERF.  
0.65:128:29  
HOMO SAPIENS (HUMAN).  
P50548

20

F-NT2RP3002311  
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).  
6.1e-46:172:54  
FELIS SILVESTRIUS CATUS (CAT).  
O19015

25

F-NT2RP3002324  
HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.  
0.012:23:65  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P53245

30

F-NT2RP3002342  
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.  
1.8e-13:219:26  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P39981

35

F-NT2RP3002353  
REGULATORY PROTEIN E2.  
0.0027:167:31  
HUMAN PAPILLOMAVIRUS TYPE 8.  
P06422

45

F-NT2RP3002409  
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEM-  
BRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE  
OF OUTER MEMBRANE TOM70).  
9.9e-09:93:34  
NEUROSPORA CRASSA.  
P23231

50

F-NT2RP3002411  
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).  
5.6e-107:254:80

55

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MUS MUSCULUS (MOUSE).  
070503

F-NT2RP3002448

5 TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).  
1.5e-05:163:33  
HOMO SAPIENS (HUMAN).  
000268

10 F-NT2RP3002571

HYPOTHETICAL 116.3 KD PROTEIN C26F1.09 IN CHROMOSOME I.  
6.4e-23:172:33  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
Q10496

15 F-NT2RP3002664

CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).  
0.062:47:29  
HOMO SAPIENS (HUMAN).  
20 P18850

F-NT2RP3002721

25 CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).  
6.2e-140:283:92  
SUS SCROFA (PIG).  
P00889

F-NT2RP3002737

30 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.9.  
4.1e-40:136:61  
MUS MUSCULUS (MOUSE).  
P97414

F-NT2RP3002738

35 SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).  
0.029:195:28  
HOMO SAPIENS (HUMAN).  
P10163

40 F-NT2RP3002790

PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
1.7e-08:130:36  
MUS MUSCULUS (MOUSE).  
P05142

45 F-NT2RP3002836

TRANSMEMBRANE PROTEIN SEX PRECURSOR.  
8.9e-24:119:43  
HOMO SAPIENS (HUMAN).  
50 P51805

F-NT2RP3002887

55 SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).  
2.9e-11:198:34  
HOMO SAPIENS (HUMAN).  
P02812

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F-NT2RP3002900  
COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).  
2.8e-18:109:41  
CRICETULUS GRISEUS (CHINESE HAMSTER).  
P49020

F-NT2RP3002958  
TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.  
6.4e-06:172:27  
RATTUS NORVEGICUS (RAT).  
P19814

F-NT2RP3002983  
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).  
4.4e-05:106:41  
BOS TAURUS (BOVINE).  
P02453

F-NT2RP3003000  
SODIUM CHANNEL PROTEIN (NA<sup>+</sup> CHANNEL).  
9.7e-30:221:31  
ELECTROPHORUS ELECTRICUS (ELECTRIC EEL).  
P02719

F-NT2RP3003076  
ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220].  
0.00033:173:30  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03200

F-NT2RP3003354  
SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.  
2.0e-54:204:51  
MUS MUSCULUS (MOUSE).  
035609

F-NT2RP3003448  
PROTEASE DEGS PRECURSOR (EC 3.4.21.-).  
4.0e-05:112:33  
ESCHERICHIA COLI.  
P31137

F-NT2RP3003469  
!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!  
1.2e-17:70:64  
HOMO SAPIENS (HUMAN).  
P39194

F-NT2RP3003473  
BACTENECIN 7 PRECURSOR (BAC7) (PR-59).  
0.0037:33:63  
BOS TAURUS (BOVINE).  
P19661

F-NT2RP3003527  
SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK).  
1.8e-53:159:69  
HOMO SAPIENS (HUMAN).

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Q13627

F-NT2RP3003532  
OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).  
2.3e-114:219:97  
HOMO SAPIENS (HUMAN).  
P41217

F-NT2RP3003535  
HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3 REGION (ORF57).  
0.98:36:30  
ASTASIA LONGA (EUGLENOPHYCEAN ALGA).  
P34774

F-NT2RP3003559  
MALE SPECIFIC SPERM PROTEIN MST84DB.  
0.047:29:48  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
Q01643

F-NT2RP3003614  
TRYPSIN INHIBITOR II (BDTI-II).  
0.98:23:39  
BRYONIA DIOICA (RED BRYONY).  
P11968

F-NT2RP3003729  
HYPOTHETICAL 42.1 KD PROTEIN IN SNZ1-YPK2 INTERGENIC REGION.  
4.1e-11:204:30  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
Q03151

F-NT2RP3003849  
PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)).  
9.7e-17:126:34  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P05130

F-NT2RP3003874  
MYOSIN I ALPHA (MMI-ALPHA).  
3.1e-64:141:84  
MUS MUSCULUS (MOUSE).  
P46735

F-NT2RP3003939  
CELL DIVISION PROTEIN FTSH HOMOLOG 4 (EC 3.4.24.-).  
7.1e-34:76:61  
SYNECHOCYSTIS SP. (STRAIN PCC 6803).  
P72991

F-NT2RP3003963  
HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.  
0.95:31:38  
HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).  
Q48251

F-NT2RP3004000  
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).

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7.1e-07:187:29

CRICETULUS GRISEUS (CHINESE HAMSTER).

P11414

5

F-NT2RP3004025

EBNA-1 NUCLEAR PROTEIN.

0.022:79:40

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

10

F-NT2RP3004067

COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.

5.0e-07:184:35

HOMO SAPIENS (HUMAN).

15

Q03692

F-NT2RP3004075

GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN PRECURSOR.

2.9e-07:92:40

20

HORDEUM VULGARE (BARLEY).

P17816

F-NT2RP3004083

ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).

25

0.013:24:45

COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).

P50682

F-NT2RP3004090

30

SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.

1.2e-07:195:29

DROSOPHILA ERECTA (FRUIT FLY).

P13730

35

F-NT2RP3004119

PEREGRIN (BR140 PROTEIN).

4.1e-40:227:43

HOMO SAPIENS (HUMAN).

P55201

40

F-NT2RP3004130

CELL SURFACE ANTIGEN 114/A10 PRECURSOR.

2.4e-08:71:42

MUS MUSCULUS (MOUSE).

45

P19467

F-NT2RP3004133

GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).

1.5e-28:111:44

50

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P43636

F-NT2RP3004202

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

55

3.0e-06:104:37

MUS MUSCULUS (MOUSE).

P05142

- 5 F-NT2RP3004294  
HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.  
8.8e-10:129:31  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P53288
- 10 F-NT2RP3004309  
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.  
1.9e-05:212:30  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P32323
- 15 F-NT2RP3004321  
REGULATORY PROTEIN SIR2 HOMOLOG (LMSIR2RP).  
2.8e-09:81:40  
LEISHMANIA MAJOR.  
Q25337
- 20 F-NT2RP3004345  
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.  
1.3e-11:75:46  
ORYZA SATIVA (RICE).  
P29834
- 25 F-NT2RP3004355  
HYDROGENASE EXPRESSION/FORMATION PROTEIN HUPV.  
0.81:154:26  
AZOTOBACTER CHROOCOCCUM MCD 1.  
Q43959
- 30 F-NT2RP3004374  
HOMEBOX PROTEIN HOX-A2.  
0.28:77:37  
GALLUS GALLUS (CHICKEN).  
Q08727
- 35 F-NT2RP3004406  
HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.  
4.9e-18:165:33  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P40544
- 40 F-NT2RP3004481  
BUTYROPHILIN PRECURSOR (BT).  
4.0e-13:152:31  
HOMO SAPIENS (HUMAN).  
Q13410
- 50 F-NT2RP3004552  
COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).  
3.4e-05:211:28  
HOMO SAPIENS (HUMAN).  
P17927
- 55 F-NT2RP3004557  
INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN PRECURSOR (IGUP I-5111).  
1.6e-23:129:35  
HOMO SAPIENS (HUMAN).

Q06323

F-NT2RP3004625

GLYCOPROTEIN X PRECURSOR.

2.4e-10:225:25

EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).

P28968

F-NT2RP3004640

ENAMELIN (TUFTELIN).

2.6e-70:167:85

BOS TAURUS (BOVINE).

P27628

F-NT2RP3004647

ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (AD-ENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).

4.6e-10:116:34

HOMO SAPIENS (HUMAN).

P12235

F-NT2RP4000108

NEUROFILAMENT TRIPLET L PROTEIN (68 KD NEUROFILAMENT PROTEIN) (NF-L) (NF68).

3.4e-107:255:87

RATTUS NORVEGICUS (RAT).

P19527

F-NT2RP4000634

MAPK/ERK KINASE KINASE 2 (EC 2.7.1.-) (MEK KINASE 2) (MEKK 2).

7.9e-142:267:88

MUS MUSCULUS (MOUSE).

Q61083

F-NT2RP4000962

SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).

1.5e-13:158:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P08458

F-NT2RP4001001

F-NT2RP4001009

POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1) (PPSEP 1).

7.7e-24:235:31

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q10071

F-NT2RP4001467

5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).

1.2e-120:237:97

HOMO SAPIENS (HUMAN).

P21589

F-NT2RP4001877

GLYCINE-RICH RNA-BINDING PROTEIN.

1.4e-08:89:34

DAUCUS CAROTA (CARROT).



# EP 1 130 094 A2

Q03878

F-NT2RP4001879

VERY HYPOTHETICAL 8.9 KD PROTEIN CY441.05 PRECURSOR.

5 0.98:49:34

MYCOBACTERIUM TUBERCULOSIS.

P71934

F-NT2RP4002187

10 PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).

4.5e-98:246:78

MUS MUSCULUS (MOUSE).

070503

F-NT2RP4002451

CUTICLE COLLAGEN 2.

0.85:92:35

CAENORHABDITIS ELEGANS.

P17656

20

F-NT2RP4002715

HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.

0.47:31:48

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

25 P53245

F-NT2RP4002750

HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).

30

3.3e-63:185:67

HOMO SAPIENS (HUMAN).

P30825

35

F-OVARC1000003

RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).

2.2e-82:197:72

40

HOMO SAPIENS (HUMAN).

Q06495

F-OVARC1000090

HOMEODOMAIN PROTEIN HOX-B1 (GHOM-LAB).

45

0.049:120:32

GALLUS GALLUS (CHICKEN).

P31259

F-OVARC1000105

UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).

50

8.6e-47:159:58

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P33296

55

F-OVARC1000137

HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION.

0.058:28:64

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P36015

F-OVARC1000208  
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!  
2.2e-12:51:74  
HOMO SAPIENS (HUMAN).  
P39195

F-OVARC1000255  
TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).  
1.1e-112:144:86  
HOMO SAPIENS (HUMAN).  
P43405

F-OVARC1000275  
GASTRIN PRECURSOR.  
0.11:59:37  
HOMO SAPIENS (HUMAN).  
P01350

F-OVARC1000298  
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).  
0.014:74:39  
MUS MUSCULUS (MOUSE).  
P05143

F-OVARC1000307  
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).  
1.0:33:54  
NICOTIANA TABACUM (COMMON TOBACCO).  
P13983

F-OVARC1000313  
PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) (CALCIUM-BINDING PRO-  
TEIN 2) (CABP2).  
4.0e-15:127:37  
RATTUS NORVEGICUS (RAT).  
P38659

F-OVARC1000331  
GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE).  
2.0e-24:64:84  
HOMO SAPIENS (HUMAN).  
P36959

F-OVARC1000410  
FIBRINOGEN-LIKE PROTEIN A PRECURSOR (FREP-A).  
1.9e-44:229:41  
PARASTICHOPUS PARVIMENSIS (SEA CUCUMBER).  
P19477

F-OVARC1000439  
SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.  
0.99:41:43  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P02841

EP 1 130 094 A2

F-OVARC1000467  
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).  
0.0061:30:63  
LYCOPERSICON ESCULENTUM (TOMATO).  
Q01157

5

F-OVARC1000529  
PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL 101 W (EC 2.7.1.-).  
1.5e-20:127:42  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P34244

10

F-OVARC1000553  
DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM).  
7.6e-26:169:40  
MUS MUSCULUS (MOUSE).  
P28843

15

F-OVARC1000775  
METALLOTHIONEIN (MT).  
0.91:31:38  
CARASSIUS AURATUS (GOLDFISH).  
P52723

20

F-OVARC1000811  
COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR) (HAF).  
2.8e-11:69:43  
HOMO SAPIENS (HUMAN).  
P00748

25

F-OVARC1000853  
CUTICLE COLLAGEN 40.  
0.00013:130:33  
CAENORHABDITIS ELEGANS.  
P34804

30

F-OVARC1000873  
MALE SPECIFIC SPERM PROTEIN MST84DB.  
0.00015:53:33  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
Q01643

40

F-OVARC1000916  
GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE P58/GTA (EC 2.7.1.-).  
2.5e-26:109:53  
MUS MUSCULUS (MOUSE).  
P24788

45

F-OVARC1000956  
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).  
0.00073:115:33  
HOMO SAPIENS (HUMAN).  
P21917

50

F-OVARC1000995  
POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2 (SNF2-ALPHA).  
0.00031:139:25  
HOMO SAPIENS (HUMAN).

55

P51531

F-OVARC1001030

5E5 ANTIGEN.

1.9e-09:89:41

RATTUS NORVEGICUS (RAT).

Q63003

F-OVARC1001049

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.

1.5e-08:146:38

GALLUS GALLUS (CHICKEN).

P02457

F-OVARC1001086

VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40].

5.3e-08:182:32

GALLUS GALLUS (CHICKEN).

P02845

F-OVARC1001132

GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9) (TCF-9).

9.2e-40:229:37

HOMO SAPIENS (HUMAN).

P16383

F-OVARC1001163

HYPOTHETICAL 49.3 KD PROTEIN C30D 11.06C IN CHROMOSOME I.

8.8e-05:38:44

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q09906

F-OVARC1001222

AMELOGENIN, CLASS I PRECURSOR.

0.72:96:31

BOS TAURUS (BOVINE).

P02817

F-OVARC1001260

F-OVARC1001336

RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANS-PORTER 2) (NA(+)/PI COTRANSporter 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RE-NAL NA+-DEPENDENT PHOSPHATE COTRANSporter 2).

1.1e-33:103:71

RATTUS NORVEGICUS (RAT).

Q06496

F-OVARC1001338

SERINE/THREONINE-PROTEIN KINASE UNC-51 (EC 2.7.1.-).

3.8e-30:89:46

CAENORHABDITIS ELEGANS.

Q23023

F-OVARC1001569

ACROSIN PRECURSOR (EC 3.4.21.10) (53 KD FUCOSE-BINDING PROTEIN).

2.2e-06:28:64

SUS SCROFA (PIG).  
P08001

F-OVARC1001570  
CATHEPSIN E PRECURSOR (EC 3.4.23.34).  
1.8e-09:121:33  
CAVIA PORCELLUS (GUINEA PIG).  
P25796

F-OVARC1001596  
REGULATORY PROTEIN E2.  
0.33:77:37  
HUMAN PAPILLOMAVIRUS TYPE 14.  
P36783

F-OVARC1001607  
ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II).  
1.0e-28:69:84  
HOMO SAPIENS (HUMAN).  
Q10469

F-OVARC1001725

F-OVARC1001727

F-OVARC1001807  
EARLY RESPONSE PROTEIN NAK1 (TR3 ORPHAN RECEPTOR).  
2.4e-51:153:75  
HOMO SAPIENS (HUMAN).  
P22736

F-OVARC1001833  
CIS-GOLGI MATRIX PROTEIN GM130.  
1.2e-55:169:75  
RATTUS NORVEGICUS (RAT).  
Q62839

F-OVARC1001952  
EBNA-1 NUCLEAR PROTEIN.  
3.5e-19:130:43  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03211

F-OVARC1001991  
HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).  
3.7e-16:141:43  
HOMO SAPIENS (HUMAN).  
Q14681

F-OVARC1002058  
LAMININ ALPHA-5 CHAIN (FRAGMENT).  
2.8e-22:163:33  
MUS MUSCULUS (MOUSE).  
Q61001

F-OVARC1002178

EP 1 130 094 A2

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).

0.12:73:36

HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).

P08393

F-PLACE1000033

VON WILLEBRAND FACTOR PRECURSOR.

1.7e-19:190:28

CANIS FAMILIARIS (DOG).

Q28295

F-PLACE1000231

DNA-BINDING PROTEIN MNB1A.

0.24:60:33

ZEA MAYS (MAIZE).

P38564

F-PLACE1000258

ZINC FINGER PROTEIN 177.

3.6e-19:55:61

HOMO SAPIENS (HUMAN).

Q13360

F-PLACE1000442

ZINC FINGER PROTEIN 136.

1.7e-80:180:72

HOMO SAPIENS (HUMAN).

P52737

F-PLACE1000560

COLICIN E9 (EC 3.1.21.1).

0.015:47:44

ESCHERICHIA COLI.

P09883

F-PLACE1000740

NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3).

1.6e-05:75:36

MUS MUSCULUS (MOUSE).

P31695

F-PLACE1000907

ZINC FINGER PROTEIN 141.

2.8e-15:43:88

HOMO SAPIENS (HUMAN).

Q15928

F-PLACE1000912

PROBABLE E4 PROTEIN (E1^E4).

0.19:46:36

HUMAN PAPILLOMAVIRUS TYPE 6B.

P06459

F-PLACE1000914

MALE SPECIFIC SPERM PROTEIN MST87F.

0.054:27:44

DROSOPHILA MELANOGASTER (FRUIT FLY).

P08175

F-PLACE1000927  
HYPOTHETICAL PROTEIN HI0044.  
3.9e-07:139:30  
HAEMOPHILUS INFLUENZAE.  
P44477

F-PLACE1000986

F-PLACE1001016  
SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT.  
2.7e-05:120:32  
RATTUS NORVEGICUS (RAT).  
P04775

F-PLACE1001100

F-PLACE1001114  
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.  
2.5e-07:250:28  
MUS MUSCULUS (MOUSE).  
P11087

F-PLACE1001123  
INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).  
6.2e-09:95:31  
HOMO SAPIENS (HUMAN).  
Q04941

F-PLACE1001183  
NONHISTONE CHROMOSOMAL PROTEIN HMG-17.  
0.31:52:34  
GALLUS GALLUS (CHICKEN).  
P02314

F-PLACE1001229  
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).  
1.0:38:47  
ARTEMIA SAUNA (BRINE SHRIMP).  
P19047

F-PLACE1001231  
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).  
4.7e-06:181:27  
ORYCTOLAGUS CUNICULUS (RABBIT).  
P11170

F-PLACE1001340  
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).  
6.5e-14:136:29  
NEUROSPORA CRASSA.  
P23231

F-PLACE1001401

EP 1 130 094 A2

HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT).

1.3e-11:103:40

RATTUS NORVEGICUS (RAT).

P13386

F-PLACE1001407

INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).

0.013:121:32

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

Q05049

F-PLACE1001464

5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).

1.4e-119:246:89

HOMO SAPIENS (HUMAN).

P21589

F-PLACE1001500

BLOOM'S SYNDROME PROTEIN.

8.3e-26:203:34

HOMO SAPIENS (HUMAN).

P54132

F-PLACE1001516

GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).

7.4e-07:204:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P08640

F-PLACE1001536

F-PLACE1001564

LEUCOCYTE ANTIGEN CD97 PRECURSOR.

2.1e-09:170:24

HOMO SAPIENS (HUMAN).

P48960

F-PLACE1001655

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DRK1).

4.0e-34:189:39

RATTUS NORVEGICUS (RAT).

P15387

F-PLACE1001788

HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I.

6.2e-21:75:58

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q09695

F-PLACE1001795

HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECURSOR.

3.8e-21:159:40

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P47032

F-PLACE1001836



EP 1 130 094 A2

ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN)[CONTAINS: OUTER MEMBRANE PROTEIN GP70;  
TRANSMEMBRANE PROTEIN P20E].

4.5e-29:134:47

BABOON ENDOGENOUS VIRUS (STRAIN M7).

P10269

F-PLACE1001918

ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-  
FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

1.5e-30:228:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32802

F-PLACE1001949

PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).

5.1e-36:210:46

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Q12697

F-PLACE1002080

HYPOTHETICAL PROTEIN KIAA0288 (HA6116).

3.5e-26:207:45

HOMO SAPIENS (HUMAN).

P56524

F-PLACE1002095

N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-  
TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANS-  
FERASE) (GT).

0.32:50:34

MUS MUSCULUS (MOUSE).

P15535

F-PLACE1002153

CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (SLAYER PROTEIN 1).

0.00021:214:26

CLOSTRIDIUM THERMOCELLUM.

Q06852

F-PLACE1002329

EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.

1.1e-35:179:44

MUS MUSCULUS (MOUSE).

Q08509

F-PLACE1002355

COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN] (FRAGMENTS).

1.0e-14:183:32

BOS TAURUS (BOVINE).

P01030

F-PLACE1002374

CATHEPSIN L PRECURSOR (EC 3.4.22.15) (MAJOR EXCRETED PROTEIN) (MEP).

9.2e-107:225:86

HOMO SAPIENS (HUMAN).

P07711

F-PLACE1002518

EP 1 130 094 A2

HYPOTHETICAL 13.2 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.

6.1e-05:59:44

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38239

5

F-PLACE1002547

MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).

10

1.0e-22:230:31

NEUROSPORA CRASSA.

P23231

F-PLACE1002726

15

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).

0.61:25:48

ORYCTOLAGUS CUNICULUS (RABBIT).

P02456

20

F-PLACE1002905

ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

5.0e-31:93:64

BOS TAURUS (BOVINE).

25

P07106

F-PLACE1002911

T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN).

6.6e-06:95:35

30

HOMO SAPIENS (HUMAN).

P40200

F-PLACE1002967

35

HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE FC RECEPTOR, BETA-SUBUNIT).

9.4e-08:95:37

MUS MUSCULUS (MOUSE).

P20490

40

F-PLACE1003135

SERINE/THREONINE-PROTEIN KINASE STE20 (EC 2.7.1.-).

1.9e-33:99:50

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Q03497

45

F-PLACE1003163

ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

9.8e-15:105:38

50

BOS TAURUS (BOVINE).

P07106

F-PLACE1003407

CLN5 PROTEIN.

55

4.2e-109:217:89

HOMO SAPIENS (HUMAN).

O75503

F-PLACE1003428  
BIOTINIDASE PRECURSOR (EC 3.5.1.12).  
1.0e-36:104:46  
HOMO SAPIENS (HUMAN).  
P43251

5

F-PLACE1003438  
HYPOTHETICAL 104.4 KD PROTEIN C17A5.16 IN CHROMOSOME I.  
1.1e-10:148:33  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
013776

10

F-PLACE1003460  
2-HYDROXY-6-KETONONA-2,4-DIENEDIOIC ACID HYDROLASE (EC 3.7.1.-).  
0.00028:134:27  
ESCHERICHIA COLI.  
P77044

15

F-PLACE1003529  
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4).  
0.00047:157:27  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P18480

25

F-PLACE1003573  
T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).  
0.022:129:25  
MUS MUSCULUS (MOUSE).  
P20937

30

F-PLACE1003598  
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).  
0.0017:102:44  
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).  
P29128

35

F-PLACE1003644  
PROTEIN Q300.  
6.7e-05:24:70  
MUS MUSCULUS (MOUSE).  
Q02722

40

F-PLACE1003737  
TOLL PROTEIN PRECURSOR.  
7.3e-08:203:27  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P08953

45

F-PLACE1003772  
SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).  
3.7e-07:141:32  
HOMO SAPIENS (HUMAN).  
P81489

50

F-PLACE1003839  
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).  
1.3e-09:201:31

55

MUS MUSCULUS (MOUSE).  
P05143

F-PLACE1003845  
PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPI-  
MERASE).  
5.0e-13:103:33  
METHANOCOCCUS JANNASCHII.  
Q57664

F-PLACE1003852  
CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).  
2.0e-18:189:29  
HOMO SAPIENS (HUMAN).  
Q14246

F-PLACE1004028  
HYPOTHETICAL 9.7 KD PROTEIN IN PURC-PURL INTERGENIC REGION.  
0.97:47:31  
BACILLUS SUBTILIS.  
P12049

F-PLACE1004078  
ADSEVERIN (SCINDERIN) (SC).  
5.3e-98:176:90  
BOS TAURUS (BOVINE).  
Q28046

F-PLACE1004166  
CREB-BINDING PROTEIN.  
9.6e-08:107:34  
HOMO SAPIENS (HUMAN).  
Q92793

F-PLACE1004168  
GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1.  
6.8e-05:147:30  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P25655

F-PLACE1004199  
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!  
4.2e-05:65:52  
HOMO SAPIENS (HUMAN).  
P39188

F-PLACE1004279  
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.  
3.6e-11:166:30  
CAENORHABDITIS ELEGANS.  
P30638

F-PLACE1004282  
HISTONE H1C (CLONE XLHW2).  
0.74:73:26  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P15866

- 5 F-PLACE1004305  
RAS-RELATED PROTEIN RAC1.  
2.3e-23:161:39  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P40792
- 10 F-PLACE1004441  
PROBABLE G PROTEIN-COUPLED RECEPTOR GPR1.  
5.4e-70:156:89  
HOMO SAPIENS (HUMAN).  
P46091
- 15 F-PLACE1004450  
AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE).  
3.1e-40:196:44  
RATTUS NORVEGICUS (RAT).  
P15684
- 20 F-PLACE1004482  
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).  
0.23:26:30  
GALLUS GALLUS (CHICKEN).  
P14093
- 25 F-PLACE1004492  
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).  
1.2e-05:150:34  
BOS TAURUS (BOVINE).  
P02453
- 30 F-PLACE1004519  
ENL PROTEIN.  
0.68:170:30  
HOMO SAPIENS (HUMAN).  
Q03111
- 35 F-PLACE1004520  
PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR.  
3.5e-50:150:74  
HOMO SAPIENS (HUMAN).  
P11462
- 40 F-PLACE1004630  
INTEGRIN BETA-6 SUBUNIT PRECURSOR.  
9.1e-31:189:39  
HOMO SAPIENS (HUMAN).  
P18564
- 50 F-PLACE1004637  
MALE SPECIFIC SPERM PROTEIN MST84DA.  
0.47:29:44  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
Q01642
- 55 F-PLACE1004648  
PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
8.4e-05:89:40  
MUS MUSCULUS (MOUSE).

P05142

F-PLACE1004816

MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.

1.0e-25:117:46

HOMO SAPIENS (HUMAN).

P55083

F-PLACE1004887

SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.

8.4e-09:195:30

DROSOPHILA ERECTA (FRUIT FLY).

P13730

F-PLACE1005003

PROTASIN PRECURSOR (EC 3.4.21.-).

1.2e-24:139:40

HOMO SAPIENS (HUMAN).

Q16651

F-PLACE1005005

UBIQUITIN-CONJUGATING ENZYME E2 G2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).

2.5e-28:51:84

HOMO SAPIENS (HUMAN).

P56554

F-PLACE1005031

CHLORINE CHANNEL PROTEIN P64.

2.7e-52:142:76

BOS TAURUS (BOVINE).

P35526

F-PLACE1005239

SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55) (FRAGMENT).

0.27:78:26

ORYCTOLAGUS CUNICULUS (RABBIT).

018776

F-PLACE1005250

HYPOTHETICAL 9.0 KD PROTEIN IN ADH4 5'REGION.

0.22:35:48

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53056

F-PLACE1005383

FIBRILLIN 1 PRECURSOR.

6.7e-09:134:32

MUS MUSCULUS (MOUSE).

Q61554

F-PLACE1005410

PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.

9.5e-105:204:100

RATTUS NORVEGICUS (RAT).

P38378

F-PLACE1005426

EP 1 130 094 A2

PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 4 PRECURSOR (PSBG-4).  
3.2e-33:184:46  
HOMO SAPIENS (HUMAN).  
Q00888

5

F-PLACE1005519  
SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).  
1.2e-23:143:41  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P38692

10

F-PLACE1005539  
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).  
5.5e-05:94:37  
BRASSICA NAPUS (RAPE).  
P40603

15

F-PLACE1005544  
CELL SURFACE A33 ANTIGEN PRECURSOR.  
0.00015:132:31  
HOMO SAPIENS (HUMAN).  
Q99795

20

F-PLACE1005569  
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).  
0.00092:122:31  
EQUUS CABALLUS (HORSE).  
Q28381

25

F-PLACE1005601  
TOXIN S4C8.  
0.34:32:37  
DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).  
P25683

30

F-PLACE1005660  
SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.  
0.99:41:43  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P02841

35

F-PLACE1005669  
COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN).  
0.0078:105:37  
HOMO SAPIENS (HUMAN).  
Q02388

45

F-PLACE1005682  
THYROID RECEPTOR INTERACTING PROTEIN 9 (TRIP9).  
2.7e-12:81:41  
HOMO SAPIENS (HUMAN).  
Q15653

50

F-PLACE1005725  
HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.  
7.5e-08:142:31  
CAENORHABDITIS ELEGANS.  
Q11073

55

- 5 F-PLACE1005736  
RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).  
9.0e-11:91:37  
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).  
P54644
- 10 F-PLACE1005745  
ORM1 PROTEIN.  
2.2e-18:137:35  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P53224
- 15 F-PLACE1005768  
NEUROTOXINS I AND I'PRECURSOR (AAH I AND AAH I').  
0.63:13:69  
ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION). P01479
- 20 F-PLACE1005815  
COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).  
1.8e-12:73:50  
HOMO SAPIENS (HUMAN).  
P23508
- 25 F-PLACE1005878  
CHLORINE CHANNEL PROTEIN P64.  
1.6e-49:115:79  
BOS TAURUS (BOVINE).  
P35526
- 30 F-PLACE1005927  
HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.  
3.2e-16:152:34  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
Q09875
- 35 F-PLACE1006071  
LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).  
4.1e-08:215:26  
MUS MUSCULUS (MOUSE).  
P02469
- 40 F-PLACE1006073  
SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).  
2.1e-05:137:34  
NEPHILA CLAVIPES (ORB SPIDER).  
P46804
- 50 F-PLACE1006079  
HOMEBOX PROTEIN DLX-3.  
1.5e-58:144:83  
HOMO SAPIENS (HUMAN).  
060479
- 55 F-PLACE1006093  
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).  
3.8e-05:72:40  
HOMO SAPIENS (HUMAN).  
P17600



# EP 1 130 094 A2

F-PLACE1006208  
EBNA-2 NUCLEAR PROTEIN.  
3.8e-15:28:75  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). P12978

5

F-PLACE1006219  
UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)  
(FRAGMENT)  
2.0e-09:38:42  
KLEBSIELLA PNEUMONIAE.  
P45602

10

F-PLACE1006277  
CELL SURFACE A33 ANTIGEN PRECURSOR.  
1.2e-07:183:29  
HOMO SAPIENS (HUMAN).  
Q99795

15

F-PLACE1006290  
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).  
8.2e-39:171:43  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P43636

20

F-PLACE1006443  
HYPOTHETICAL 60.0 KD PROTEIN IN IMP1-HLJ1 INTERGENIC REGION.  
0.0010:155:27  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
Q03795

25

F-PLACE1006515  
ZINC FINGER Y-CHROMOSOMAL PROTEIN 1.  
0.046:98:28  
MUS MUSCULUS (MOUSE).  
P10925

30

F-PLACE1006716  
30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC  
PROTEIN ADIPOQ).  
3.6e-25:177:35  
MUS MUSCULUS (MOUSE).  
Q60994

40

F-PLACE1006786  
PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (BASIC PROTEIN) (WBP) (FRAGMENT).  
1.0:19:42  
TRITICUM AESTIVUM (WHEAT).  
P26913

45

F-PLACE1006809  
SLS1 PROTEIN PRECURSOR.  
0.0011:37:51  
YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).  
Q99158

50

F-PLACE1006959  
PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
5.3e-05:96:41

55

EP 1 130 094 A2

MUS MUSCULUS (MOUSE).  
P05142

5 F-PLACE1007028  
EBNA-1 NUCLEAR PROTEIN.  
5.9e-09:219:33  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03211

10 F-PLACE1007040  
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAG-  
MENT).  
0.68:138:24  
HOMO SAPIENS (HUMAN).  
15 P02812

F-PLACE1007077  
SERINE/THREONINE-PROTEIN KINASE CLA4 (EC 2.7.1.-).  
0.73:177:25  
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P48562

F-PLACE1007081  
COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).  
25 3.0e-20:182:39  
BOS TAURUS (BOVINE).  
Q28107

F-PLACE1007096  
30 HYPOTHETICAL SYMPORTER SLL1374.  
2.8e-14:162:30  
SYNECHOCYSTIS SP. (STRAIN PCC 6803).  
P74168

35 F-PLACE1007296  
ER LUMEN PROTEIN RETAINING RECEPTOR 1 (KDEL RECEPTOR 1).  
9.4e-50:120:86  
HOMO SAPIENS (HUMAN).  
P24390

40 F-PLACE1007591  
MEIOTIC RECOMBINATION PROTEIN REC104.  
0.68:73:31  
45 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P33323

F-PLACE1007626  
PTB-ASSOCIATED SPLICING FACTOR (PSF).  
0.00083:97:34  
50 HOMO SAPIENS (HUMAN).  
P23246

F-PLACE1007702  
55 ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.  
1.9e-08:87:36  
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).  
P40602

F-PLACE1007845  
 GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).  
 1.3e-16:158:40  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
 P43636

5

F-PLACE1007881  
 HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.  
 1.2e-11:113:37  
 CAENORHABDITIS ELEGANS.  
 Q19425

10

F-PLACE1007971  
 METALLOTHIONEIN 20-III ISOFORMS A AND B (MT-20-IIIA AND MT-20-IIIB).  
 1.0:32:43  
 MYTILUS EDULIS (BLUE MUSSEL).  
 P80253

15

F-PLACE1008282  
 HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).  
 8.1e-87:178:87  
 ORYCTOLAGUS CUNICULUS (RABBIT).  
 P33279

20

F-PLACE1008297  
 MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).  
 3.6e-17:187:33  
 DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).  
 P90648

25

F-PLACE1008359  
 BEM46 PROTEIN (FRAGMENT).  
 4.9e-07:103:33  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
 P54069

30

F-PLACE1008469  
 D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).  
 0.0018:78:37  
 HOMO SAPIENS (HUMAN).  
 P21917

40

F-PLACE1008549  
 FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).  
 0.0034:89:30  
 HOMO SAPIENS (HUMAN).  
 Q01543

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F-PLACE1008657  
 ADSEVERIN (SCINDERIN) (SC).  
 6.7e-127:257:91  
 BOS TAURUS (BOVINE).  
 Q28046

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F-PLACE1008716  
 ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II).

55

4.5e-20:66:78  
HOMO SAPIENS (HUMAN).  
Q10469

5 F-PLACE1008744  
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN) (PRP).  
3.6e-19:221:33  
HOMO SAPIENS (HUMAN).  
P04003

10 F-PLACE1008984  
BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (EC 6.4.1.2) (BC-CP).  
0.089:61:31  
15 GLYCINE MAX (SOYBEAN).  
Q42783

F-PLACE1008985  
20 SYNAPTOTAGMIN V.  
8.6e-09:123:35  
HOMO SAPIENS (HUMAN).  
000445

F-PLACE1009067  
25 HYPOTHETICAL 33.4 KD PROTEIN.  
4.3e-09:60:50  
HOMO SAPIENS (HUMAN).  
Q04323

30 F-PLACE1009196  
SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).  
0.050:23:34  
GORILLA GORILLA GORILLA (LOWLAND GORILLA).  
P35303

35 F-PLACE1009279  
8.6 KD TRANSGLUTAMINASE SUBSTRATE.  
1.4e-07:62:35  
40 TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).  
P81281

F-PLACE1009527  
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).  
0.037:71:38  
45 HOMO SAPIENS (HUMAN).  
Q02817

F-PLACE1009546  
50 PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
5.9e-07:86:39  
MUS MUSCULUS (MOUSE).  
P05142

F-PLACE1009600  
55 TETRACYCLINE RESISTANCE PROTEIN, CLASS H (TETA(H)).  
1.7e-08:113:31  
PASTEURELLA MULTOCIDA.  
P51564

F-PLACE1009735

TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE1 10) (VMW110) (ALPHA-0 PROTEIN).

2.6e-09:182:35

5 HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).  
P08393

F-PLACE1009982

REGULATORY PROTEIN E2.

10 0.99:94:28

HUMAN PAPILLOMAVIRUS TYPE 8.

P06422

F-PLACE1010011

15 DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2-DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT).

2.8e-20:119:42

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P17898

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F-PLACE1010078

ORM1 PROTEIN.

3.4e-20:137:37

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

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P53224

F-PLACE1010081

SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37).

1.5e-11:147:32

30 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

Q05609

F-PLACE1010251

NEL-LIKE PROTEIN (FRAGMENT).

35

1.8e-10:73:42

HOMO SAPIENS (HUMAN).

Q92832

F-PLACE1010445

40

HYPOTHETICAL BHLF1 PROTEIN.

0.0042:227:33

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03181

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F-PLACE1010713

PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).

1.5e-77:177:80

MUS MUSCULUS (MOUSE).

070503

50

F-PLACE1010784

P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (6H1).

1.7e-18:102:40

GALLUS GALLUS (CHICKEN).

55

P32250

F-PLACE1010827

COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).

2.8e-18:109:41  
CRICETULUS GRISEUS (CHINESE HAMSTER).  
P49020

5 F-PLACE1010968  
PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE  
PHOSPHOHYDROLASE).  
2.3e-06:191:28  
10 DROSOPHILA MELANOGASTER (FRUIT FLY).  
P16621

F-PLACE1011045  
HYPOTHETICAL 71.4 KD PROTEIN IN NMD3-ENO2 INTERGENIC REGION.  
6.0e-14:153:34  
15 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P38862

F-PLACE1011116  
20 GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-  
GLUCAN GLUCOHYDROLASE).  
2.3e-06:195:27  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P08640

25 F-PLACE1011181  
MSP1 PROTEIN HOMOLOG.  
4.3e-06:93:25  
CAENORHABDITIS ELEGANS.  
P54815

30 F-PLACE1011236  
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.  
4.1e-17:180:28  
CAENORHABDITIS ELEGANS.  
35 P30638

F-PLACE1011364  
HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II.  
2.1e-24:158:41  
40 CAENORHABDITIS ELEGANS.  
Q09298

F-PLACE1011407  
45 ZINC FINGER PROTEIN 140.  
3.8e-10:47:74  
HOMO SAPIENS (HUMAN).  
P52738

F-PLACE1011516  
50 HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.  
1.6e-13:117:34  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P53073

55 F-PLACE1011708  
DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR (EC 3.4.24.-).  
9.9e-22:203:32  
DROSOPHILA MELANOGASTER (FRUIT FLY).

P25723

F-PLACE1011824

SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTIVATED KINASE 3) (CDC42/RAC EFFECTOR KINASE PAK-B).

1.6e-15:103:36

MUS MUSCULUS (MOUSE).

Q61036

F-PLACE1011978

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

3.3e-55:188:50

HOMO SAPIENS (HUMAN).

Q03923

F-PLACE2000118

EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

2.8e-23:169:43

NICOTIANA TABACUM (COMMON TOBACCO).

P13983

F-PLACE2000219

MALE SPECIFIC SPERM PROTEIN MST84DA.

0.11:29:41

DROSOPHILA MELANOGASTER (FRUIT FLY).

Q01642

F-PLACE3000181

CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).

9.5e-26:193:37

DROSOPHILA MELANOGASTER (FRUIT FLY).

P33450

F-PLACE3000213

COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).

2.3e-23:191:34

HOMO SAPIENS (HUMAN).

P17927

F-PLACE4000354

E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).

3.2e-25:150:30

ORYCTOLAGUS CUNICULUS (RABBIT).

P27113

F-PLACE4000455

IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT).

0.66:52:36

HOMO SAPIENS (HUMAN).

P04433

F-SKNMC1000004

OPTOMOTOR-BLIND PROTEIN (LETHAL(1)OPTOMOTOR-BLIND) (L(1)OMB) (BIFID PROTEIN).

0.079:88:30

DROSOPHILA MELANOGASTER (FRUIT FLY).

Q24432

- 5 F-SKNMC1000014  
SCO-SPONDIN (FRAGMENT).  
0.63:60:36  
BOS TAURUS (BOVINE).  
P98167
- 10 F-SKNMC1000082  
PUTATIVE MITOCHONDRIAL CARRIER YGR096W.  
2.4e-10:93:34  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P53257
- 15 F-THYRO1000036  
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).  
0.72:69:36  
MUS MUSCULUS (MOUSE).  
P05143
- 20 F-THYRO1000061  
COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).  
0.0068:70:38  
BOS TAURUS (BOVINE).  
P25508
- 25 F-THYRO1000099  
SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).  
0.0063:207:28  
NEPHILA CLAVIPES (ORB SPIDER).  
P46804
- 30 F-THYRO1000196  
RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD).  
1.6e-10:134:32  
GALLUS GALLUS (CHICKEN).  
P24503
- 35 F-THYRO1000400  
ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).  
3.9e-28:163:38  
MUS MUSCULUS (MOUSE).  
P54116
- 40 F-THYRO1000580  
RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).  
3.3e-15:64:62  
MUS MUSCULUS (MOUSE).  
Q61751
- 50 F-THYRO1000584  
EPIDIDYMI-SPECIFIC ALPHA-MANNOSIDASE (EC 3.2.1.24) (ALPHA-D-MANNOSIDE MANNOHYDROLASE)  
(135 KD PROTEIN).  
1.5e-89:197:72  
SUS SCROFA (PIG).  
Q28949
- 55 F-THYRO1000678  
GAP JUNCTION BETA-6 PROTEIN (CONNEXIN 30) (CX30).  
7.7e-39:89:87



MUS MUSCULUS (MOUSE).  
P70689

F-THYRO1000776  
5 HIGH AFFINITY SULPHATE TRANSPORTER 2.  
3.0e-25:83:50  
STYLOSANTHES HAMATA.  
P53392

10 F-THYRO1000795  
MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN (OGCP).  
1.2e-33:227:37  
BOS TAURUS (BOVINE).  
P22292

15 F-THYRO1000846  
CUTICLE COLLAGEN 12 PRECURSOR.  
6.7e-09:190:33  
CAENORHABDITIS ELEGANS.  
20 P20630

F-THYRO1000866  
HYPOTHETICAL 146.8 KD PROTEIN C34E10.5 IN CHROMOSOME III.  
0.12:85:31  
25 CAENORHABDITIS ELEGANS.  
P46580

F-THYRO1000956  
30 PROBABLE G PROTEIN-COUPLE1) RECEPTOR APJ.  
1.3e-68:165:84  
HOMO SAPIENS (HUMAN).  
P35414

F-THYRO1000964  
35 TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).  
0.015:170:34  
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).  
P29128

40 F-THYRO1000999  
CRYPTDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C).  
0.28:40:45  
MUS MUSCULUS (MOUSE).  
P50715

45 F-THYRO1001063  
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-  
TIDE IB-6; PEPTIDE P-H].  
3.5e-05:232:32  
50 HOMO SAPIENS (HUMAN).  
P04280

F-THYRO1001071  
55 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).  
0.00061:131:33  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
P17437

EP 1 130 094 A2

- 5 F-THYRO1001102  
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).  
0.25:94:38  
HOMO SAPIENS (HUMAN).  
000268
- 10 F-THYRO1001113  
SYNAPTOTAGMIN III (SYTIII).  
2.0e-08:102:35  
MUS MUSCULUS (MOUSE).  
035681
- 15 F-THYRO1001128  
GLYCOPROTEIN X PRECURSOR.  
6.8e-07:182:31  
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).  
P28968
- 20 F-THYRO1001205  
NEUROGRANIN (NG) (PROTEIN KINASE C SUBSTRATE 7.5 KD PROTEIN) (RC3).  
0.91:33:42  
RATTUS NORVEGICUS (RAT).  
Q04940
- 25 F-THYRO1001237  
HYPOTHETICAL PROTEIN IN NIFH2 3 REGION (FRAGMENT).  
4.0e-07:68:38  
METHANOCOCCUS THERMOLITHOTROPHICUS.  
P05410
- 30 F-THYRO1001242  
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).  
1.0:104:35  
HOMO SAPIENS (HUMAN).  
35 P17600
- 40 F-THYRO1001266  
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).  
4.3e-09:119:27  
ORYCTOLAGUS CUNICULUS (RABBIT).  
P11170
- 45 F-THYRO1001327  
HYPOTHETICAL 23.7 KD PROTEIN IN CYR1-OST1 INTERGENIC REGION.  
1.7e-06:141:24  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P41544
- 50 F-THYRO1001456  
HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.  
1.1e-11:88:48  
MYCOBACTERIUM TUBERCULOSIS.  
Q10555
- 55 F-THYRO1001457  
PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).  
2.1e-68:228:59

HOMO SAPIENS (HUMAN).  
Q15139

5 F-THYRO1001471  
COLLAGEN 1(X) CHAIN PRECURSOR.  
3.9e-05:204:30  
GALLUS GALLUS (CHICKEN).  
P08125

10 F-THYRO1001478  
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.  
0.038:162:31  
HOMO SAPIENS (HUMAN).  
Q03692

15 F-THYRO1001495  
!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!  
4.8e-19:50:82  
HOMO SAPIENS (HUMAN).  
20 P39193

F-THYRO1001523  
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!  
5.0e-13:66:62  
25 HOMO SAPIENS (HUMAN).  
P39195

F-THYRO1001529  
SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT  
30 2).  
1.6e-27:115:53  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
Q09925

35 F-THYRO1001593  
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).  
3.3e-92:225:77  
HOMO SAPIENS (HUMAN).  
40 P27448

F-THYRO1001608  
PROLINE-RICH PROTEIN MP-2 PRECURSOR.  
1.2e-07:127:35  
45 MUS MUSCULUS (MOUSE).  
P05142

F-THYRO1001641  
NUC-1 NEGATIVE REGULATORY PROTEIN PREG.  
0.0039:98:31  
50 NEUROSPORA CRASSA.  
Q06712

F-THYRO1001700  
INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE (EC 2.7.1.-) (INTERFER-  
55 ON-INDUCIBLE RNA-DEPENDENT PROTEIN KINASE) (P68 KINASE) (P1/EIF-2A PROTEIN KINASE).  
3.3e-09:65:43  
HOMO SAPIENS (HUMAN).  
P19525

F-THYRO1001702  
 MYELOID UPREGULATED PROTEIN.  
 7.8e-62:161:78  
 MUS MUSCULUS (MOUSE).  
 035682

F-THYRO1001725  
 PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).  
 0.00061:82:41  
 RATTUS NORVEGICUS (RAT).  
 P20468

F-THYRO1001770  
 PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).  
 1.0e-20:165:35  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
 P53974

F-THYRO1001803  
 GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).  
 3.6e-07:221:30  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
 P08640

F-Y79AA1000030  
 TRANSCRIPTIONAL ACTIVATOR FE65.  
 4.5e-09:43:46  
 RATTUS NORVEGICUS (RAT).  
 P46933

F-Y79AA1000127  
 FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).  
 1.3e-05:72:43  
 HOMO SAPIENS (HUMAN).  
 P48023

F-Y79AA1000207  
 STANNIOCALCIN PRECURSOR (STC) (CORPUSCLES OF STANNIUS PROTEIN) (CS) (HYPOCALCIN) (TELEOCALCIN).  
 1.0:100:27  
 ANGUILLA AUSTRALIS (AUSTRALIAN EEL).  
 P18301

F-Y79AA1000226  
 HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV.  
 2.6e-07:188:28  
 CAENORHABDITIS ELEGANS.  
 P49049

F-Y79AA1000270  
 VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).  
 1.6e-102:233:87  
 BOS TAURUS (BOVINE).  
 P40682

F-Y79AA1000426  
 INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).

1.1e-14:149:38

HOMO SAPIENS (HUMAN).

P55103

5

F-Y79AA1000521

MALE SPECIFIC SPERM PROTEIN MST84DD.

0.00079:60:36

DROSOPHILA MELANOGASTER (FRUIT FLY).

Q01645

10

F-Y79AA1000750

EBNA-1 NUCLEAR PROTEIN.

2.0e-09:131:38

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

15

P03211

F-Y79AA1000776

CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).

20

0.080:44:40

SUS SCROFA (PIG).

P35323

F-Y79AA1000777

25

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

4.2e-33:204:39

THERMOMONOSPORA CURVATA.

P49695

30

F-Y79AA1000876

PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLASE BETA SUB-UNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55).

4.6e-16:115:38

BOS TAURUS (BOVINE).

35

P05307

F-Y79AA1000888

TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE).

40

2.0e-09:159:35

TREPONEMA PALLIDUM.

083802

F-Y79AA1000959

45

HOMEBOX PROTEIN HOX-B3 (HOX-2.7) (MH-23).

8.8e-08:72:38

MUS MUSCULUS (MOUSE).

P09026

F-Y79AA1000967

50

CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).

1.1e-37:202:42

RATTUS NORVEGICUS (RAT).

Q63450

55

F-Y79AA1001013

SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS : PEPTIDE P-D] (FRAGMENT).

0.038:128:28

# EP 1 130 094 A2

HOMO SAPIENS (HUMAN).  
P10162

5 F-Y79AA1001056  
HYPOTHETICAL 7.1 KD PROTEIN IN TK-VS INTERGENIC REGION.  
0.41:42:30  
BACTERIOPHAGE T4.  
P13307

10 F-Y79AA1001062  
TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).  
9.9e-13:132:38  
HOMO SAPIENS (HUMAN).  
Q13829

15 F-Y79AA1001090  
ANKYRIN HOMOLOG PRECURSOR.  
4.0e-19:176:34  
CHROMATIUM VINOSUM.  
20 Q06527

F-Y79AA1001212  
HYPOTHETICAL PROTEIN MJ0110.  
0.095:55:34  
25 METHANOCOCCUS JANNASCHII.  
Q57574

F-Y79AA1001264  
HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.  
30 3.3e-53:177:55  
CAENORHABDITIS ELEGANS.  
Q10005

F-Y79AA1001272  
35 ACROSIN PRECURSOR (EC 3.4.21.10).  
6.3e-08:78:46  
ORYCTOLAGUS CUNICULUS (RABBIT).  
P48038

40 F-Y79AA1001328  
DELTA-LIKE PROTEIN 1 PRECURSOR (DELTA1).  
1.3e-08:118:39  
RATTUS NORVEGICUS (RAT).  
P97677

45 F-Y79AA1001426  
BAND 3 ANION TRANSPORT PROTEIN.  
1.7e-18:156:32  
GALLUS GALLUS (CHICKEN).  
50 P15575

F-Y79AA1001427  
INDUCIBLE NITRATE REDUCTASE 2 (EC 1.6.6.1) (NR).  
1.1e-49:131:51  
55 GLYCINE MAX (SOYBEAN).  
P39870

F-Y79AA1001430

# EP 1 130 094 A2

RING CANAL PROTEIN (KELCH PROTEIN).  
2.5e-24:157:40  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
Q04652

5

F-Y79AA1001523  
TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).  
6.2e-15:141:39  
HOMO SAPIENS (HUMAN).  
Q13263

10

F-Y79AA1001530  
TUBULIN BETA-5 CHAIN.  
8.0e-76:204:76  
HOMO SAPIENS (HUMAN).  
P04350

15

F-Y79AA1001592  
PTB-ASSOCIATED SPLICING FACTOR (PSF).  
0.42:104:33  
HOMO SAPIENS (HUMAN).  
P23246

20

F-Y79AA1001727  
AMALGAM PROTEIN PRECURSOR.  
1.9e-09:185:28  
DROSOPHILA MELANOGASTER (FRUIT FLY).  
P15364

25

F-Y79AA1001787  
PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).  
7.6e-43:210:45  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
Q12697

30

F-Y79AA1001793  
CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).  
0.077:44:40  
SUS SCROFA (PIG).  
P35323

40

F-Y79AA1001795  
HYPOTHETICAL BHLF1 PROTEIN.  
0.00014:210:31  
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).  
P03181

45

F-Y79AA1001799  
MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.  
2.8e-18:107:44  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P23500

50

F-Y79AA1001803  
SECRETOGRANIN III PRECURSOR (SGIII).  
1.3e-68:182:76

55

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MUS MUSCULUS (MOUSE).  
P47867

F-Y79AA1001863  
GLYCOPROTEIN J.

0.030:61:32

HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).  
P06480

F-Y79AA1002022

WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).  
9.8e-08:127:37

HOMO SAPIENS (HUMAN).  
P42768

F-Y79AA1002058

CCAAT/ENHANCER BINDING PROTEIN DELTA (C/EBP DELTA) (NUCLEAR FACTOR NF-IL6-BETA) (NF-IL6-BETA).

0.28:56:42

HOMO SAPIENS (HUMAN).  
P49716

F-Y79AA1002121

D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN).  
0.71:57:36

MUS MUSCULUS (MOUSE).  
Q60925

F-Y79AA1002129

TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).  
0.98:158:24

PSEUDOMONAS AERUGINOSA.  
P15276

F-Y79AA1002213

HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.  
4.7e-39:218:41

CAENORHABDITIS ELEGANS.  
Q03567

F-Y79AA1002334

HYPOTHETICAL PROTEIN MJ1345.  
1.8e-08:164:26

METHANOCOCCUS JANNASCHII.  
Q58741

F-Y79AA1002373

CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).

0.083:44:40

SUS SCROFA (PIG).  
P35323

F-Y79AA1002376

DYNEIN INTERMEDIATE CHAIN 2, CYTOSOLIC (DH IC-2).  
3.0e-91:214:83

RATTUS NORVEGICUS (RAT).  
Q62871



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F-Y79AA1002378  
ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).  
1.0e-59:163:74  
MUS MUSCULUS (MOUSE).  
Q07231

F-Y79AA1002381  
CELL DIVISION CONTROL PROTEIN 28 (EC 2.7.1.-).  
9.5e-41:179:38  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
P00546

Homology search result 6

[0296] The result of the homology search in the GenBank(<http://www.ncbi.nlm.nih.gov/web/GenBank/>) using the clone sequences of the 5'-ends. except EST and STS sequences

Indicated are from the top,  
the name of the clone sequence,  
definition of the top hit data,  
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),  
the Accession No. of the top hit data.

[0297] Data were not shown for the clones in which the P-value was higher than 1.

F-BNGH41000020  
H.sapiens mitochondrial DNA, complete genome.  
6.0e-188:913:97  
X93334

F-BNGH41000087  
Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.  
7.1e-32:176:99  
AL034418

F-BNGH41000091  
Homo sapiens potassium channel h-eag.  
1.6e-79:687:76  
AJ001366

F-HEMBA1000006  
S.erythraea second and third ORF's of eryA gene, complete cds.  
0.95:243:64  
M63677

F-HEMBA1000121  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SE-  
QUENCE.  
5.9e-70:450:89  
AL031291

F-HEMBA1000128  
Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-14, complete sequence.  
1.0:274:59  
Z98549

F-HEMBA1000275

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Herpes simplex virus type 2 (strain HG52), complete genome.  
0.036:625:55  
Z86099

- 5 F-HEMBA1000300  
Homo sapiens chromosome 17, clone hRPK.178\_C\_3, complete sequence.  
1.4e-40:343:80  
AC005702
- 10 F-HEMBA1000349  
Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence.  
7.5e-65:451:72  
AC005922
- 15 F-HEMBA1000443  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING DRAFT SE-  
QUENCE.  
8.1e-77:216:95  
Z93241
- 20 F-HEMBA1000462  
Caenorhabditis elegans cosmid C49H3.  
3.7e-06:98:82  
U42436
- 25 F-HEMBA1000477  
Mus musculus BALB/c putative growth factor GDF7 (Gdf7) gene, partial cds.  
9.1e-05:190:65  
U08339
- 30 F-HEMBA1000590  
Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphig-  
lycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG  
island, complete sequence.  
3.0e-102:209:99  
AL021578
- 35 F-HEMBA1000634  
\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1,  
WORKING DRAFT SEQUENCE, 15 unordered pieces.  
2.0e-95:460:99  
AC004480
- 40 F-HEMBA1000671  
Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.  
1.5e-28:259:69  
AC006116
- 45 F-HEMBA1000713  
Homo sapiens 10kD protein (BC10) mRNA, complete cds.  
6.5e-126:442:97  
AF053470
- 50 F-HEMBA1000732  
Homo sapiens clone IMAGE Consortium 302831 latent transforming growth factor-beta binding protein 4 mRNA,  
partial cds.  
1.7e-45:258:94  
AF054502
- 55

F-HEMBA1000745

Streptomyces coelicolor cosmid 3F9.

3.5e-06:360:61

AL023862

5

F-HEMBA1000835

Homo sapiens fibrillin mRNA, complete cds.

1.3e-07:151:69

L13923

10

F-HEMBA1000875

Human Krueppel-type zinc finger protein (ZNF169) gene, partial cds.

2.6e-28:249:81

U28322

15

F-HEMBA1000907

Spermatozopsis similis mRNA for 95 kD basal apparatus-protein.

3.4e-09:599:60

AJ001438

20

F-HEMBA1000940

Homo sapiens connexin46.6 (Cx46.6) gene, complete cds.

1.7e-16:307:66

AF014643

25

F-HEMBA1000962

Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.

0.00040:497:59

AC004228

30

F-HEMBA1001184

Homo sapiens SH3 domain binding glutamic acid-rich-like protein (SH3BGRL) mRNA, complete cds.

8.8e-23:404:67

AF042081

35

F-HEMBA1001221

Human transmembrane protein mRNA, complete cds.

2.4e-42:858:63

U19878

40

F-HEMBA1001228

Human germline oligomeric matrix protein (COMP) mRNA, complete cds.

1.9e-82:470:91

L32137

45

F-HEMBA1001272

Human Ig gamma-2 heavy chain switch region.

0.032:549:60

U39934

50

F-HEMBA1001296

H.sapiens mRNA for PQ-rich protein.

6.9e-07:73:98

Z50194

55

F-HEMBA1001297

Homo sapiens putative transcription factor CA150 mRNA, complete cds.

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9.3e-14:143:81  
AF017789

F-HEMBA1001390

Mus musculus polymerase I-transcript release factor mRNA, complete cds.  
2.5e-56:464:81  
AF036249

F-HEMBA1001563

Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo) gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.  
3.1e-06:210:68  
AL022165

F-HEMBA1001621

Human G protein-coupled receptor APJ gene, complete cds.  
2.0e-98:516:95  
U03642

F-HEMBA1001878

Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.  
1.0e-170:810:98  
AF090988

F-HEMBA1001886

Human repressor transcriptional factor (ZNF85) mRNA, complete cds.  
3.3e-114:849:80  
U35376

F-HEMBA1002048

HS\_3058\_B2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=22 Row=B, genomic survey sequence.  
3.8e-11:244:66  
AQ103440

F-HEMBA1002131

Homo sapiens mRNA for KIAA0584 protein, partial cds.  
3.5e-44:709:66  
AB011156

F-HEMBA1002163

Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.  
2.3e-28:373:71  
AC002489

F-HEMBA1002164

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SE-  
QUENCE.  
1.3e-127:493:99  
AL031427

F-HEMBA1002167

Rattus norvegicus neuroligin I mRNA, complete cds.  
8.1e-155:850:91  
U22952

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F-HEMBA1002178

Homo sapiens mRNA for KIAA0584 protein, partial cds.

2.6e-46:794:65

AB011156

5

F-HEMBA1002195

Human lysosomal alpha-mannosidase (manB) gene, 5' flanking region and exon 1.

7.7e-35:255:86

U60885

10

F-HEMBA1002227

Homo sapiens mRNA for 80K-L protein, complete cds.

3.8e-137:382:95

D10522

15

F-HEMBA1002239

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-485G10, complete sequence.

4.5e-43:452:74

AC003049

20

F-HEMBA1002316

Homo sapiens DNA sequence from PAC 29C18 on chromosome 22.

3.0e-22:609:67

Z97192

25

F-HEMBA1002420

Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.

4.2e-142:322:98

AC005632

30

F-HEMBA1002421

Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.

1.3e-165:778:98

J04621

35

F-HEMBA1002524

Homo sapiens clone UWGC:y55c025 from 6p21, complete sequence.

1.3e-153:313:96

AC004209

40

F-HEMBA1002551

Human potential CENP-C binding target sequence, 0.7 kb clone, partial sequence 2.

6.1e-16:108:97

U57994

45

F-HEMBA1002767

Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.

1.4e-168:798:98

AF038660

50

F-HEMBA1002985

HS\_3165\_A2\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3165 Col=16 Row=E, genomic survey sequence.

1.7e-08:127:76

AQ142051

55

F-HEMBA1002992

RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67815, genomic survey sequence.

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2.7e-11:119:86  
AQ201833

5 F-HEMBA1003047  
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.  
4.5e-187:873:99  
AF034611

10 F-HEMBA1003072  
Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.  
4.1e-50:515:73  
U68380

15 F-HEMBA1003101  
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.  
5.3e-139:671:98  
AF049891

20 F-HEMBA1003120  
Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.  
3.3e-44:213:73  
AC006116

25 F-HEMBA1003230  
Homo sapiens UP50 mRNA, complete cds.  
5.5e-183:856:98  
AF093118

30 F-HEMBA1003294  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 495010, WORKING DRAFT SE-  
QUENCE.  
4.2e-38:558:69  
AL031121

35 F-HEMBA1003315  
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence.  
1.2e-61:737:68  
AB013390

40 F-HEMBA1003392  
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.  
2.9e-183:851:99  
AF074264

45 F-HEMBA1003399  
Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.  
8.7e-16:215:74  
AC005282

50 F-HEMBA1003487  
H.sapiens DNA sequence.  
0.0075:158:67  
Z22340

55 F-HEMBA1003497  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2705, WORKING DRAFT SEQUENCE.  
1.1e-109:538:98  
AL033529

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5 F-HEMBA1003530  
S.scrofa mRNA for BM88 antigen.  
2.8e-47:644:69  
X82027

10 F-HEMBA1003602  
Human (lambda) DNA for immunoglobulin light chain.  
2.5e-94:551:91  
D86997

15 F-HEMBA1003732  
Homo sapiens clone DJ0935K16, complete sequence.  
6.1e-151:777:96  
AC006011

20 F-HEMBA1003945  
Homo sapiens clone 638 unknown mRNA, complete sequence.  
1.8e-76:310:93  
AF091085

25 F-HEMBA1004007

30 F-HEMBA1004067  
Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S  
ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.  
8.7e-133:718:94  
AL031864

35 F-HEMBA1004085  
Homo sapiens, clone hRPK.2\_A\_1, complete sequence.  
2.7e-58:256:80  
AC006197

40 F-HEMBA1004110  
Homo sapiens intersectin short form mRNA, complete cds.  
3.8e-159:779:96  
AF064243

45 F-HEMBA1004250  
Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.  
1.2e-183:863:99  
AC005752

50 F-HEMBA1004391  
H.sapiens gene for neural cell adhesion molecule L1.  
0.51:426:59  
Z29373

55 F-HEMBA1004444  
Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.  
3.3e-147:463:93  
AC004938

F-HEMBA1004454  
Homo sapiens tetraspan NET-4 mRNA, complete cds.  
0.00036:230:62  
AF065389

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F-HEMBA1004505

D.melanogaster mRNA for alpha 1,2 mannosidase.

5.5e-17:663:58

X82640

5

F-HEMBA1004785

Gallus gallus mRNA for chromobox protein (CHCB3), complete cds.

6.6e-19:322:68

AB005619

10

F-HEMBA1004797

Haemonchus contortus GT microsatellite DNA sequence.

3.0e-08:175:71

U84474

15

F-HEMBA1004952

Mus musculus recombinant quaking gene sequence.

4.8e-15:398:65

U44942

20

F-HEMBA1004971

F-HEMBA1004982

25

F-HEMBA1005070

Human mRNA for KIAA0310 gene, complete cds.

2.5e-65:370:93

AB002308

30

F-HEMBA1005084

Mouse transcriptional control element.

0.0024:189:63

M17284

35

F-HEMBA1005145

Pseudorabies virus glycoprotein gp50 gene, complete cds.

0.00022:395:60

AF092447

40

F-HEMBA1005230

Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.

2.8e-102:302:94

AC006116

45

F-HEMBA1005246

Homo sapiens CAGH44 mRNA, partial cds.

5.0e-29:429:66

U80741

50

F-HEMBA1005267

Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.

1.0e-43:320:87

AF042089

55

F-HEMBA1005337

Plasmodium falciparum MAL3P6, complete sequence.

4.1e-08:84:89



Z98551

F-HEMBA1005430

5 F-HEMBA1005449  
T.aestivum mRNA for a proline-rich protein.  
0.00097:385:61  
X52472

10 F-HEMBA1005489  
Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na<sup>+</sup>-isocitrate dehydrogenase gamma subunit (IDH), and trans-locon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq281u1 gene and cytochrome C (CCp) pseudogene.  
15 7.8e-16:405:62  
U52111

F-HEMBA1005522  
O.cuniculus rACNG mRNA for aorta CNG channel.  
20 5.9e-47:344:85  
X59668

F-HEMBA1005545  
Human m3 muscarinic acetylcholine receptor (CHRM3) gene, complete cds.  
25 5.1e-173:810:98  
U29589

F-HEMBA1005698

30 F-HEMBA1005913  
HS\_2249\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2249  
Col=1 Row=J, genomic survey sequence.  
0.17:215:61  
AQ072649

35 F-HEMBA1005929  
Homo sapiens chromosome 19, cosmid R31237, complete sequence.  
7.0e-107:285:93  
AC005581

40 F-HEMBA1005945  
Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete cds.  
1.8e-46:670:65  
AF004161

45 F-HEMBA1006016  
CIT-HSP-2334L16.TF CIT-HSP Homo Sapiens genomic clone 2334L16, genomic survey sequence.  
2.1e-13:246:69  
AQ038406

50 F-HEMBA1006171

F-HEMBA1006276  
Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.  
55 1.4e-144:416:93  
AC005261

F-HEMBA1006299

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F-HEMBA1006311

F-HEMBA1006335

Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.

9.6e-61:370:91

AL023582

F-HEMBA1006357

Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds.

2.3e-26:389:67

AF005038

F-HEMBA1006430

Caenorhabditis elegans cosmid T12A2.

4.6e-23:283:72

U13019

F-HEMBA1006482

Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.

1.9e-144:575:98

AF026852

F-HEMBA1006517

F-HEMBA1006544

Homo sapiens suppressor of white-apricot homolog 2 (SWAP2) gene, exons 12 and 13.

2.3e-151:732:97

AF042809

F-HEMBA1006572

HS\_3058\_B2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=22 Row=B, genomic survey sequence.

1.9e-45:245:96

AQ103440

F-HEMBA1006658

Homo sapiens mRNA for KIAA0687 protein, partial cds.

3.6e-127:646:95

AB014587

F-HEMBA1006707

Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

1.7e-118:397:98

AL021578

F-HEMBA1006724

H.sapiens CpG island DNA genomic Mse1 fragment, clone 40c2, forward read cpg40c2.ft1k.

1.4e-53:282:97

Z55440

F-HEMBA1006749

Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

3.9e-116:457:98

AL021578

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- 5 F-HEMBA1006770  
Xenopus laevis elav-type ribonucleoprotein (etr-1) mRNA, complete cds.  
1.6e-53:280:81  
U16800
- 10 F-HEMBA1006902  
Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.  
4.9e-122:462:98  
AL021578
- 15 F-HEMBA1006912
- 20 F-HEMBA1006916  
Homo sapiens Grb14 mRNA, complete cds.  
1.6e-118:651:92  
L76687
- 25 F-HEMBA1006960  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 110F11, WORKING DRAFT SEQUENCE.  
0.20:298:60  
AL033526
- 30 F-HEMBA1007013  
Rattus norvegicus repeat element associated with the Rasgrf1 gene.  
8.0e-07:531:59  
AF056927
- 35 F-HEMBA1007057  
Human DNA sequence from clone 522J7 on chromosome 22q13.3. Contains part of a 60S Ribosomal protein L5 pseudogene and a Peregrin (BR140) LIKE gene downstream of a putative CpG island. Contains ESTs, STSs and GSSs, complete sequence.  
0.27:277:64  
Z98885
- F-HEMBA1007063
- 40 F-HEMBA1007226  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310013, WORKING DRAFT SEQUENCE.  
0.00033:488:63  
AL031658
- 45 F-HEMBA1007241  
Caenorhabditis elegans cosmid T15B7.  
0.068:304:59  
AF022985
- 50 F-HEMBA1007291  
Homo sapiens chromosome 19, fosmid 37502, complete sequence.  
6.2e-123:587:98  
AC004755
- 55 F-HEMBA1007332  
Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.  
1.3e-30:172:97  
U56430

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F-HEM BB1000106

Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudogene similar to U-SNRNP-associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete sequence.  
0.033:332:61

AL030995

F-HEM BB1000276

Dictyostelium discoideum gene encoding a novel glycoprotein.  
0.00070:440:60

AJ005262

F-HEM BB1000309

Homo sapiens zinc finger protein (MBLL) mRNA, complete cds.  
7.6e-34:180:100

AF061261

F-HEM BB1000407

Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces. 0.16:228:64  
AC000384

F-HEM BB1000447

Homo sapiens JWA protein mRNA, complete cds.  
1.4e-158:750:98

AF070523

F-HEM BB1000542

Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.

4.3e-141:874:89

Z99496

F-HEM BB1000567

Human DNA for insulin-like growth factor II (IGF-2); exon 7 and additional ORF.  
9.7e-122:572:99

X07868

F-HEM BB1000642

F-HEM BB1000668

Caenorhabditis elegans cosmid K06A5.  
0.00041:174:64

AF039038

F-HEM BB1000679

C.familiaris mRNA for TRAM-protein.  
6.1e-100:756:80

X63678

F-HEM BB1000881

Danio rerio mRNA for MINDIN2, complete cds.  
6.2e-40:581:66

AB006085

F-HEM BB1000905

Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.  
4.9e-91:209:94

AC005089

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5 F-HEMBB1001026  
Human p76 mRNA, complete cds.  
1.9e-06:410:61  
U81006

10 F-HEMBB1001048  
Human Hpast (HPAST) mRNA, complete cds.  
6.8e-55:524:75  
AF001434

15 F-HEMBB1001200  
Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9  
unordered pieces.  
4.4e-12:794:59  
AC004157

20 F-HEMBB1001407  
Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1  
ordered pieces.  
2.7e-43:281:91  
AC004150

25 F-HEMBB1001530  
HS\_2255\_B1\_F05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens  
genomic clone Plate=2255 Col=9 Row=L, genomic survey sequence.  
2.1e-14:95:97  
AQ131814

30 F-HEMBB1001547  
S.cerevisiae chromosome VII reading frame ORF YGL236c.  
1.1e-19:550:61  
Z72758

35 F-HEMBB1001573  
Homo sapiens 12p13.3 PAC RPCI5-951N9 (Roswell Park Cancer Institute Human PAC library) complete se-  
quence.  
2.7e-07:467:60  
AC004672

40 F-HEMBB1001847  
H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read cpg13d12.r11c.  
1.1e-14:94:100  
Z64565

45 F-HEMBB1001959  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SE-  
QUENCE.  
1.2e-82:492:90  
AL034405

50 F-HEMBB1001978  
Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.  
7.0e-23:239:76  
AC005386

55 F-HEMBB1002039  
Human DNA sequence from cosmid 315B17, between markers DXS366 and DXS87 on chromosome X contains  
ESTs.

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3.5e-49:605:71  
Z73967

F-HEM BB1002041

R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).  
3.5e-09:501:60  
X83546

F-HEM BB1002051

Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds.  
3.1e-95:454:99  
AF049703

F-HEM BB1002120

F-HEM BB1002162

Homo sapiens genethonin 1 mRNA, complete cds.  
7.0e-67:328:99  
AF062534

F-HEM BB1002228

Homo sapiens unknown mRNA, complete cds.  
1.6e-39:208:98  
AF047439

F-HEM BB1002245

Rattus norvegicus prostaglandin F2a receptor regulatory protein precursor, mRNA, complete cds.  
3.7e-68:424:87  
U26595

F-HEM BB1002302

RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey sequence.  
2.7e-15:101:98  
B88081

F-HEM BB1002427

Homo sapiens chromosome 9q34, clone 70C11, complete sequence.  
2.9e-123:249:90  
AC002319

F-HEM BB1002465

Mouse short chain acyl-CoA dehydrogenase mRNA, complete cds.  
7.9e-18:545:61  
L11163

F-HEM BB1002661

Drosophila melanogaster; Chromosome 2R; Region 44A1-44A2; P1 clone DS07435, WORKING DRAFT SE-  
QUENCE, 2 unordered pieces.  
1.9e-07:187:67

AC005445

F-HEM BB1002663

F-HEM BB1002693

Homo sapiens full length insert cDNA, clone ZD85G07.  
2.1e-20:136:93  
AF086462

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F-MAMMA1000046

CIT-HSP-2166017.TF CIT-HSP Homo sapiens genomic clone 2166017, genomic survey sequence.

2.0e-60:345:92

B92334

5

F-MAMMA1000102

Human DNA sequence from cosmid B33F2 on chromosome 22 Contains ESTs.

3.0e-161:766:98

Z79996

10

F-MAMMA1000106

Rat gene for alpha 1B adrenergic receptor, promoter region and partial cds.

0.0025:247:64

D32045

15

F-MAMMA1000118

Canis familiaris beta1 adrenergic receptor (dogbeta1) gene, complete cds.

6.1e-06:545:60

U73207

20

F-MAMMA1000141

Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.

1.5e-10:151:78

AC004024

25

F-MAMMA1000204

Homo Sapiens mRNA for LGMD2B protein.

2.1e-166:781:98

AJ007670

30

F-MAMMA1000226

\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.

2.9e-35:188:100

AC004064

35

F-MAMMA1000403

Human vascular addressin MAdCAM-1 mRNA, complete cds.

0.00043:538:59

U82483

40

F-MAMMA1000449

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317C6, WORKING DRAFT SEQUENCE.

0.090:514:60

Z97651

45

F-MAMMA1000457

H.sapiens mRNA for NADH-cytochrome b5 reductase.

5.5e-36:469:68

Y09501

50

F-MAMMA1000473

Caenorhabditis elegans cosmid B0491, complete sequence.

0.0052:187:64

Z49907

55

F-MAMMA1000496

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Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.  
1.2e-81:318:92  
AC004997

5 F-MAMMA1000528  
P.falciparum complete gene map of plastid-like DNA (IR-B).  
0.016:343:58  
X95276

10 F-MAMMA1000591  
Mus musculus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase-T3 mRNA, complete cds.  
1.2e-24:493:63  
U70538

15 F-MAMMA1000614  
\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1,  
WORKING DRAFT SEQUENCE, 21 unordered pieces.  
7.5e-13:615:60  
AC004670

20 F-MAMMA1000652  
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.  
1.6e-59:451:82  
AC004638

25 F-MAMMA1000681  
Homo sapiens mRNA for putative G-protein coupled receptor, EDG6.  
1.2e-32:636:65  
AJ000479

30 F-MAMMA1000706  
\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0110D16; HTGS phase 1,  
WORKING DRAFT SEQUENCE, 7 unordered pieces.  
6.8e-06:428:62  
35 AC004578

F-MAMMA1000788  
HS\_3080\_A2\_B03\_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080  
Col=6 Row=C, genomic survey sequence.  
40 4.9e-35:204:94  
AQ128409

F-MAMMA1000810  
Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.  
45 5.8e-06:246:65  
AL022098

F-MAMMA1000814  
Anadara trapezia (alpha 3.15L) hemoglobin alpha-chain (HBA) gene, exons 2 and 3, intron 2, including hypervar-  
50 iable microsatellite polymorphic repeat regions.  
1.0e-12:176:75  
L25098

F-MAMMA1000881  
55 Rattus norvegicus serum and glucocorticoid-regulated kinase (sgk) mRNA, complete cds.  
2.8e-07:283:63  
L01624



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F-MAMMA1000986

Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.

1.8e-166:306:99

AF001550

5

F-MAMMA1000994

Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.

0.75:260:61

AL021897

10

F-MAMMA1001043

H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2).

0.038:376:60

Z37976

15

F-MAMMA1001066

Homo sapiens DNA from chromosome 19-cosmid f24590 containing CAPNS and POL2RI, genomic sequence.

4.4e-15:162:72

AD001527

20

F-MAMMA1001094

Homo sapiens clone 243 unknown mRNA, complete sequence.

6.2e-181:844:99

AF091094

25

F-MAMMA1001141

Cams familiaris beta1 adrenergic receptor (dogbeta1) gene, complete cds.

1.3e-10:602:59

U73207

30

F-MAMMA1001150

M.musculus (Balb/c) mRNA for serine/threonine protein kinase.

7.7e-57:447:67

Z34524

35

F-MAMMA1001237

Rattus norvegicus monocarboxylate transporter MCT3 mRNA, complete cds.

1.5e-08:306:65

AF059258

40

F-MAMMA1001284

HS\_3076\_A1\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3076 Col=15 Row=K, genomic survey sequence.

5.2e-53:307:93

AQ120674

45

F-MAMMA1001310

1(2)09851 Drosophila melanogaster P lethal line Drosophila melanogaster genomic Sequence recovered from 3' end of P element, genomic survey sequence.

0.00072:209:66

AQ025672

50

F-MAMMA1001344

Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit homolog (CCA1) and putative protein 2 (PUT2) genes, partial cds, complete sequence.

5.2e-05:164:67

55

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AF026198

F-MAMMA1001418

Human Na<sup>+</sup>/nucleoside cotransporter (hCNT1a) mRNA, complete cds.

6.0e-35:622:63

U62966

F-MAMMA1001532

Homo sapiens PAC clone DJ0728D04, complete sequence.

5.2e-46:538:74

AC004865

F-MAMMA1001609

Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence. 0.00031:592:57

AC005886

F-MAMMA1001615

H.sapiens CpG island DNA genomic MseI fragment, clone 71h9, reverse read cpg71h9.rt1a.

1.2e-25:146:99

Z62710

F-MAMMA1001623

Homo sapiens 12q24.2 BAC RPCI11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

3.9e-69:471:85

AC006065

F-MAMMA1001634

Human DNA sequence from PAC 93C23 on chromosome X. Contains steroid 5-alpha-reductase pseudogene, ESTs and STS.

2.2e-22:228:79

AL008713

F-MAMMA1001893

HS\_3067\_B2\_H09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=18 Row=P, genomic survey sequence.

2.5e-29:188:93

AQ138065

F-MAMMA1001901

Human DNA sequence from clone 354J5 on chromosome 6q21-22. Contains pseudogene similar to zinc finger protein (ZPR1), EST, STS, GSS, complete sequence.

2.0e-23:287:71

Z95118

F-MAMMA1001957

Drosophila melanogaster, chromosome 2L, region 21C5-21D1, P1 clone DS07610, complete sequence.

1.5e-14:192:66

AC004573

F-MAMMA1001978

Human immunoglobulin S(u) like sequence.

0.60:150:66

X15517

F-MAMMA1002070

Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.

3.9e-116:250:93

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AC002073

F-MAMMA1002080

Mus musculus chromosome 11, clone mCIT.268\_P\_23, complete sequence.

5 1.1e-59:493:78

AC004807

F-MAMMA1002087

HS-1047-B2-A09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=18 Row=B, genomic survey sequence.

10 2.1e-31:174:98

B38457

F-MAMMA1002091

Homo sapiens CD39L2 (CD39L2) mRNA, complete cds.

15 1.6e-156:743:98

AF039916

F-MAMMA1002095

Rat alternatively spliced mRNA.

20 4.9e-126:691:91

M93017

F-MAMMA1002128

Mus musculus C2C12 unknown mRNA, partial cds.

25 5.0e-41:353:77

U31629

F-MAMMA1002142

30

F-MAMMA1002165

Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.

1.2e-34:219:90

AF100780

35

F-MAMMA1002205

Homo Sapiens Chromosome X clone bWXD691, complete sequence.

8.1e-33:535:67

AC004386

40

F-MAMMA1002224

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.

1.2e-31:274:82

Z86090

45

F-MAMMA1002234

Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).

9.8e-145:736:91

X53744

50

F-MAMMA1002586

Drosophila melanogaster cosmid clone 86E4.

0.0071:306:58

AL021086

55

F-MAMMA1002633

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.

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3.9e-33:297:79  
AL031680

5 F-MAMMA1003126  
Human Hpast (HPAST) mRNA, complete cds.  
1.7e-82:801:74  
AF001434

10 F-NT2RM1000407  
Cloning vector pUC-GM-INT, complete sequence.  
9.4e-141:673:98  
AF025392

15 F-NT2RM1000462  
, complete sequence.  
1.5e-86:232:82  
AC005300

20 F-NT2RM1000542  
Mouse beta-galactosidase (BGAL) gene, complete cds.  
4.4e-17:468:62  
M57734

25 F-NT2RM1000580  
Caenorhabditis elegans cosmid F09E5.  
1.6e-08:352:61  
U37429

30 F-NT2RM1000789  
Homo sapiens mRNA for hTCF-4.  
1.1e-94:299:92  
Y11306

35 F-NT2RM1000855  
Canis familiaris sec61 homologue mRNA, complete cds.  
6.6e-110:671:87  
M96629

40 F-NT2RM1000858  
tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].  
2.0e-65:716:70  
S70011

45 F-NT2RM1000899  
S.pombe chromosome I cosmid c8C9.  
0.0010:300:59  
Z99168

50 F-NT2RM2000241  
Homo sapiens chromosome 12p13.3 clone RPC11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.  
0.99:201:65  
AC005844

55 F-NT2RM2000306  
Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.  
1.1e-142:595:97

AL021878

F-NT2RM2000410

*S.gregaria* Abd-B gene.

0.076:172:66

X69161

F-NT2RM2000423

*Arthrobacter* sp. beta-galactosidase gene, complete cds.

4.2e-06:606:57

U78028

F-NT2RM2000497

*Homo sapiens* chromosome 17, clone hRPK.215\_P\_18, complete sequence.

1.2e-55:285:81

AC005969

F-NT2RM2000514

F-NT2RM2000565

*Caenorhabditis elegans* cosmid F28C5, complete sequence.

4.2e-18:539:62

Z68315

F-NT2RM2000582

*P.zebra* microsatellite locus DNA, 429bp.

0.00015:160:69

X99784

F-NT2RM2000589

*Bos taurus* myosin X, complete cds.

3.4e-139:817:88

U55042

F-NT2RM2000622

*H.sapiens* MFH-1 gene.

0.0010:466:57

Y08223

F-NT2RM2000632

*Homo sapiens* mRNA for TBP-associated factor 170 (TAFII170).

0.0052:331:59

AJ001017

F-NT2RM2000773

*Oryctolagus cuniculus* serum amyloid A-activating factor SAF-8 mRNA, partial cds.

2.9e-91:496:93

AF076786

F-NT2RM2001126

*Homo sapiens* multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds.

1.6e-161:663:99

AF093419

F-NT2RM2001558

*Homo sapiens* protein kinase A binding protein AKAP110 mRNA, complete cds.

1.2e-164:770:98

AF093408

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F-NT2RM2001626

F.rubripes GSS sequence, clone 060E22bA4, genomic survey sequence.

4.5e-46:606:68

Z88651

5

F-NT2RM2001643

HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT775  
Col=18 Row=J, genomic survey sequence.

2.5e-06:181:66

B41504

10

F-NT2RM2001738

S.capreolus ard2 gene and orf2, orf4 and orf5.

0.41:273:63

Y11036

15

F-NT2RM2001767

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.

8.0e-18:130:92

AL034380

20

F-NT2RM2001792

Homo sapiens mRNA for serum lectin P35, complete cds.

2.5e-12:244:67

D49353

25

F-NT2RM2001818

F-NT2RM2001902

Drosophila melanogaster mRNA for p21 activated kinase related protein.

7.2e-74:683:75

AJ011578

30

F-NT2RM2001939

Human G protein-coupled receptor GPR-NGA gene, complete cds.

1.4e-140:702:96

U55312

35

F-NT2RM2001941

Human gene for muscarinic acetylcholine receptor HM1.

6.3e-20:488:62

X15263

40

F-NT2RM4000100

Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.

7.7e-25:162:74

AC004827

45

F-NT2RM4000115

F-NT2RM4000198

F-NT2RM4000284

Human IgG Fc receptor hFcRn mRNA, complete cds.

7.3e-37:194:98

U12255

55

F-NT2RM4000295

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Streptomyces chrysomallus actinomycin synthetase II (acmB) gene, complete cds.  
1.6e-05:642:59  
AF047717

5 F-NT2RM4000326  
Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.  
1.0e-127:340:92  
AJ003147

10 F-NT2RM4000417  
Oncorhynchus kisutch microsatellite OKi20 DNA.  
0.44:144:66  
AF055444

15 F-NT2RM4000444  
S.salar mRNA for transport-associated protein Tap2A.  
1.7e-27:577:62  
Z83328

20 F-NT2RM4000587  
Homo sapiens chromosome 19, cosmid R28058, complete sequence.  
7.7e-16:388:64  
AC005615

25 F-NT2RM4000593

F-NT2RM4000648  
M.musculus mRNA for K-glypican.  
30 1.4e-50:610:70  
X83577

F-NT2RM4000761  
Human mitochondrial DNA, fragment M1, encoding transfer RNAs, cytochrome oxidase I, and 2 URFs.  
35 4.8e-167:787:98  
M10546

F-NT2RM4000965  
S.scrofa mRNA for calcium release channel (CRC).  
40 0.044:356:60  
X62880

F-NT2RM4000997

45 F-NT2RM4001321  
HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=18 Row=J, genomic survey sequence.  
1.3e-06:181:67  
B41504

50 F-NT2RM4001325  
Homo sapiens mRNA for chondroitin 6-sulfotransferase, complete cds.  
6.6e-12:384:64  
AB012192

55 F-NT2RM4001377  
Homo sapiens mRNA for KIAA0638 protein, partial cds.  
9.7e-155:719:99

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AB014538

F-NT2RM4001735

5 Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 483K16, WORKING DRAFT SE-  
QUENCE.

1.3e-162:679:96

AL034374

F-NT2RM4001768

10 Human HepG2 partial cDNA, clone hrnd3a07m5.

2.7e-52:271:98

D17020

F-NT2RM4001843

15

F-NT2RM4002352

Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.

1.4e-155:761:97

AB009462

20

F-NT2RP1000002

Mouse cAMP-dependent protein kinase beta subunit gene, exon 1.

1.7e-06:252:65

M21096

25

F-NT2RP1000050

Human HepG2 partial cDNA, clone hmd3g02m5.

7.1e-18:115:97

D17047

30

F-NT2RP1000181

Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),  
complete sequence.

4.2e-139:427:98

AC004228

35

F-NT2RP1000239

Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.

1.4e-90:524:91

U92989

40

F-NT2RP1000261

Homo sapiens hPMS1 gene, promoter region and exon 1.

2.5e-14:132:85

AB006462

45

F-NT2RP1000271

Homo sapiens DNA-binding protein mRNA, complete cds.

4.3e-139:678:97

AF038951

50

F-NT2RP1000300

Homo sapiens, complete sequence.

0.012:146:69

AC005854

55

F-NT2RP1000325

H.sapiens gene for phosphate carrier.



4.2e-110:438:98  
X77337

5 F-NT2RP1000448  
Streptomyces coelicolor cosmid 1A6.  
0.79:209:61  
AL023496

10 F-NT2RP1000465  
Mus musculus nuclear protein NIP45 mRNA, complete cds.  
2.2e-29:489:68  
U76759

15 F-NT2RP1000468  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SE-  
QUENCE.  
1.6e-49:306:91  
AL034405

20 F-NT2RP1000551  
Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds.  
7.5e-139:742:93  
U09585

25 F-NT2RP1000579  
Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds.  
3.6e-140:798:91  
L21936

30 F-NT2RP1000613  
Sequence 1 from patent US 5589579.  
8.1e-10:468:58  
I32995

35 F-NT2RP1000679  
Homo sapiens chromosome 17, clone hRPC.4\_G\_17, complete sequence.  
1.3e-112:448:89  
AC003688

40 F-NT2RP1000740  
H.sapiens CpG island DNA genomic Mse1 fragment, clone 34a2, reverse read cpg34a2.rt1a.  
9.3e-14:211:73  
Z60772

45 F-NT2RP1000903  
HS\_2256\_B1\_E10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2256  
Col=19 Row=J, genomic survey sequence.  
9.0e-21:197:84  
AQ084622

50 F-NT2RP1000981  
F-NT2RP1001004  
Danio rerio mRNA for MINDIN2, complete cds.  
4.1e-22:472:63  
55 AB006085

F-NT2RP1001020  
Mus musculus clone OST66, genomic survey sequence.

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1.5e-47:352:81  
AF046696

F-NT2RP1001031

CIT-HSP-2330P23.TR CIT-HSP Homo sapiens genomic clone 2330P23, genomic survey sequence.  
8.0e-26:145:99  
AQ035969

F-NT2RP1001563

Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces. 0.096:405:59  
AC004971

F-NT2RP2000092

Human zinc finger protein ZNF136.  
1.8e-54:652:70  
U09367

F-NT2RP2000178

Streptomyces coelicolor cosmid 3F9.  
0.92:217:64  
AL023862

F-NT2RP2000240

Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.  
2.9e-96:534:90  
AF001550

F-NT2RP2000394

Gallus gallus p52 pro-apototic protein mRNA, complete cds.  
2.9e-19:380:65  
AF029071

F-NT2RP2000447

Homo sapiens clone DJ1129D05, complete sequence.  
1.3e-109:289:98  
AC005630

F-NT2RP2000479

Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal protein L29 pseudo-gene, ESTs and STSs.  
0.0039:219:63  
AL008627

F-NT2RP2000514

Homo sapiens roundabout 2 (robo2) mRNA, partial cds.  
3.7e-89:461:95  
AF040991

F-NT2RP2000533

Mus musculus cornichon mRNA, complete cds.  
1.4e-113:677:89  
AF022811

F-NT2RP2000610

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SE-  
QUENCE.  
4.3e-25:177:89  
AL034405

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F-NT2RP2000616

RPC111-75J11.TK MCI11 Homo sapiens genomic clone R-75J11, genomic survey sequence.

8.4e-34:135:91

AQ268877

5

F-NT2RP2000649

Homo sapiens CAAX prenyl protease (STE24) mRNA, complete cds.

1.2e-165:802:97

AF064867

10

F-NT2RP2000663

Human DNA sequence from cosmid U61B11, between markers DXS366 and DXS87 on chromosome X contains ESTs.

1.6e-106:365:97

15

Z73913

F-NT2RP2000694

Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.

4.2e-112:561:96

20

AJ012159

F-NT2RP2000712

HS\_3071\_A2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=10 Row=G, genomic survey sequence.

7.6e-78:389:97

25

AQ166085

F-NT2RP2000739

Human mRNA for KIAA0326 gene, partial cds.

6.4e-24:574:62

30

AB002324

F-NT2RP2000818

Drosophila melanogaster, chromosome 2R, region 38A5-38B4, BAC clone BACR48M05, complete sequence.

0.00047:304:61

35

AC005719

F-NT2RP2000903

Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.

2.6e-110:541:97

40

AJ012159

F-NT2RP2001200

Homo sapiens mRNA for KIAA0676 protein, partial cds.

3.3e-1 10:540:96

45

AB014576

F-NT2RP2001223

HS-1054-B2-C02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=4 Row=F, genomic survey sequence.

7.2e-10:128:77

50

B41982

F-NT2RP2001276

Mouse regulatory protein (npdc-1) mRNA, complete cds.

1.2e-38:296:81

55

L03814

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F-NT2RP2001388  
RPCI11-30G23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30G23, genomic survey sequence.  
0.32:53:94  
B87787

F-NT2RP2001469  
M.musculus tex292 mRNA (5'region).  
4.2e-10:120:83  
X80434

F-NT2RP2001480  
Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.  
9.0e-140:686:96  
L38969

F-NT2RP2001495  
Human transporter protein (g17) mRNA, complete cds.  
1.9e-35:581:64  
U49082

F-NT2RP2001514  
Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.  
3.7e-22:475:62  
AC005115

F-NT2RP2001529  
Homo sapiens mRNA for ZIP-kinase, complete cds.  
4.6e-152:757:96  
AB007144

F-NT2RP2001538  
Sequence 11 from patent US 5624818.  
1.4e-88:528:88  
I41141

F-NT2RP2001562  
Homo sapiens GLE1 (GLE1) mRNA, complete cds.  
2.3e-117:572:97  
AF058922

F-NT2RP2001662  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.  
6.1e-107:365:91  
AL031662

F-NT2RP2001755  
Sequence 9 from patent US 5750502.  
1.5e-53:518:75  
AR007441

F-NT2RP2001769  
A.sativa Aspk11 mRNA.  
4.7e-17:537:60  
X79992

F-NT2RP2001817  
Candida albicans SIR2 (SIR2) gene, complete cds.  
4.6e-10:285:61

AF045774

F-NT2RP2001878

Mus musculus repeat element upstream of the Rasgrf1/Cdc25Mm gene.

5.0e-06:554:60

AF021791

F-NT2RP2001903

M.musculus mRNA for m-calpain.

3.1e-06:337:60

Y10139

F-NT2RP2001915

Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.

6.8e-28:488:65

AC005670

F-NT2RP2001921

Homo sapiens clone NH0332L11, complete sequence.

1.1e-77:148:99

AC005538

F-NT2RP2001948

Sequence 2 from patent US 5541311.

0.59:284:57

I24091

F-NT2RP2001956

Feline c-sis proto-oncogene, segment 4.

0.99:101:69

M25356

F-NT2RP2002015

HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775

Col=18 Row=J, genomic survey sequence.

3.0e-06:181:65

B41504

F-NT2RP2002063

Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.

1.3e-108:418:94

AC004050

F-NT2RP2002188

Rattus norvegicus neuroligin 3 mRNA, complete cds.

1.0e-125:700:90

U41663

F-NT2RP2002232

F-NT2RP2002304

Human FMR1 gene, 5' end.

0.12:93:67

L19476

F-NT2RP2002409

Myxococcus xanthus response regulator FrzZ (frzZ) gene, partial cds; alanine dehydrogenase (aldA), putative ECF sigma factor RpoE1 (rpoE1), and response regulator homolog (frzS) genes, complete cds; and unknown

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genes.

9.0e-10:553:59

AF049107

5

F-NT2RP2002510

Mus musculus (129SV) DNA, unmapped BAC 10817, complete sequence.

4.2e-27:573:62

AC004093

10

F-NT2RP2002527

Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.

3.2e-110:439:99

AC004228

15

F-NT2RP2002533

Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds.

6.4e-141:726:95

20

AF040709

F-NT2RP2002564

Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence.

2.6e-112:403:98

25

AC004941

F-NT2RP2002674

HS\_3122\_B2\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3122 Col=4 Row=B, genomic survey sequence.

4.8e-13:86:100

30

AQ182907

F-NT2RP2002721

35

F-NT2RP2002824

Arabidopsis thaliana BAC T19D16 genomic sequence.

1.3e-12:135:69

U95973

40

F-NT2RP2002942

Homo sapiens mRNA for KIAA0806 protein, complete cds.

6.1e-145:758:94

AB018349

45

F-NT2RP2002974

Mus musculus mRNA for Six5, partial cds.

8.0e-84:588:82

D83146

50

F-NT2RP2002976

H.sapiens gene for phospholipase C beta 3, exon 14.

0.93:210:61

Z37557

55

F-NT2RP2003042

G.gallus mRNA for lecithin-cholesterol acyltransferase.

9.1e-26:462:65

X91011

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F-NT2RP2003138

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.

3.9e-142:702:96

AL031662

5

F-NT2RP2003179

Homo sapiens mRNA for KIAA0537 protein, complete cds.

3.3e-42:587:70

AB011109

10

F-NT2RP2003210

Mus musculus fatty acid transport protein 4 mRNA, partial cds.

2.6e-112:726:85

AF072759

15

F-NT2RP2003302

Human zinc finger protein ZNF136.

5.5e-63:691:69

U09367

20

F-NT2RP2003369

Homo sapiens chromosome 7q22 sequence, complete sequence.

2.0e-49:249:95

AF053356

25

F-NT2RP2003383

Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA, complete cds.

1.5e-159:817:95

AF016005

30

F-NT2RP2003390

Homo sapiens SEC63 (SEC63) mRNA, complete cds.

7.0e-115:554:98

AF100141

35

F-NT2RP2003469

Genomic sequence from Human 9q34, complete sequence.

5.6e-38:210:97

AC001644

40

F-NT2RP2003545

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.

2.2e-48:579:71

AF024636

45

F-NT2RP2003593

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 971N18, WORKING DRAFT SEQUENCE.

1.8e-90:326:99

AL021396

50

F-NT2RP2003599

F-NT2RP2003655

M.musculus tex261 mRNA.

5.3e-77:513:85

X81058

55

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F-NT2RP2003664

Homo sapiens mRNA for leptin receptor gene-related protein.

1.7e-132:630:98

Y12670

5

F-NT2RP2003931

Homo sapiens chromosome 19, overlapping cosmids R27918 and R33775, complete sequence.

1.3e-114:411:97

AC004447

10

F-NT2RP2003940

Human ZNF43 mRNA.

1.4e-97:693:82

X59244

15

F-NT2RP2003950

Sequence 1 from patent US 5648238.

6.9e-13:143:79

I55887

20

F-NT2RP2004069

F-NT2RP2004108

Human zinc finger protein ZNF136.

1.5e-67:548:78

U09367

25

F-NT2RP2004141

Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon.

8.0e-10:487:62

U87960

30

F-NT2RP2004179

Homo sapiens chromosome 11 from 11p15.5 region, complete sequence.

0.56:600:57

AF015416

35

F-NT2RP2004205

Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence.

0.32:431:55

AC005356

40

F-NT2RP2004447

Homo sapiens Chromosome 11q13 BAC Clone 18h3, WORKING DRAFT SEQUENCE, 7 ordered pieces.

2.0e-23:252:79

AC000353

45

F-NT2RP2004495

Human transporter protein (g17) mRNA, complete cds.

3.6e-25:497:61

U49082

50

F-NT2RP2004524

Genomic sequence from Human 9q34, complete sequence.

5.9e-60:203:98

AC001644

55

F-NT2RP2004556



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HS\_3022\_A1\_A11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022  
Col=21 Row=A, genomic survey sequence.

1.3e-51:419:79

AQ119143

5

F-NT2RP2004606

cDNA encoding NIC(Natural Inhibitor of Collagenase).

1.2e-113:617:92

E00985

10

F-NT2RP2004648

Felis catus lysosomal beta-galactosidase (Bgal) mRNA, complete cds.

1.5e-15:403:64

AF006749

15

F-NT2RP2004670

Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.

1.1e-73:493:85

L22557

20

F-NT2RP2004794

Mus musculus mRNA for B-IND1 protein.

5.6e-12:109:86

Z97207

25

F-NT2RP2004837

Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.

2.8e-39:352:78

AC006030

30

F-NT2RP2004847

CIT-HSP-2357D24.TR CIT-HSP Homo sapiens genomic clone 2357D24, genomic survey sequence.

2.5e-35:196:96

AQ074738

35

F-NT2RP2005027

Human glucose transporter-like protein-III (GLUT3), complete cds.

2.2e-145:713:96

M20681

40

F-NT2RP2005069

Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.

9.4e-51:200:90

U35245

45

F-NT2RP2005163

Mouse DNA fragment that hybridizes to HSV-1 Smal A fragment.

1.4e-08:231:67

M11041

50

F-NT2RP2005181

Mus musculus cationic amino acid trmsporter (CAT3) mRNA, complete cds.

1.6e-96:575:85

U70859

55

F-NT2RP2005247

Mus musculus ret finger protein mRNA, complete cds.

1.8e-13:310:66

L46855

F-NT2RP2005378

RPCI11-21D23.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21D23, genomic survey sequence.

3.0e-12:131:80

B85846

F-NT2RP2005391

S.muris mRNA for microneme antigen.

2.5e-10:345:61

Z26947

F-NT2RP2005425

Homo sapiens mRNA for KIAA0803 protein, partial cds.

1.0e-116:566:97

AB018346

F-NT2RP2005463

F-NT2RP2005514

F-NT2RP2005535

Homo sapiens DNA-binding protein mRNA, complete cds.

2.3e-125:726:90

AF038951

F-NT2RP2005541

CIT-HSP-2386E2.TF.1 CIT-HSP Homo sapiens genomic clone 2386E2, genomic survey sequence.

6.2e-20:152:88

AQ240341

F-NT2RP2005597

D.melanogaster mRNA for rotated abdomen protein.

0.088:270:57

X95956

F-NT2RP2005632

Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.

2.0e-07:207:67

U47276

F-NT2RP2005666

Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.

1.0:328:57

AC005849

F-NT2RP2005774

Human zinc finger protein ZNF136.

4.0e-44:451:74

U09367

F-NT2RP2005878

Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.

5.1e-16:382:63

AF064635

F-NT2RP2005883

Human DNA sequence from clone 248E1 on chromosome 6q23.1-23.3 Contains DOPAMINE-BETA-MONOOXY-

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GENASE PRECURSOR, EF-1-ALPHA-2 pseudogene EST GSS and CA repeat, complete sequence.  
1.5e-30:191:95  
AL023578

5 F-NT2RP2005887

Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.  
1.8e-50:394:79  
AC006030

10 F-NT2RP2005941

Human DNA sequence from cosmid CFAT5, chromosome region 11p13 contains PAX6 exons 1-4, EST and CpG Islands.  
9.5e-93:468:96  
Z95332

15

F-NT2RP2005994

Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.  
1.6e-139:692:96  
AC004050

20

F-NT2RP2006004

CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.  
6.6e-39:206:98  
AQ080257

25

F-NT2RP2006042

Human mRNA for KIAA0144 gene, complete cds.  
1.7e-10:220:69  
D63478

30

F-NT2RP2006092

Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.  
3.6e-121:562:82  
AC005214

35

F-NT2RP2006099

Human Chromosome 11 pac pDJ392a17, complete sequence.  
8.7e-76:383:92  
AC000385

40

F-NT2RP2006134

Homo sapiens Chromosome 22q11.2 Cosmid Clone 91c In DGCR Region, complete sequence. 0.055:125:71  
AC000091

45

F-NT2RP2006269

D.melanogaster mRNA for rotated abdomen protein.  
5.4e-05:357:58  
X95956

50

F-NT2RP2006512

Sequence 1 from Patent EP 0285405.  
3.7e-102:659:85  
I05465

55

F-NT2RP3000011

RPCI11-43E12.TJ RPCI11 Homo sapiens genomic clone R-43E12, genomic survey sequence.  
1.8e-10:113:84  
AQ195722

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F-NT2RP3000022

Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.

6.7e-116:284:99

AL031178

F-NT2RP3000059

R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).

0.0031:511:59

X83546

F-NT2RP3000063

Homo sapiens chromosome 19, fosmid 37502, complete sequence.

0.20:544:57

AC004755

F-NT2RP3000125

HS\_3025\_A1\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence.

1.0e-21:161:88

AQ101452

F-NT2RP3000148

Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.

5.2e-40:257:77

AC002310

F-NT2RP3000169

Homo sapiens MRS1 mRNA, complete cds.

3.4e-106:501:99

AF093239

F-NT2RP3000171

Mus musculus mRNA for B-IND1 protein.

1.8e-97:571:89

Z97207

F-NT2RP3000172

Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.

2.0e-123:702:86

L22557

F-NT2RP3000201

Homo sapiens mRNA for KIAA0687 protein, partial cds.

9.2e-170:792:98

AB014587

F-NT2RP3000232

HS\_3238\_B2\_D04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=8 Row=H, genomic survey sequence.

9.2e-24:174:88

AQ219879

F-NT2RP3000304

Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.

3.3e-171:797:98

AF074264

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F-NT2RP3000378

Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.

5.8e-137:774:89

L38621

5

F-NT2RP3000427

Mouse cAMP-dependent protein kinase beta subunit gene, exon 1.

1.5e-18:390:65

M21096

10

F-NT2RP3000436

cDNA encoding a human novel protein disulfide isomerase like enzyme,EP52.

4.5e-05:353:59

E13330

15

F-NT2RP3000444

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117715, WORKING DRAFT SEQUENCE.

9.7e-75:203:97

AL022315

20

F-NT2RP3000460

Canis familiaris sec61 homologue mRNA, complete cds.

7.1e-131:643:88

M96629

25

F-NT2RP3000481

Homo sapiens RanBP7/importin 7 mRNA, complete cds.

1.7e-162:770:98

AF098799

30

F-NT2RP3000616

Homo sapiens KIAA0405 mRNA, complete cds.

4.7e-31:579:62

AB007865

35

F-NT2RP3000645

Human chromosome 12p13 sequence, complete sequence.

5.9e-07:484:61

U47924

40

F-NT2RP3000652

Human ZNF43 mRNA.

4.4e-131:853:84

X59244

45

F-NT2RP3000676

Homo sapiens mRNA for KIAA0446 protein, complete cds.

2.7e-86:420:98

AB007915

50

F-NT2RP3000677

Human estrogen receptor-related protein (variant ER from breast cancer) mRNA, complete cds.

2.9e-21:125:100

M69296

55

F-NT2RP3000721

HS\_2221\_A2\_C01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221

Col=2 Row=E, genomic survey sequence.

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0.94:254:60  
AQ253443

F-NT2RP3000789

Mus musculus coding region determinant binding protein mRNA, complete cds.

5.4e-139:827:87

AF061569

F-NT2RP3000818

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 94M16, WORKING DRAFT SEQUENCE.

3.0e-28:218:86

Z97201

F-NT2RP3000820

Mus musculus WSB-1 mRNA, complete cds.

1.1e-77:477:87

AF033186

F-NT2RP3000838

Homo sapiens mRNA for KIAA0638 protein, partial cds.

2.6e-77:682:79

AB014538

F-NT2RP3000871

Homo sapiens retinoblastoma-interacting protein (RBBP8) mRNA, complete cds.

5.8e-07:350:60

AF043431

F-NT2RP3000907

Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.

1.7e-13:330:62

AC005115

F-NT2RP3000921

cDNA GA3-43 encoding novel polypeptide which appear when differentiate from embryo-tumor cell P19 to nerve cell.

6.8e-68:812:69

E12950

F-NT2RP3001012

cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).

2.4e-129:692:92

E12829

F-NT2RP3001044

Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.

3.7e-60:393:79

AC006030

F-NT2RP3001061

F.rubripes GSS sequence, clone 154E17aC12, genomic survey sequence.

1.8e-07:239:62

AL018519

F-NT2RP3001159

Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.

4.4e-24:156:72

AC004770

F-NT2RP3001170

Homo sapiens mRNA for KIAA0784 protein, partial cds.

2.3e-181:859:98

AB018327

F-NT2RP3001195

Genomic sequence from Human 9q34, complete sequence.

3.8e-53:253:92

AC001644

F-NT2RP3001240

Canis familiaris sec61 homologue mRNA, complete cds.

1.4e-133:740:87

M96629

P-NT2RP3001271

Homo sapiens chromosome 19, cosmid F20237, complete sequence.

0.082:370:60

AC005775

F-NT2RP3001322

Homo sapiens mRNA for KIAA0566 protein, partial cds.

1.9e-38:728:63

AB011138

F-NT2RP3001388

Rattus norvegicus synaptotagmin XI mRNA, complete cds.

1.2e-103:701:83

AF000423

F-NT2RP3001542

Human Chromosome 11 Cosmid cSRL34e5, complete sequence.

8.6e-17:293:65

U73643

F-NT2RP3001560

Mouse mRNA for thymic epithelial cell surface antigen, complete cds.

7.8e-135:742:91

D67067

F-NT2RP3001592

Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.

7.2e-12:188:71

U22398

F-NT2RP3001650

Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.

1.9e-26:374:72

AC005281

F-NT2RP3001685

Homo sapiens 12q13.1 Cosmid C174F5 (Lawrence Livermore LL12NC01 or LL12NC02 human cosmid libraries) complete sequence.

4.6e-73:284:98

AC004550

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F-NT2RP3001738

Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.

1.8e-21:186:67

AC004770

F-NT2RP3001754

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.

5.0e-21:131:96

AL034380

F-NT2RP3001858

Homo sapiens mRNA for KIAA0584 protein, partial cds.

5.9e-39:770:63

AB011156

F-NT2RP3001976

M.domesticus (C57B1/6J) mRNA for zinc finger protein 30.

2.0e-37:536:70

Z30174

F-NT2RP3002015

Homo sapiens huntingtin gene, partial exon.

0.024:175:65

L49359

F-NT2RP3002160

Homo sapiens chromosome 9q34, clone 70C11, complete sequence.

1.6e-95:249:91

AC002319

F-NT2RP3002281

Homo sapiens mRNA for KIAA0765 protein, partial cds.

1.6e-149:713:98

AB018308

F-NT2RP3002286

Mus musculus EGF repeat transmembrane protein mRNA, complete cds.

2.0e-136:756:92

U57368

F-NT2RP3002311

Mouse beta-galactosidase (BGAL) gene, complete cds.

1.0e-29:624:63

M57734

F-NT2RP3002324

Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.

5.7e-122:655:93

Z69890

F-NT2RP3002342

Human transporter protein (g17) mRNA, complete cds.

9.8e-36:565:65

U49082

F-NT2RP3002353



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Streptomyces phaeochromogenes plasmid pJV1, complete sequence.  
0.15:466:60  
U23762

- 5 F-NT2RP3002409  
Homo sapiens mRNA for KIAA0719 protein, complete cds.  
2.0e-189:897:98  
AB018262
- 10 F-NT2RP3002411  
Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.  
7.8e-122:796:84  
AF064635
- 15 F-NT2RP3002448  
R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).  
4.0e-11:403:64  
X83546
- 20 F-NT2RP3002571  
Bos taurus mRNA for lyncein.  
8.7e-114:652:90  
Y17923
- 25 F-NT2RP3002664  
H.sapiens CpG island DNA genomic Mse1 fragment, clone 34a2, reverse read cpg34a2.rt1a.  
6.1e-14:211:72  
Z60772
- 30 F-NT2RP3002721  
Homo sapiens citrate synthase mRNA, complete cds.  
7.5e-179:873:96  
AF047042
- 35 F-NT2RP3002737  
Homo sapiens mRNA for HNSPC, complete cds.  
1.4e-42:409:75  
D82346
- 40 F-NT2RP3002738  
Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.  
8.9e-122:812:83  
D29766
- 45 F-NT2RP3002790  
Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.  
2.2e-15:626:62  
U22398
- 50 F-NT2RP3002836  
Homo sapiens mRNA for KIAA0463 protein, partial cds.  
6.8e-152:717:99  
AB007932
- 55 F-NT2RP3002887  
R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).  
2.0e-05:491:59  
X83546

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F-NT2RP3002900

Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.

7.3e-13:327:66

U26264

F-NT2RP3002958

Mus musculus IgK chain (6S) intron with insertion/deletion mutations.

5.6e-22:403:66

L12153

F-NT2RP3002983

Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.

1.2e-118:339:99

AP000047

F-NT2RP3003000

Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds.

7.9e-88:555:88

AF051946

F-NT2RP3003076

Streptomyces coelicolor cosmid 2A11.

0.15:505:59

AL031184

F-NT2RP3003354

Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds.

1.2e-34:625:64

AF005038

F-NT2RP3003448

CIT-HSP-721P7.TV CIT-HSP Homo sapiens genomic clone 721P7, genomic survey sequence.

1.2e-16:126:89

B50017

F-NT2RP3003469

Homo sapiens chromosome 19, cosmid F23990, complete sequence.

2.0e-18:126:94

AC005262

F-NT2RP3003473

Homo sapiens chromosome 17, clone hRPK.1003\_J\_3, complete sequence.

7.1e-68:474:71

AC005181

F-NT2RP3003527

Homo sapiens mRNA for protein kinase Dyrk1B.

1.4e-160:769:98

Y17999

F-NT2RP3003532

Mus musculus cell surface molecule OX-2 mRNA, complete cds.

1.3e-96:712:80

AF004023

F-NT2RP3003535

Drosophila melanogaster (P1 DS02368 (D205)) DNA sequence, complete sequence. 0.027:155:65

AC004313

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F-NT2RP3003559

H.sapiens CpG island DNA genomic Mse1 fragment, clone 171h5, reverse read cpg171h5.rt1a.

3.9e-50:261:97

Z59762

5

F-NT2RP3003614

Mus musculus semaphorin VIa mRNA, complete cds.

1.7e-131:811:86

AF030430

10

F-NT2RP3003729

Homo sapiens chromosome 10 clone LA10NC01\_15\_E\_11 map 10q26.3, WORKING DRAFT SEQUENCE, 3 un-ordered pieces.

1.4e-97:259:91

AC006171

15

F-NT2RP3003849

F-NT2RP3003874

M.musculus mRNA for myosin I heavy chain.

2.9e-151:863:89

X69987

20

F-NT2RP3003939

T24C19TF TAMU Arabidopsis thaliana genomic clone T24C19, genomic survey sequence.

1.4e-19:293:68

B29025

25

F-NT2RP3003963

CIT-HSP-2050C19.TF CIT-HSP Homo sapiens genomic clone 2050C19, genomic survey sequence.

1.3e-16:111:95

B80539

30

F-NT2RP3004000

Homo sapiens klotho gene, exon 1.

0.042:430:60

AB009666

35

F-NT2RP3004025

Human DNA sequence from Fosmid 49D8 on chromosome 22, complete sequence.

0.062:197:65

Z82186

40

F-NT2RP3004067

Human mRNA for KIAA0375 gene, complete cds.

1.7e-33:556:66

AB002373

45

F-NT2RP3004075

jd187 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 5H9, genomic survey sequence.

1.5e-12:438:61

B13419

50

F-NT2RP3004083

F-NT2RP3004090

Dog alpha-L-iduronidase (IDUA) gene, exons 7-12.

55

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1.4e-06:469:60  
L01060

F-NT2RP30041 19  
Human mRNA for KIAA0215 gene, complete cds.  
1.3e-72:640:75  
D86969

F-NT2RP3004130

F-NT2RP3004133  
Pseudomonas aeruginosa phage phi CTX DNA, complete genome.  
0.0018:421:60  
Y13918

F-NT2RP3004202

F-NT2RP3004294  
Xenopus laevis ER1 mRNA, complete cds.  
5.0e-77:335:78  
AF015454

F-NT2RP3004309  
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.  
9.6e-25:231:65  
AC004770

F-NT2RP3004321  
Homo sapiens chromosome 11 from 11p15.5 region, complete sequence.  
3.7e-80:279:95  
AF015416

F-NT2RP3004345  
Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.  
7.2e-12:188:71  
U22398

F-NT2RP3004355  
HS\_3212\_A1\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=15 Row=E, genomic survey sequence.  
0.061:266:65  
AQ176625

F-NT2RP3004374  
HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=18 Row=J, genomic survey sequence.  
1.3e-06:181:67  
B41504

F-NT2RP3004406  
CIT-HSP-2340N18.TF CIT-HSP Homo sapiens genomic clone 2340N18, genomic survey sequence.  
9.9e-74:359:99  
AQ058326

F-NT2RP3004481  
Mus musculus bassoon gene, exon 6 to 11.  
0.0060:528:59

Y17038

F-NT2RP3004552

Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.

5 7.6e-40:731:64

D64009

F-NT2RP3004557

Human Ki nuclear autoantigen mRNA, complete cds.

10 8.1e-120:626:94

U11292

F-NT2RP3004625

Homo sapiens I-1 receptor candidate protein mRNA, complete cds.

15 9.8e-151:710:98

AF082516

F-NT2RP3004640

Bos taurus tuftelin mRNA, complete cds.

20 8.2e-104:565:87

AF105228

F-NT2RP3004647

Homo sapiens mRNA for KIAA0446 protein, complete cds.

25 2.1e-109:524:98

AB007915

F-NT2RP4000108

Human gene for neurofilament subunit NF-L.

30 7.0e-158:862:93

X05608

F-NT2RP4000634

Sequence 11 from patent US 5753446.

35 2.9e-155:828:92

AR008281

F-NT2RP4000962

Mus musculus clone OST66, genomic survey sequence.

40 6.0e-48:352:81

AF046696

F-NT2RP4001001

Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.

45 4.8e-47:360:84

AC005915

F-NT2RP4001009

Homo sapiens CAAX prenyl protease (STE24) mRNA, complete cds.

50 5.9e-175:828:98

AF064867

F-NT2RP4001467

Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).

55 3.3e-159:742:98

X55740

F-NT2RP4001877

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1.7e-27:401:69  
AC005637

F-NT2RP4001879

F-NT2RP4002187

Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.

4.2e-115:777:83  
AF064635

F-NT2RP4002451

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING DRAFT SEQUENCE.

6.1e-86:452:96  
Z98200

F-NT2RP4002715

Homo sapiens clone NH0523H20, complete sequence.

3.6e-59:410:77  
AC005041

F-NT2RP4002750

Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.

3.4e-105:586:87  
U70859

F-OVARC1000003

B.taurus mRNA for sodium dependent phosphate transporter.

9.0e-125:823:83  
X81699

F-OVARC1000090

RPCI11-25E14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-25E14, genomic survey sequence.

1.9e-06:151:74  
B86784

F-OVARC1000105

S.cerevisiae UBC6 gene.

4.6e-25:525:64  
X73234

F-OVARC1000137

Human SNARE protein Ykt6 (YKT6) mRNA, complete cds.

1.2e-33:184:98  
U95735

F-OVARC1000208

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-761H5, complete sequence.

1.7e-79:362:91  
AC002544

F-OVARC1000255

Porcine protein-tyrosine kinase (syk) mRNA, complete cds.

4.9e-116:424:88  
M73237

F-OVARC1000275

Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.

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0.32:314:61  
AJ011930

F-OVARC1000298

5 Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.  
2.5e-121:306:98  
AC005632

F-OVARC1000307

10 Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].  
0.017:162:67  
X94677

F-OVARC1000313

15 Homo sapiens mRNA for KIAA0573 protein, partial cds.  
1.7e-119:585:97  
AB011145

F-OVARC1000331

20 Sequence 2 from patent US 5756332.  
1.9e-48:290:91  
AR009648

F-OVARC1000410

25 Homo sapiens mRNA for angiopoietin-like factor.  
4.6e-26:538:62  
Y16132

F-OVARC1000439

30 F-OVARC1000467  
HS\_3008\_A2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone  
Plate=3008 Col=24 Row=G, genomic survey sequence.  
2.0e-11:132:82  
35 AQ116995

F-OVARC1000529

40 HS\_3092\_B2\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092  
Col=22 Row=F, genomic survey sequence.  
8.2e-12:115:84  
AQ127947

F-OVARC1000553

45 Homo sapiens chromosome 19, cosmid R26894, complete sequence.  
6.5e-92:221:96  
AC005594

F-OVARC1000775

50 Human chromosome 3p21.1 gene sequence.  
6.9e-69:380:95  
L13435

F-OVARC1000811

55 Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.  
6.7e-77:500:86  
AC004235

F-OVARC1000853

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HS\_3234\_A1\_F05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=9 Row=K, genomic survey sequence.

4.6e-05:111:71

AQ191345

5

F-OVARC1000873

Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.

8.2e-42:234:96

10

AL034418

F-OVARC1000916

Sequence 3 from patent US 5674748.

2.0e-55:422:84

15

I68139

F-OVARC1000956

Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains polymorphic VNTR pYNZ32.

1.2e-107:540:97

20

Z69708

F-OVARC1000995

H.sapiens genomic DNA (chromosome 3; clone NL1106D).

4.3e-28:166:95

25

X87478

F-OVARC1001030

Human mRNA for KIAA0339 gene, complete cds.

2.1e-10:334:64

30

AB002337

F-OVARC1001049

\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.

5.4e-12:420:62

35

AC004670

F-OVARC1001086

Homo sapiens cyclin T2a mRNA, complete cds.

1.9e-164:761:99

40

AF048731

F-OVARC1001132

Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.

1.5e-89:328:75

45

AP000038

F-OVARC1001163

Caenorhabditis elegans cosmid F40E10, complete sequence.

3.8e-26:337:71

50

Z69792

F-OVARC1001222

CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey sequence.

1.2e-08:171:70

55

B57734



F-OVARC1001260

F-OVARC1001336

B.taurus mRNA for sodium dependent phosphate transporter.

5 5.4e-83:622:80

X81699

F-OVARC1001338

HS\_2181\_B2\_E11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2181

10 Col=22 Row=J, genomic survey sequence.

2.3e-17:144:86

AQ022764

F-OVARC1001569

15 Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.

2.9e-06:241:63

AF100904

F-OVARC1001570

20 Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.

1.6e-10:235:64

AJ011929

F-OVARC1001596

25 Homo sapiens chromosome 17, clone hRPK.372\_K\_20, complete sequence.

2.2e-45:498:73

AC005951

F-OVARC1001607

30 Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.

1.7e-38:323:80

U15128

F-OVARC1001725

35 Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.

3.5e-172:821:98

AF064800

F-OVARC1001727

40 Human DNA sequence from clone 48A11 on chromosome 20p12 Contains EST, STS, GSS, complete sequence.

2.2e-132:633:98

AL031132

F-OVARC1001807

45 Human TR3 orphan receptor mRNA, complete cds.

7.1e-90:566:87

L13740

F-OVARC 1001833

50 Rattus norvegicus cis-Golgi matrix protein GM130 mRNA, complete cds.

5.2e-46:364:79

U35022

F-OVARC1001952

55 Homo sapiens FGFR-4 gene.

1.7e-14:392:62

Y13901

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F-OVARC1001991  
Human Chromosome 11 Cosmid cSRL34e5, complete sequence.  
2.3e-06:298:64  
U73643

5

F-OVARC1002058  
, complete sequence.  
1.3e-108:617:92  
AC005500

10

F-OVARC1002178  
Herpes simplex virus type 2 (strain HG52), complete genome.  
0.43:234:63  
Z86099

15

F-PLACE1000033  
Mus musculus otogelin mRNA, complete cds.  
5.9e-18:579:59  
U96411

20

F-PLACE1000231  
Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds.  
1.1e-18:273:68  
AF037272

25

F-PLACE1000258  
Human KRAB zinc finger protein (ZNP177) mRNA, complete cds.  
1.2e-13:241:70  
U37263

30

F-PLACE1000442  
Human zinc finger protein ZNF136.  
2.3e-87:774:76  
U09367

35

F-PLACE1000560  
Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.  
4.1e-107:318:96  
AC005368

40

F-PLACE1000740  
Rat notch 2 mRNA.  
1.1e-37:399:74  
M93661

45

F-PLACE1000907  
RPCI11-73M20.TJ RPCI11 Homo sapiens genomic clone R-73M20, genomic survey sequence.  
3.5e-21:147:92  
AQ269030

50

F-PLACE1000912

F-PLACE1000914  
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.  
1.8e-74:206:93  
AC002093

55

F-PLACE1000927

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Cowpox virus strain GRI-90 DNA (49 kb fragment).  
6.8e-75:683:74  
Y15035

- 5 F-PLACE1000986  
RPCI11-75H23.TK RPCI11 Homo sapiens genomic clone R-75H23, genomic survey sequence.  
1.0:316:57  
AQ268409
- 10 F-PLACE1001016  
Human dihydropyridine-sensitive L-type calcium channel alpha-1 subunit (CACNL1A3) mRNA, complete cds.  
0.28:432:59  
L33798
- 15 F-PLACE1001100  
RPCI11-32N5.TK RPCI-11 Homo sapiens genomic clone RPCI-11-32N5, genomic survey sequence.  
0.48:145:64  
AQ047336
- 20 F-PLACE1001114  
Lysobacter enzymogenes beta-lactamase gene sequence.  
0.033:349:60  
M97392
- 25 F-PLACE1001123  
F.rubripes GSS sequence, clone 084A20aC12, genomic survey sequence.  
9.7e-05:138:64  
AL015804
- 30 F-PLACE1001183  
Homo sapiens BAC clone RG318C11 from 7p14-p15, complete sequence.  
0.15:576:59  
AC005091
- 35 F-PLACE1001229  
F.rubripes GSS sequence, clone 144D13aC10, genomic survey sequence.  
2.2e-21:271:70  
AL017986
- 40 F-PLACE1001231  
Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.  
6.4e-102:677:84  
AF026554
- 45 F-PLACE1001340  
Homo sapiens mRNA for KIAA0719 protein, complete cds.  
1.3e-130:636:97  
AB018262
- 50 F-PLACE1001401  
CIT-HSP-2323H22.TR CIT-HSP Homo sapiens genomic clone 2323H22, genomic survey sequence.  
6.4e-13:165:76  
AQ028562
- 55 F-PLACE1001407  
Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.  
2.4e-28:228:85  
AL023582

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F-PLACE1001464

Human placental cDNA coding for 5 nucleotidase (EC 3.1.3.5).

5.0e-151:742:96

X55740

F-PLACE1001500

CIT-HSP-2368L16.TR CIT-HSP Homo sapiens genomic clone 2368L16, genomic survey sequence.

1.1e-25:150:97

AQ078655

F-PLACE1001516

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.

1.2e-139:676:98

AC002425

F-PLACE1001536

Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.

1.7e-142:513:97

AC004387

F-PLACE1001564

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SE-  
QUENCE.

2.9e-104:373:89

AL033377

F-PLACE1001655

Homo sapiens Shab-related delayed-rectifier K<sup>+</sup> channel alpha subunit (KCNS3) mRNA, complete cds.

1.3e-123:585:98

AF043472

F-PLACE1001788

Homo sapiens mRNA for HYA22, complete cds.

9.9e-21:234:75

D88153

F-PLACE1001795

Drosophila melanogaster; Chromosome 3L; Region 83F1-83F2; P1 clone DS07437, WORKING DRAFT SE-  
QUENCE, 3 unordered pieces.

1.4e-05:218:64

AC005985

F-PLACE1001836

Homo sapiens BAC clone GS155M11 from 7q21-q22, complete sequence.

4.9e-79:577:82

AC004022

F-PLACE1001918

Arabidopsis thaliana BAC T19D16 genomic sequence.

3.7e-24:417:63

U95973

F-PLACE1001949

S.cerevisiae chromosome XV reading frame ORF YOR291w.

3.6e-16:255:70

Z75199

F-PLACE1002080

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Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.  
7.5e-129:622:98  
AF039691

5 F-PLACE1002095  
Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.  
2.3e-48:551:71  
AC004219

10 F-PLACE1002153  
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.  
8.3e-161:764:98  
AF095791

15 F-PLACE1002329  
Sequence 12 from Patent WO 9000403.  
6.9e-05:380:63  
I09634

20 F-PLACE1002355  
Homo sapiens protease-activated receptor 4 mRNA, complete cds.  
2.8e-17:190:77  
AF055917

25 F-PLACE1002374  
Human mRNA for pro-cathepsin L(major excreted protein MEP).  
6.2e-162:716:94  
X12451

30 F-PLACE 1002518  
HS\_3091\_A1\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3091  
Col=15 Row=K, genomic survey sequence.  
3.2e-74:316:94  
AQ123005

35 F-PLACE1002547  
Homo sapiens mRNA for KIAA0719 protein, complete cds.  
2.6e-171:819:98  
AB018262

40 F-PLACE1002726  
CIT-HSP-2369G10.TR CIT-HSP Homo sapiens genomic clone 2369G10, genomic survey sequence.  
4.8e-18:135:88  
AQ075115

45 F-PLACE1002905  
Drosophila melanogaster DNA sequence (P1 DS00906 (D99)), complete sequence.  
3.7e-06:235:66  
AC004154

50 F-PLACE1002911  
Bovine herpesvirus 1 complete genome.  
0.93:264:63  
AJ004801

55 F-PLACE1002967  
Homo sapiens IgE receptor beta chain (HTm4) mRNA, complete cds.  
0.0041:302:60

L35848

F-PLACE1003135

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.

4.7e-49:450:75

AF024636

F-PLACE1003163

Homo sapiens DBI-related protein mRNA, complete cds.

4.7e-152:722:98

AF069301

F-PLACE1003407

Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.

6.3e-141:682:97

AF068227

F-PLACE1003428

Human DNA sequence from clone 55C23 on chromosome 6q22.3-23.3 contains vanin-like genes VNN1 and VNN2, ESTs, GSSs,, complete sequence.

1.2e-116:286:100

AL032821

F-PLACE1003438

Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.

0.13:468:60

AF092918

F-PLACE1003460

HS\_3234\_A1\_F05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=9 Row=K, genomic survey sequence.

5.8e-05:111:71

AQ191345

F-PLACE1003529

Homo sapiens clone DJ0981O07, complete sequence.

5.8e-134:457:97

AC006017

F-PLACE1003573

Sequence 2 from patent US 5792648.

0.93:186:62

AR022348

F-PLACE1003598

Mus musculus mismatch repair protein (MSH6) gene, exon 1.

3.3e-07:311:63

AF031085

F-PLACE1003644

Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence.

1.8e-06:138:74

AC001234

F-PLACE1003737

Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.

1.4e-165:791:98

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AC005859

F-PLACE1003772

Human p300/CBP-associated factor (P/CAF) mRNA, complete cds.

5 2.2e-07:448:61

U57317

F-PLACE1003839

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.

10 2.0e-106:525:97

AC004131

F-PLACE1003845

Caenorhabditis elegans cosmid D2096.

15 9.8e-26:386:69

U40800

F-PLACE1003852

Homo sapiens mRNA for KIAA0758 protein, partial cds.

20 7.4e-171:814:98

AB018301

F-PLACE1004028

25 F-PLACE1004078

Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.

2.0e-116:274:98

AC005281

30 F-PLACE1004166

HS\_3223\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=17 Row=O, genomic survey sequence.

0.77:304:58

AQ193346

35

F-PLACE1004168

F-PLACE1004199

CIT-HSP-2328F14.TR CIT-HSP Homo sapiens genomic clone 2328F14, genomic survey sequence.

40 9.4e-16:186:76

AQ042262

F-PLACE1004279

Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds.

45 1.2e-18:456:62

AF057039

F-PLACE1004282

50 F-PLACE1004305

Homo sapiens mRNA for KIAA0740 protein, complete cds.

2.7e-121:612:96

AB018283

55 F-PLACE1004441

Human G protein-coupled receptor (GPR1) gene, complete cds.

2.4e-104:537:95

U13666

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F-PLACE1004450

Pleuronectes americanus aminopeptidase N (ampN) mRNA, complete cds.

3.1e-20:601:60

AF012465

F-PLACE1004482

HS\_3032\_B1\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=F, genomic survey sequence.

1.1e-86:423:98

AQ129106

F-PLACE1004492

Human DNA sequence from PAC 434P1 on chromosome 22. Contains inward rectifier potassium channel 4, (potassium channel, inwardly rectifying, subfamily J, member 4) (hippocampal inward rectifier) (HIR) (HRK1) (HIRK2) (KIR2.3), ESTs similar to lumen protein retaining receptor 2 (KDEL receptor 2), DEAD-box protein P72, ESTs, CpG islands.

0.17:180:67

Z97056

F-PLACE1004519

Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.

1.1e-75:432:84

AL021808

F-PLACE1004520

Human pregnancy-specific beta-1-glycoprotein mRNA PSG95, complete cds.

4.1e-109:606:92

M34715

F-PLACE1004630

Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds.

6.2e-138:749:92

AB008375

F-PLACE1004637

HS-1061-B1-E10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 783 Col=19 Row=J, genomic survey sequence.

0.013:92:75

B45487

F-PLACE1004648

F-PLACE1004816

Homo sapiens mRNA for Hakata antigen, complete cds.

3.8e-98:590:90

D88587

F-PLACE1004887

Dog alpha-L-iduronidase (IDUA) gene, exons 7-12.

1.2e-06:469:60

L01060

F-PLACE1005003

Human SNC19 mRNA sequence.

4.8e-20:472:63

U20428



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F-PLACE1005005

Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.

7.8e-143:650:97

5 AJ011930

F-PLACE1005031

Bovine chlorine channel protein (p64) mRNA, complete cds.

7.1e-62:463:83

10 L16547

F-PLACE1005239

Homo sapiens mRNA for HIRIP3 protein, clone pH4-31.

2.2e-14:115:85

15 AJ223349

F-PLACE1005250

Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.

3.3e-40:370:77

20 U50734

F-PLACE1005383

Homo sapiens UP50 mRNA, complete cds.

2.7e-126:633:96

25 AF093118

F-PLACE1005410

Rattus rattus sec61 homologue mRNA, complete cds.

1.9e-115:771:85

30 M96630

F-PLACE1005426

Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.

7.2e-113:391:96

35 AC005392

F-PLACE1005519

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.

1.0e-53:521:74

40 AF024636

F-PLACE1005539

c-erbB=proto-oncogene {exon 1, promoter} [chickens, Genomic, 700 nt].

3.6e-05:434:62

45 S66408

F-PLACE1005544

Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.

3.3e-56:575:74

50 U89915

F-PLACE1005569

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.

1.1e-118:381:96

55 AL034397

F-PLACE1005601

Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.

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3.9e-143:697:98  
AC002073

F-PLACE1005660

F-PLACE1005669  
Fruit fly (D.melanogaster) Glued mRNA, complete cds.  
3.4e-14:275:66  
J02932

F-PLACE1005682  
Mus musculus Ankhzn mRNA, complete cds.  
0.75:347:57  
AB011370

F-PLACE1005725  
Homo sapiens huntingtin (HD) gene, exon 1.  
1.4e-06:425:62  
L27350

F-PLACE1005736

F-PLACE1005745  
HS\_3039\_B1\_F12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039  
Col=23 Row=L, genomic survey sequence.  
1.0:283:59  
AQ155068

F-PLACE1005768  
Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.  
1.5e-141:719:96  
Z82185

F-PLACE1005815  
Sequence 1 from patent US 5571905.  
0.088:199:62  
I28535

F-PLACE1005878  
Bovine chlorine channel protein (p64) mRNA, complete cds.  
2.5e-54:394:84  
L16547

F-PLACE1005927  
HS\_3138\_B2\_B03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3138  
Col=6 Row=D, genomic survey sequence.  
8.0e-32:162:95  
AQ183333

F-PLACE1006071  
1.6e-180:877:96  
AF028816

F-PLACE1006073  
Homo sapiens mRNA for glucuronyltransferase I, complete cds.  
1.7e-94:464:98  
AB009598

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F-PLACE1006079

Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.

5.2e-107:423:96

AF028233

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F-PLACE1006093

jd187 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 5H9, genomic survey sequence.

0.00018:316:60

10

B13419

F-PLACE1006208

Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.

1.4e-12:421:64

15

L14320

F-PLACE1006219

Caenorhabditis elegans cosmid D2096.

6.4e-25:386:69

20

U40800

F-PLACE1006277

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.

7.2e-135:381:97

25

AL034397

F-PLACE1006290

Caenorhabditis elegans cosmid F09E5.

1.4e-08:354:61

30

U37429

F-PLACE1006443

Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.

2.9e-80:168:95

35

AC002093

F-PLACE1006515

Homo sapiens mRNA for KIAA0576 protein, partial cds.

4.2e-140:655:99

40

AB011148

F-PLACE1006716

Human DNA sequence from PAC 151B14 on chromosome 22q12-qter contains somatostatin receptor subtype 3 (SSTR3), tRNA, ESTs, CpG island and STS.

2.2e-51:621:70

45

Z86000

F-PLACE1006786

CITBI-E1-2502A9.TR CITBI-E1 Homo sapiens genomic clone 2502A9, genomic survey sequence.

0.43:237:64

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AQ264473

F-PLACE1006809

HS\_2255\_B1\_F05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=9 Row=L, genomic survey sequence.

2.1e-14:95:97

55

AQ131814

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F-PLACE1006959

HS\_3247\_B1\_E03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247 Col=5 Row=J, genomic survey sequence.

1.1e-09:199:70

AQ220414

F-PLACE1007028

Homo sapiens Chromosome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2 (CDKN1C) gene, complete sequence.

2.0e-24:658:62

AC005950

F-PLACE1007040

Mus musculus neuronal intermediate filament protein (alpha-internexin) gene, complete cds.

8.8e-09:585:62

L27220

F-PLACE1007077

F-PLACE1007081

RPCI11-31D7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-31D7, genomic survey sequence.

2.3e-42:228:97

AQ016433

F-PLACE1007096

F-PLACE1007296

Human mRNA for a presumptive KDEL receptor.

1.3e-71:542:83

X55885

F-PLACE1007591

Homo sapiens full length insert cDNA clone YP44A02.

1.1e-18:141:90

AF085890

F-PLACE1007626

Homo sapiens unknown mRNA, complete cds.

7.8e-104:516:97

AF047439

F-PLACE1007702

Homo sapiens chromosome 17, clone 363G12, WORKING DRAFT SEQUENCE, 11 unordered pieces.

7.5e-50:439:77

AC002348

F-PLACE1007845

Caenorhabditis elegans cosmid F09E5.

4.4e-08:355:62

U37429

F-PLACE1007881

CITBI-E1-2517N6.TF CITBI-E1 Homo sapiens genomic clone 2517N6, genomic survey sequence.

1.4e-14:104:95

AQ279407

F-PLACE1007971

HS\_3237\_B2\_F09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237

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Col=18 Row=L, genomic survey sequence.  
1.2e-12:169:76  
AQ206052

- 5 F-PLACE1008282  
Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.  
4.5e-101:192:100  
AC005995
- 10 F-PLACE1008297  
Mycoplasma genitalium random genomic clone hg1, partial cds.  
0.099:193:60  
U02109
- 15 F-PLACE1008359  
Homo sapiens DNA for (CGG)<sub>n</sub> trinucleotide repeat region, isolate CL16-1 (Chr.16).  
0.53:185:65  
AJ001218
- 20 F-PLACE1008469  
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.  
1.2e-93:213:98  
AC002093
- 25 F-PLACE1008549  
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds.  
5.7e-144:693:98  
AF049703
- 30 F-PLACE1008657  
Bovine mRNA for adseverin, complete cds.  
5.6e-140:782:90  
D26549
- 35 F-PLACE1008716  
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.  
1.1e-133:648:97  
U15128
- 40 F-PLACE1008744  
Sequence 1 from patent US 5691147.  
8.4e-91:475:95  
I76197
- 45 F-PLACE1008984  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SE-  
QUENCE.  
4.2e-103:493:99  
AL031427
- 50 F-PLACE1008985  
Mus musculus synaptotagmin VIII mRNA, partial cds.  
1.1e-23:289:72  
U20107
- 55 F-PLACE1009067  
H.sapiens CpG island DNA genomic Mse1 fragment, clone 52e12, forward read cpg52e12.ft1a.  
1.2e-28:164:96

Z61442

F-PLACE1009196

- 5 F-PLACE1009279  
H.sapiens mRNA for serine protease.  
6.0e-10:327:64  
Y07921
- 10 F-PLACE1009527  
Human DNA-binding protein ABP/ZF mRNA, complete cds.  
2.0e-19:125:96  
U82613
- 15 F-PLACE1009546  
S.lividans mercury resistance operon.  
0.56:358:59  
X65467
- 20 F-PLACE1009600  
Mouse mRNA for tetracycline transporter-like protein, complete cds.  
2.1e-128:718:91  
D88315
- 25 F-PLACE1009735  
Homo sapiens clone NH0523H20, complete sequence.  
2.9e-128:613:99  
AC005041
- 30 F-PLACE1009982  
  
F-PLACE1010011  
, complete sequence.  
2.1e-26:234:83
- 35 AC005409  
  
F-PLACE1010078  
Saccharomyces cerevisiae chromosome XII cosmid 8300.  
0.066:273:58
- 40 U19028  
  
F-PLACE1010081  
Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.  
7.0e-150:733:97
- 45 AF027706  
  
F-PLACE1010251  
Sequence 1 from patent US 5665588.  
0.0012:309:62
- 50 I64695  
  
F-PLACE1010445  
Herpes simplex virus type 2 (strain HG52), complete genome.  
9.4e-07:511:58
- 55 Z86099  
  
F-PLACE1010713  
Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.

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2.1e-89:612:83  
AF064635

5 F-PLACE1010784  
Sequence 1 from patent US 5686597.  
2.5e-103:505:98  
I73723

10 F-PLACE1010827  
Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.  
7.3e-13:327:66  
U26264

15 F-PLACE1010968  
O.cuniculus mRNA for titin.  
0.44:165:64  
X64696

20 F-PLACE1011045  
Homo sapiens E1-like protein mRNA, complete cds.  
1.8e-127:595:99  
AF094516

25 F-PLACE1011116  
HS\_2033\_A2\_E05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033  
Col=10 Row=I, genomic survey sequence.  
8.3e-29:192:92  
AQ229784

30 F-PLACE1011181  
H.sapiens CpG island DNA genomic Mse1 fragment, clone 99f2, reverse read cpg99f2.rt1a.  
4.8e-35:200:95  
Z64239

35 F-PLACE1011236  
Mus musculus mRNA for RST, complete cds.  
4.5e-54:717:66  
AB005451

40 F-PLACE1011364  
Homo sapiens protein kinase/endoribonulcease (IRE1) mRNA, complete cds.  
0.13:502:57  
AF059198

45 F-PLACE1011407  
M.domesticus (C57B1/6J) mRNA for zinc finger protein 30.  
7.2e-15:313:68  
Z30174

50 F-PLACE1011516  
Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SE-  
QUENCE, 4 unordered pieces.  
1.8e-16:317:66  
AC005720

55 F-PLACE1011708  
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.  
1.8e-143:722:96

AF034611

F-PLACE1011824

Human Ste20-like kinase (MST2) mRNA, complete cds.

5.0e-100:561:92

U26424

F-PLACE 101 1978

Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.

9.6e-76:722:74

M27877

F-PLACE2000118

Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence), complete sequence.

5.2e-112:568:95

AL022578

F-PLACE2000219

Homo sapiens Down Syndrome critical region, partial sequence.

0.0059:144:71

AF015262

F-PLACE3000181

Sequence 102 from patent US 5643781.

4.1e-127:745:90

I51041

F-PLACE3000213

F-PLACE4000354

HS\_3071\_A2\_B06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071

Col=12 Row=C, genomic survey sequence.

4.4e-12:335:64

AQ137396

F-PLACE4000455

Homo sapiens transcriptional enhancer factor (TEF1) DNA, complete CDS.

9.5e-118:563:98

M63896

F-SKNMC1000004

Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.

2.9e-141:292:98

AC005632

F-SKNMC1000014

CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.

0.89:136:67

AQ075724

F-SKNMC1000082

H.sapiens CpG island DNA genomic MseI fragment, clone 26g3, reverse read cpg26g3.rt1b.

5.6e-06:60:98

265216



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F-THYRO1000036

F-THYRO1000061

Homo sapiens chromosome 19, cosmid R28991, complete sequence.

5 2.4e-105:425:94

AC004623

F-THYRO1000099

Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon.

10 0.35:609:57

U87960

F-THYRO1000196

Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.

15 5.1e-125:475:98

AF016272

F-THYRO1000400

Mycobacterium tuberculosis sequence from clone y423.

20 1.0:264:59

AD000014

F-THYRO1000580

HS\_3216\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3216

25 Col=17 Row=O, genomic survey sequence.

2.8e-25:157:96

AQ184086

F-THYRO1000584

Boar mRNA for 135kDa protein, complete cds.

30 2.0e-104:787:80

D28521

F-THYRO1000678

M.musculus Cx30 gene.

35 6.9e-41:285:85

Z70023

F-THYRO1000776

Drosophila melanogaster DNA sequence (P1 DS08948 (D168)), complete sequence.

40 2.7e-10:389:59

AC004288

F-THYRO1000795

Rattus norvegicus mRNA for mitochondrial dicarboxylate carrier.

45 1.2e-107:736:83

AJ223355

F-THYRO1000846

CITBI-E1-2505H6.TR CITBI-E1 Homo sapiens genomic clone 2505H6, genomic survey sequence.

50 0.00025:351:61

AQ260270

F-THYRO1000866

Homo sapiens SKB1Hs mRNA, complete cds.

55 3.3e-91:529:89

AF015913

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F-THYRO1000956

Human G protein-coupled receptor APJ gene, complete cds.

3.8e-148:724:97

U03642

F-THYRO1000964

Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.

5.0e-37:714:64

AF091624

F-THYRO1000999

CITBI-E1-2508B3.TF CITBI-E1 Homo sapiens genomic clone 2508B3, genomic survey sequence.

1.2e-06:280:62

AQ261426

F-THYRO1001063

H.sapiens (xs174) mRNA, 300bp.

1.6e-41:298:85

Z36825

F-THYRO1001071

Human mRNA for KIAA0154 gene, partial cds.

7.4e-16:197:73

D63876

F-THYRO1001102

Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.

3.5e-10:128:83

AC004997

F-THYRO1001113

Homo sapiens mRNA for LGMD2B protein.

8.8e-52:684:68

AJ007670

F-THYRO1001128

Homo sapiens chromosome 9q34, clone 63G10, complete sequence.

1.2e-141:227:97

AC002096

F-THYRO1001205

F-THYRO1001237

Mus musculus interleukin-2 (Il-2) gene, 5'end.

0.77:78:74

L07576

F-THYRO1001242

Mouse mRNA for thymic epithelial cell surface antigen, complete cds.

5.1e-127:721:90

D67067

F-THYRO1001266

Human sodium iodide symporter mRNA, complete cds.

2.7e-41:806:62

U66088

F-THYRO1001327

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Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

3.1e-117:374:96

5 AL021578

F-THYRO1001456

F-THYRO1001457

10 M.musculus (Balb/c) mRNA for serine/threonine protein kinase.

1.8e-57:491:69

Z34524

F-THYRO1001471

15 Sequence 52 from Patent WO9712992.

0.00019:546:58

A62364

F-THYRO1001478

20

F-THYRO1001495

Homo sapiens clone DJ1163L11, complete sequence.

4.4e-20:222:76

AC005230

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F-THYRO1001523

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 407F17, WORKING DRAFT SEQUENCE.

8.8e-21:538:62

30

Z83845

F-THYRO1001529

M.musculus mRNA for serine palmitoyltransferase subunit B.

5.8e-32:448:66

35

X95642

F-THYRO1001593

Homo sapiens chromosome 19, cosmid R31237, complete sequence.

5.8e-91:213:98

40

AC005581

F-THYRO1001608

Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.

45

0.0028:335:65

AE000662

F-THYRO1001641

Leishmania major chromosome 3 clone L6290 strain Friedlin, WORKING DRAFT SEQUENCE, 2 ordered pieces.

50

0.92:378:61

AC005928

F-THYRO1001700

HS\_3220\_A1\_B08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=15 Row=C, genomic survey sequence.

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1.0e-49:265:96

AQ184388

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F-THYRO1001702

Mus musculus mRNA for myeloid associated differentiation protein.

1.4e-70:502:82

AJ001616

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F-THYRO1001725

F.rubripes GSS sequence, clone 133B16aE1, genomic survey sequence.

3.8e-06:249:65

AL004967

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F-THYRO1001770

S.cerevisiae chromosome II reading frame ORF YBR059c.

1.5e-07:320:62

Z35928

15

F-THYRO1001803

Homo sapiens chromosome 10 clone CRI-JC2019 map 10q22.1-10q22.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.

1.2e-38:234:94

AC006108

20

F-Y79AA1000030

Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.

9.9e-92:389:98

AC005214

25

F-Y79AA1000127

Homo sapiens genomic DNA, chromosome 21q11.1, segment 5/28, WORKING DRAFT SEQUENCE.

9.2e-131:359:100

AP000034

30

F-Y79AA1000207

Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.

2.2e-151:302:98

AC005562

35

F-Y79AA1000226

Drosophila melanogaster, chromosome 2L, region 21C5-21D1, P1 clone DS07610, complete sequence.

1.1e-50:549:67

AC004573

40

F-Y79AA1000270

Bos taurus vacuolar H<sup>+</sup> ATPase subunit Ac45 mRNA, complete cds.

6.4e-111:771:83

U10039

45

F-Y79AA1000426

Mus musculus activin beta E subunit mRNA, complete cds.

2.4e-87:703:76

U96386

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F-Y79AA1000521

Homo sapiens LERK-6 (EPLG6) gene, exon 1.

0.0092:148:68

U92893

55

F-Y79AA1000750

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-761H5, complete sequence.

9.0e-07:143:74  
AC002544

F-Y79AA1000776

5

F-Y79AA1000777  
Podospora anserina beta transducin-like protein (het-e1) gene, complete cds.  
6.6e-17:760:59  
L28125

10

F-Y79AA1000876  
Homo sapiens long form transcription factor C-MAF (c-maf) mRNA, complete cds.  
3.3e-10:323:66  
AF055377

15

F-Y79AA1000888  
Streptomyces coelicolor cosmid 8A6.  
3.1e-06:665:59  
AL031013

20

F-Y79AA1000959  
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.  
1.6e-52:277:96  
AF093420

25

F-Y79AA1000967  
Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.  
2.9e-131:752:86  
L22557

30

F-Y79AA1001013

F-Y79AA1001056  
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.  
1.2e-85:676:79  
U50734

35

F-Y79AA1001062  
Human Chromosome 11 Cosmid cSRL34e5, complete sequence.  
8.6e-17:293:65  
U73643

40

F-Y79AA1001090  
Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.  
1.9e-05:223:63  
AC004596

45

F-Y79AA1001212  
Homo sapiens SL15 protein mRNA, complete cds.  
4.7e-162:763:98  
AF038961

50

F-Y79AA1001264  
Drosophila melanogaster DNA sequence (P1s DS00764 (D273) and DS00501 (D274)), complete sequence.  
1.2e-32:599:63  
AC005269

55

F-Y79AA1001272

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Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from cosmid 5L5, WORKING DRAFT SEQUENCE.  
1.2e-11:356:67  
AJ009613

5 F-Y79AA1001328  
Rattus norvegicus Delta 3 mRNA, complete cds.  
2.1e-51:443:76  
AF084576

10 F-Y79AA1001426  
HS\_3146\_A1\_A10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146  
Col=19 Row=A, genomic survey sequence.  
9.0e-23:106:91  
AQ141090

15 F-Y79AA1001427  
Bovine cytochrome b5 reductase mRNA, partial cds.  
1.4e-55:670:70  
M83104

20 F-Y79AA1001430  
Homo sapiens mRNA for KIAA0469 protein, complete cds.  
8.6e-123:577:99  
AB007938

25 F-Y79AA1001523  
Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds.  
3.3e-91:496:93  
AF009353

30 F-Y79AA1001530  
Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.  
1.8e-126:764:89  
AL030996

35 F-Y79AA1001592  
40 HS\_3219\_A2\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219  
Col=24 Row=I, genomic survey sequence.  
5.2e-36:234:89  
AQ180547

45 F-Y79AA1001727

F-Y79AA1001787  
S.pombe chromosome III cosmid c1672.  
8.8e-11:409:58  
50 AL031324

F-Y79AA1001793  
Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.  
0.12:131:70  
55 AL025355

F-Y79AA1001795  
Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BINGS gene, exons 11

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- to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RINGS), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and GSSs, complete sequence.  
1.2e-140:672:98  
AL031228
- 5
- 10 F-Y79AA1001799  
S.pombe chromosome I cosmid c8C9.  
0.00031:300:60  
Z99168
- 15 F-Y79AA1001803  
Mus musculus secretogranin III (SgIII) mRNA, complete cds.  
4.6e-101:516:82  
U02982
- 20 F-Y79AA1001863  
Homo sapiens DNA, anonymous heat-stable fragment RP5-6A.  
5.2e-85:410:99  
AB012170
- 25 F-Y79AA1002022  
CIT-HSP-2053H1.TF CIT-HSP Homo sapiens genomic clone 2053H1, genomic survey sequence.  
4.3e-20:130:95  
B68526
- 30 F-Y79AA1002058  
Homo sapiens clone 24733 mRNA sequence.  
5.3e-153:740:98  
AF052149
- 35 F-Y79AA1002121  
  
F-Y79AA1002129  
Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.  
5.5e-12:565:61  
L14320
- 40 F-Y79AA1002213  
Rattus norvegicus brain specific Na<sup>+</sup>-dependent inorganic phosphate cotransporter mRNA, complete cds.  
4.0e-12:434:60  
U07609
- 45 F-Y79AA1002334  
F.rubripes GSS sequence, clone 174E24aB10, genomic survey sequence.  
3.0e-10:171:72  
AL019366
- 50 F-Y79AA1002373  
Rattus norvegicus Smad8 mRNA, complete cds.  
0.96:420:61  
AF012347
- 55 F-Y79AA1002376  
Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.

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1.1e-132:805:88  
U39045

F-Y79AA1002378

Mus musculus mRNA for zinc finger protein, complete cds, clone:CTfin51.  
1.9e-64:521:78  
D10630

F-Y79AA1002381

O.sativa mRNA for cdc2+/CDC28-related protein kinase.  
3.3e-21:431:60  
X58194

## Homology search result 7

**[0298]** The result of the homology search in the GenBank(<http://www.ncbi.nlm.nih.gov/web/GenBank/>) using the clone sequences of the 3'-ends. except EST and STS sequences.

Indicated are from the top,  
the name of the clone sequence,  
definition of the top hit data,  
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),  
the Accession No. of the top hit data.

**[0299]** Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone. Data were not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000006

R-HEMBA1000121

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SE-  
QUENCE.  
2.2e-43:355:80  
AL031291

R-HEMBA1000128

Homo sapiens chromosome X, PAC 671D9, complete sequence.  
0.99:389:60  
AF031078

R-HEMBA1000275

Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG  
island.  
3.4e-10:212:66  
Z93023

R-HEMBA1000300

{Alu RNA transcript, clone NE461} [human, embryonal carcinoma cells, NTera2D1 pluripotent cells, Other RNA,  
282 nt].  
4.6e-42:246:89  
S42653

R-nnnnnnnnnnnnn

Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence.  
1.0e-71:192:95  
AC005922

R-HEMBA1000462



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Homo sapiens clone 243 unknown mRNA, complete sequence.  
8.3e-90:313:94  
AF091094

5 R-HEMBA1000477  
Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 8/11.  
0.22:377:60  
AB020865

10 R-HEMBA1000590  
Homo sapiens mRNA for matrilin-4, partial.  
8.0e-101:547:93  
AJ007581

15 R-HEMBA1000634  
\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1, WORKING DRAFT SEQUENCE, 15 unordered pieces.  
0.95:186:62  
20 AC004480

R-HEMBA1000671  
RPC111-65E1.TJ RPC111 Homo sapiens genomic clone R-65E1, genomic survey sequence.  
2.1e-09:165:73  
25 AQ237194

R-HEMBA1000713  
Homo sapiens 10kD protein (BC10) mRNA, complete cds.  
1.2e-117:575:97  
30 AF053470

R-HEMBA1000732  
Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.  
1.4e-108:581:93  
35 Y13622

R-nnnnnnnnnnnnn

40 R-HEMBA1000875  
Homo sapiens chromosome 17, clone hRPK.1090\_M\_7, complete sequence.  
0.044:253:64  
AC005274

45 R-HEMBA1000940  
\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.  
1.9e-33:222:82  
U14567

50 R-HEMBA1000962

R-HEMBA1001184  
Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.  
0.00044:466:58  
55 AC004688

R-HEMBA1001221  
Sequence 1 from patent US 5633147.

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7.1e-11:232:65  
I43819

R-HEMBA1001228

5 Human germline oligomeric matrix protein (COMP) mRNA, complete cds.  
7.8e-89:358:96  
L32137

R-HEMBA1001272

10 nbxb0003bDO1r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003G00r, genomic survey sequence.  
0.00014:201:64  
AQ050116

R-HEMBA1001296

15 Homo sapiens PAC clone DJ1168D11 from 7p21-p22, complete sequence.  
0.13:440:58  
AC004614

R-HEMBA1001297

20 Homo sapiens putative transcription factor CA150 mRNA, complete cds.  
5.0e-92:466:96  
AF017789

R-HEMBA1001390

25 CIT-HSP-2314K10.TR CIT-HSP Homo sapiens genomic clone 2314K10, genomic survey sequence.  
3.4e-43:196:85  
AQ027191

R-HEMBA1001563

30 H.sapiens villin gene, exon 1.  
2.1e-43:342:81  
X71058

R-HEMBA1001621

35 Human G protein-coupled receptor APJ gene, complete cds.  
1.2e-41:288:87  
U03642

R-HEMBA1001878

40 Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.  
2.0e-79:434:93  
AF090988

R-HEMBA1001886

45 Human zinc finger protein (ZNF141) mRNA, complete cds.  
1.8e-59:530:80  
L15309

R-HEMBA1002048

50 Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60), complete sequence.  
0.36:322:61  
AC005355

R-HEMBA1002131

55 Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.  
0.22:233:61  
AL031730

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5 R-HEMBA1002163  
Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.  
1.1e-16:275:69  
AC002489

10 R-HEMBA1002167  
Rattus norvegicus neuroligin I mRNA, complete cds.  
8.7e-23:193:84  
U22952

15 R-HEMBA1002178

R-HEMBA1002195  
Homo sapiens DHPS gene, exons 8 to 9.  
1.4e-19:114:100  
AJ001704

20 R-HEMBA1002227  
Homo sapiens mRNA for 80K-L protein, complete cds.  
6.1e-115:567:97  
D10522

25 R-HEMBA1002316  
Homo sapiens mRNA for putative GTP-binding protein.  
1.5e-18:161:85  
Y14391

30 R-HEMBA1002420  
Caenorhabditis elegans cosmid C27A7, complete sequence.  
0.88:214:62  
Z81041

35 R-HEMBA1002421  
Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.  
6.0e-90:443:97  
J04621

40 R-HEMBA1002524  
Human MHC Class I region proline rich protein mRNA, complete cds.  
3.2e-110:551:96  
U63336

45 R-HEMBA1002551  
Mouse Bac 276o8, WORKING DRAFT SEQUENCE, 25 unordered pieces.  
7.0e-06:397:61  
AC003022

50 R-HEMBA1002767  
Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.  
4.2e-110:568:96  
AC005038

55 R-HEMBA1002985  
Homo sapiens chromosome 17, clone hRPK.15\_K\_2, complete sequence.  
3.4e-23:184:86  
AC005901

R-HEMBA1003047

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Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.

5.0e-114:571:96

AF034611

5 R-HEMBA1003072  
HS-1014-B1-F12-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 789  
Col=23 Row=L, genomic survey sequence.  
1.5e-62:340:94  
B32084

10 R-HEMBA1003101  
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.  
3.8e-116:575:97  
AF049891

15 R-HEMBA1003120  
HS\_3220\_A1\_F04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220  
Col=7 Row=K, genomic survey sequence.  
3.6e-61:354:92  
20 AQ184345

R-HEMBA1003230  
Homo sapiens UP50 mRNA, complete cds.  
1.3e-42:258:93  
25 AF093118

R-HEMBA1003294  
HS\_3220\_A1\_D03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220  
Col=5 Row=G, genomic survey sequence.  
30 0.0095:204:63  
AQ190655

R-HEMBA1003315  
Sus scrofa DNA for LH beta, exons 1, 2, 3, complete cds.  
35 6.6e-24:163:79  
D00579

R-HEMBA1003392  
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.  
40 2.6e-115:557:98  
AF074264

R-HEMBA1003399  
Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.  
45 1.8e-63:166:100  
AC004971

R-HEMBA1003487

50 R-HEMBA1003497  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27O5, WORKING DRAFT SEQUENCE.  
1.4e-119:592:97  
AL033529

55 R-HEMBA1003530

R-HEMBA1003602  
Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.

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9.4e-79:468:91  
AC002041

5 R-HEMBA1003732  
Homo sapiens clone DJ0935K16, complete sequence.  
2.0e-118:586:98  
AC006011

10 R-HEMBA1003945  
Human calcineurin B mRNA, complete cds.  
8.9e-82:410:97  
M30773

15 R-HEMBA1004007  
Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.  
6.7e-56:404:75  
AC004851

20 R-HEMBA1004085  
G.gallus microsatellite DNA (LEI0311 (= EC12A05)).  
0.66:144:65  
Z95196

25 R-nnnnnnnnnnnnn  
Homo sapiens intersectin short form mRNA, complete cds.  
2.1e-115:569:97  
AF064243

30 R-HEMBA1004250  
Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.  
3.8e-98:478:98  
AC005752

35 R-HEMBA1004391  
Plasmodium falciparum MAL3P8, complete sequence.  
0.29:126:65  
AL034560

40 R-HEMBA1004444  
Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.  
8.4e-52:308:78  
AC004938

45 R-HEMBA1004454  
CIT-HSP-2337122.TF CIT-HSP Homo sapiens genomic clone 2337122, genomic survey sequence.  
0.78:59:77  
AQ038475

50 R-HEMBA1004505

R-HEMBA1004785

R-HEMBA1004797

55 R-HEMBA1004952  
Mus musculus diabetic embryopathy (Dep-1) mRNA.  
3.4e-39:327:82  
AF032130

R-HEMBA1004971

Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.

0.00040:251:66

AC005099

5

R-HEMBA1004982

Strongyloides fulleborni 18S ribosomal RNA and 5.8S ribosomal RNA genes, partial sequence, and internal transcribed spacer 1, complete sequence.

0.092:191:63

10

U43581

R-HEMBA1005070

Human mRNA for KIAA0310 gene, complete cds.

1.2e-94:381:91

15

AB002308

R-HEMBA1005084

R-HEMBA1005145

20

Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.

5.7e-58:283:84

AJ003147

25

R-HEMBA1005230

CIT-HSP-2333N15.TR CIT-HSP Homo sapiens genomic clone 2333N15, genomic survey sequence.

5.5e-31:363:73

AQ040189

30

R-HEMBA1005246

Homo sapiens full length insert cDNA clone YX52E07.

1.6e-11:173:72

AF086040

35

R-HEMBA1005267

Sequence 1 from patent US 5618695.

2.4e-73:536:81

I40055

40

R-HEMBA1005337

Caenorhabditis elegans cosmid K07D4.

0.16:157:63

AF077534

45

R-HEMBA1005430

R-HEMBA1005449

R-HEMBA1005489

50

Anopheles rangeli NADH dehydrogenase subunit 2 gene, mitochondrial gene encoding mitochondrial product, partial cds.

0.020:271:61

U35272

55

R-HEMBA1005522

R-HEMBA1005545

Human m3 muscarinic acetylcholine receptor (CHRM3) gene, complete cds.

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1.8e-115:579:96  
U29589

5 R-HEMBA1005698  
0.0065:223:65  
AG004952

10 R-HEMBA1005913  
Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.  
3.7e-15:272:68  
AC003037

15 R-HEMBA1005929  
Homo sapiens chromosome 19, cosmid R31237, complete sequence.  
9.4e-55:502:76  
AC005581

20 R-HEMBA1005945  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING DRAFT SE-  
QUENCE.  
0.45:245:62  
AL034410

25 R-HEMBA1006016  
Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.  
3.5e-25:415:66  
AC005562

30 R-HEMBA1006171  
Human DNA sequence from PAC 433M19 on chromosome Xq26.3-Xq27.1. Contains ESTs, STSs and polymorphic  
CA repeat.  
1.0:176:64  
Z95703

35 R-HEMBA1006276  
Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.  
2.8e-118:592:96  
AC005261

40 R-HEMBA1006299  
  
R-HEMBA1006311

45 R-HEMBA1006335  
Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.  
6.1e-111:578:96  
AL023582

50 R-HEMBA1006357  
Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.  
4.8e-11:174:74  
AC004469

55 R-HEMBA1006430  
Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.  
8.7e-45:402:79  
AC004086

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R-HEMBA1006482

Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.

1.7e-105:537:96

AF026852

5

R-HEMBA1006517

345A19.TV CIT978SKA1 Homo sapiens genomic clone A-345A19, genomic survey sequence.

1.5e-44:176:88

B15409

10

R-HEMBA1006544

Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.

2.5e-66:310:83

AC004997

15

R-HEMBA1006572

Homo sapiens reduced folate carrier (RFC1) gene, exons 1a, 1c and 1b.

0.028:255:64

U92868

20

R-HEMBA1006658

Homo sapiens mRNA for KIAA0687 protein, partial cds.

7.3e-1 11:570:94

AB014587

25

R-HEMBA1006707

Homo sapiens mRNA for matrilin-4, partial.

5.1e-78:389:97

AJ007581

30

R-HEMBA1006724

HS\_2052\_B1\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=15 Row=F, genomic survey sequence.

2.6e-46:309:88

AQ305998

35

R-HEMBA1006749

Homo sapiens mRNA for matrilin-4, partial.

3.2e-88:472:94

AJ007581

40

R-HEMBA1006770

Homo sapiens CAGH4 mRNA, partial cds.

6.5e-25:145:82

U80746

45

R-HEMBA1006902

Homo sapiens mRNA for matrilin-4, partial.

9.3e-112:540:98

AJ007581

50

R-HEMBA1006912

\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.

6.6e-48:279:92

U14571

55

R-HEMBA1006916

Homo sapiens Grb14 mRNA, complete cds.



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1.8e-114:346:99  
L76687

5 R-HEMBA1006960  
Homo sapiens chromosome 19, cosmid F16403, complete sequence.  
0.78:203:62  
AC005777

10 R-HEMBA1007013  
Human mRNA for DNA-binding protein TAXREB302, complete cds.  
6.3e-31:163:100  
D28468

15 R-HEMBA1007057  
CIT-HSP-517F5.TP CIT-HSP Homo sapiens genomic clone 517F5, genomic survey sequence.  
1.0:128:67  
B49904

20 R-HEMBA1007063  
Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.  
5.0e-43:300:88  
AL022069

25 R-HEMBA1007241  
HIV-1 RNA V3 region (patient Y, sample Y1, clone 05).  
0.74:148:66  
Z47529

30 R-HEMBA1007291  
Homo sapiens chromosome 19, fosmid 37502, complete sequence.  
3.6e-36:300:80  
AC004755

35 R-HEMBA1007332  
Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.  
7.3e-15:148:80  
U56430

40 R-HEMBA1000106  
Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's.  
8.0e-05:313:60  
L40609

45 R-HEMBA1000276  
HS\_3048\_A2\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=14 Row=E, genomic survey sequence.  
0.91:234:58  
AQ099411

50 R-HEMBA1000309

R-HEMBA1000407  
Mus musculus clone OST5976, genomic survey sequence.  
55 6.4e-28:226:81  
AF046768

R-HEMBA1000447

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Homo sapiens JWA protein mRNA, complete cds.

1.7e-107:533:97

AF070523

- 5 R-HEM BB1000542  
Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.  
4.4e-72:547:80  
AF084259
- 10 R-HEM BB1000567  
Human insulin-like growth factor (IGF-II) gene, exon 1 of 4.  
4.3e-60:368:88  
M13970
- 15 R-HEM BB1000642  
Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.  
2.9e-42:431:75  
Z84483
- 20 R-HEM BB1000668  
CITBI-E1-2508D15.TR CITBI-E1 Homo sapiens genomic clone 2508D15, genomic survey sequence.  
2.5e-40:249:91  
AQ261535
- 25 R-HEM BB1000679  
HS\_3061\_A1\_C03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061  
Col=5 Row=E, genomic survey sequence.  
1.8e-48:257:96  
AQ127602
- 30 R-HEM BB1000881  
CIT-HSP-2350020.TR CIT-HSP Homo sapiens genomic clone 2350O20, genomic survey sequence.  
0.0072:248:61  
AQ062620
- 35 R-HEM BB1000905  
Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.  
2.5e-104:547:94  
AC005089
- 40 R-HEM BB1001026  
  
R-HEM BB1001048
- 45 R-HEM BB1001200  
P.falciparum complete gene map of plastid-like DNA (IR-A).  
1.5e-11:521:59  
X95275
- 50 R-HEM BB1001407  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2705, WORKING DRAFT SEQUENCE.  
3.0e-29:308:77  
AL033529
- 55 R-HEM BB1001530  
Homo sapiens chromosome 19, cosmid R30538, complete sequence.  
0.040:373:63  
AC005943

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R-HEMBB1001547

Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4.

0.027:291:62

AJ235270

5

R-HEMBB1001573

CIT-HSP-2307C1.TR CIT-HSP Homo sapiens genomic clone 2307C1, genomic survey sequence.

1.3e-13:90:98

AQ020395

10

R-HEMBB1001847

Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence.

3.4e-27:147:80

AF064864

15

R-HEMBB1001959

Homo sapiens clone 24781 mRNA sequence.

4.4e-103:504:97

AF070640

20

R-HEMBB1001978

CIT-HSP-2328G6.TF CIT-HSP Homo sapiens genomic clone 2328G6, genomic survey sequence.

7.9e-29:220:86

AQ040310

25

R-HEMBB1002039

Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.

2.7e-37:550:68

AC005014

30

R-HEMBB1002041

Sequence 1 from patent US 5633147.

2.7e-23:322:70

I43819

35

R-HEMBB1002051

Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.

9.2e-35:302:79

AC004825

40

R-HEMBB1002120

Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.

6.0e-05:479:59

AC003106

45

R-HEMBB1002162

Human DNA sequence from clone 739H11 on chromosome 1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS, complete sequence.

3.7e-30:238:84

AL031289

50

R-HEMBB1002228

Homo sapiens BAC clone NH0436H22 from 2, complete sequence.

6.6e-57:274:86

AC005234

55

R-HEMBB1002245

Sequence 25 from patent US 5747660.

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4.8e-30:361:73  
AR005295

R-HEMBB1002302

5 Methanococcus jannaschii section 84 of 150 of the complete genome.  
0.00019:362:59  
U67542

R-HEMBB1002427

10 Genomic sequence from Human 9q34, complete sequence.  
3.9e-105:533:96  
AC001643

R-HEMBB1002465

15 Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.  
2.9e-05:335:62  
AE001382

R-HEMBB1002661

20 R-HEMBB1002663  
\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.  
8.3e-43:268:89  
U14573

R-HEMBB1002693

25 Human BAC clone RG126M09 from 7q21-q22, complete sequence.  
2.4e-24:220:76  
AC002067

R-MAMMA1000046

30 Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.  
0.032:402:57  
AC005505

R-MAMMA1000102

40 Human DNA sequence from cosmid B33F2 on chromosome 22 Contains ESTs.  
2.0e-84:428:96  
Z79996

R-MAMMA1000106

45 Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.  
0.095:138:66  
AP000031

R-MAMMA1000118

R-MAMMA1000141

50 Homo sapiens 12q24.2 PAC RPCI1-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.  
9.0e-91:480:95  
AC004024

R-MAMMA1000204

55 Homo sapiens mRNA for LGMD2B protein.  
1.5e-107:544:96  
AJ007670

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R-MAMMA1000226

H.sapiens VASP gene, exons 4 to 13.

0.99:244:63

X98534

5

R-MAMMA1000403

CIT-HSP-2372A15.TF CIT-HSP Homo sapiens genomic clone 2372A15, genomic survey sequence.

8.0e-38:187:81

AQ112406

10

R-MAMMA1000449

Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.

1.2e-41:422:76

AC004491

15

R-MAMMA1000457

Homo sapiens clone 638 unknown mRNA, complete sequence.

7.4e-116:570:97

AF091084

20

R-MAMMA1000473

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.

9.6e-09:136:77

AC004131

25

R-MAMMA1000496

Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.

2.6e-48:272:93

AC004997

30

R-MAMMA1000528

Human BAC clone RG114A06 from 7q31, complete sequence.

1.8e-13:109:80

AC002542

35

R-MAMMA1000591

Human cosmid g1572c264, complete sequence.

1.6e-22:329:71

AC000359

40

R-MAMMA1000614

R-MAMMA1000652

H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28A10.

0.81:158:65

Z84499

45

R-MAMMA1000681

Homo sapiens full length insert cDNA clone YY85D04.

1.0e-107:560:94

AF088014

50

R-MAMMA1000706

Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.

1.1e-46:232:100

AF067223

55

R-MAMMA1000788

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Bos taurus P14 (p14) mRNA, complete cds.  
3.8e-72:493:84  
AF037349

5 R-MAMMA1000810  
Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence.  
5.0e-37:318:79  
AC003002

10 R-MAMMA1000814  
Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.  
7.7e-15:140:85  
AC003071

15 R-MAMMA1000881  
Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.  
8.8e-46:457:75  
20 AL031311

R-MAMMA1000986  
Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.  
7.7e-44:343:82  
25 AF001550

R-MAMMA1000994  
Homo sapiens mRNA for ISLR, complete cds.  
3.6e-108:552:96  
30 AB003184

R-MAMMA1001043

35 R-MAMMA1001066  
Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.  
1.3e-42:302:82  
AC006120

40 R-MAMMA1001094  
Homo sapiens clone 243 unknown mRNA, complete sequence.  
5.4e-115:567:97  
AF091094

45 R-MAMMA1001141  
HS\_3059\_B1\_H06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3059 Col=11 Row=P, genomic survey sequence.  
1.3e-68:388:92  
AQ214896

50 R-MAMMA1001150  
H.sapiens mRNA for protein kinase C mu.  
5.4e-20:340:66  
X75756

55 R-MAMMA1001237  
Mouse DNA fragment that hybridizes to HSV- 1 SmaI A fragment.  
0.15:222:65  
M11041

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R-MAMMA1001284

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.

1.2e-33:344:76

AL034423

R-MAMMA1001310

Human Bruton agammaglobulinemia (BTK) gene, exons 10-12.

1.8e-39:332:80

L31565

R-MAMMA1001418

Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.

4.4e-42:411:76

U07563

R-MAMMA1001532

Homo sapiens PAC clone DJ0728D04, complete sequence.

2.3e-10:196:73

AC004865

R-MAMMA1001609

HS-1054-B2-H01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=2 Row=P, genomic survey sequence.

1.6e-34:170:79

B42016

R-MAMMA1001615

R-MAMMA1001623

Homo sapiens 12q24.2 BAC RPCI11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

8.8e-21:180:82

AC006065

R-MAMMA1001634

Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.

2.6e-40:283:86

AC005695

R-MAMMA1001893

Homo sapiens clone DJ0782K24, WORKING DRAFT SEQUENCE, 16 unordered pieces.

0.73:132:67

AC006003

R-MAMMA1001901

Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.

4.0e-43:288:77

Z93023

R-MAMMA1001957

Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.

1.2e-41:298:86

AC005212

R-MAMMA1001978

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- 5 R-MAMMA1002070  
Homo sapiens clone DJ400N23, WORKING DRAFT SEQUENCE, 10 unordered pieces.  
2.1e-104:530:97  
AC005003
- 10 R-MAMMA1002080 rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt].  
5.9e-47:449:76  
S72304
- 15 R-MAMMA1002087  
Human Cosmid g1572c037 from 7q31.3, complete sequence.  
1.7e-11:120:83  
AC000125
- 20 R-MAMMA1002095  
Rat alternatively spliced mRNA.  
5.3e-30:289:74  
M93018
- 25 R-MAMMA1002128  
R-MAMMA1002142  
R-MAMMA1002165  
Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence.  
1.1e-28:350:72  
AC005871
- 30 R-MAMMA1002205  
Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING  
PROTEIN (CNBP) like gene and STSs.  
1.2e-42:282:75  
Z83843
- 35 R-MAMMA1002224  
Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project).  
0.99:210:60  
AL022224
- 40 R-MAMMA1002234  
Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).  
1.7e-61:310:81  
X53744
- 45 R-MAMMA1002586  
Streptomyces collinus coenzyme B12-dependent mutase (meaA) gene, complete cds.  
0.99:348:60  
AF008569
- 50 R-MAMMA1002633  
Homo sapiens, clone hRPK. 1\_A\_1, complete sequence.  
2.6e-13:381:64  
AC006196
- 55 R-MAMMA1003126  
R-NT2RM4000100  
Plasmodium falciparum MAL3P2, complete sequence.



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0.00047:296:61  
AL034558

R-NT2RM4000115

5 Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SE-  
QUENCE.

0.079:270:64  
AL031746

10 R-NT2RM4000198

Homo sapiens chromosome 10 clone LA10NC01\_15\_E\_11 map 10q26.3, WORKING DRAFT SEQUENCE, 3 un-  
ordered pieces.

7.7e-24:244:78  
AC006171

15 R-NT2RM4000284

Human IgG Fc receptor hFcRn mRNA, complete cds.

1.7e-93:440:100  
U12255

20 R-NT2RM4000295

, complete sequence.

0.89:351:58  
AC005663

25 R-NT2RM4000326

Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterra-  
nean Fever gene disease.

2.3e-112:602:94  
AJ003147

30 R-NT2RM4000417

Human DNA sequence from PAC 326L13 containing brain-4 mRNA ESTs and polymorphic CA repeat.

0.78:229:62  
Z82170

R-NT2RM4000444

R-NT2RM4000587

40 R-NT2RM4000593

R-NT2RM4000648

0.010:260:61  
AG005508

R-NT2RM4000761

H.sapiens mitochondrial genome (consensus sequence).

3.2e-95:476:97  
X62996

R-NT2RM4000965

R-NT2RM4000997

55 R-NT2RM4001321

Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3'part of the DNA-bind-  
ing Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.

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6.0e-19:282:73  
AL031277

R-NT2RM4001325

R-NT2RM4001377  
Homo sapiens mRNA for KIAA0638 protein, partial cds.  
2.9e-111:553:96  
AB014538

R-NT2RM4001735  
Homo sapiens clone 23904 mRNA sequence.  
4.6e-106:553:94  
AF052129

R-NT2RM4001768  
Human HepG2 3'region Mbol cDNA, clone hmd3c03m3.  
4.1e-29:187:91  
D17194

R-NT2RM4001843  
Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.  
0.95:366:58  
AC005828

R-NT2RM4002352  
Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.  
5.5e-108:557:95  
AB009462

R-NT2RP2000092  
HS\_3070\_B1\_B04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3070  
Col=7 Row=D, genomic survey sequence.  
1.1e-23:247:77  
AQ120714

R-NT2RP2000178  
E.amylovora lon gene.  
1.1e-15:422:62  
X77706

R-NT2RP2000240  
\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1,  
WORKING DRAFT SEQUENCE, 15 unordered pieces.  
0.00010:260:62  
AC004480

R-NT2RP2000394  
HS\_3211\_B2\_G06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211  
Col=12 Row=N, genomic survey sequence.  
1.1e-61:316:97  
AQ174850

R-NT2RP2000447  
Homo sapiens clone DJ1129D05, complete sequence.  
8.7e-67:357:94  
AC005630

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- 5 R-NT2RP2000479  
Homo sapiens chromosome 17, clone 193h18, complete sequence.  
5.7e-51:551:73  
AC002546
- 10 R-NT2RP2000514  
P.falciparum parasite antigen reactive with the parasite inhibitory mouse monoclonal antibody (mMAb) 43E5, clone #366, partial cds.  
2.1e-08:192:68  
M21323
- 15 R-NT2RP2000533  
Mus musculus cornichon mRNA, complete cds.  
3.5e-59:243:82  
AF022811
- 20 R-NT2RP2000616  
Human DNA sequence from clone 694E4 on chromosome 22 Contains exon similar to phosphatidylserine decarboxylase, EST, GSS, complete sequence.  
0.0064:105:67  
AL031255
- 25 R-NT2RP2000649  
Homo sapiens mRNA for Hs Ste24p, complete cds.  
1.4e-65:326:98  
AB016068
- 30 R-NT2RP2000663  
Human DNA sequence from cosmid U61B11, between markers DXS366 and DXS87 on chromosome X contains ESTs.  
7.9e-110:555:96  
Z73913
- 35 R-NT2RP2000712  
Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.  
9.8e-32:308:78  
AC006001
- 40 R-NT2RP2000739  
Bos taurus TATA box binding protein (TBP) gene, partial cds.  
0.19:128:68  
L47974
- 45 R-NT2RP2000818  
Caenorhabditis elegans cosmid C48D5, complete sequence.  
0.010:429:58  
Z36237
- 50 R-NT2RP2000903  
H.sapiens 5T4 gene for 5T4 Oncofetal antigen.  
4.0e-99:505:96  
Z29083
- 55 R-NT2RP2001200  
Homo sapiens mRNA for KIAA0676 protein, partial cds.  
2.0e-57:306:95  
AB014576

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R-NT2RP2001223

R-NT2RP2001276

Mouse regulatory protein (npdc-1) mRNA, complete cds.

5.8e-14:353:65

L03814

R-NT2RP2001388

Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.

1.7e-31:291:77

AC004971

R-NT2RP2001469

M.musculus tex292 mRNA (3'region).

3.7e-26:188:89

X80433

R-NT2RP2001480

Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.

6.6e-83:426:95

L38969

R-NT2RP2001495

transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].

6.3e-43:238:96

S77359

R-NT2RP2001514

Homo sapiens cyclin K (CPR4) mRNA, complete cds.

6.6e-06:57:100

AF060515

R-NT2RP2001538

Mus musculus transcriptional regulatory protein (mSin3) gene, complete cds.

6.9e-12:179:75

L36831

R-NT2RP2001562

Human PAC clone DJ0800B09 from 7q11.23-q21, complete sequence.

0.074:257:61

AC004028

R-NT2RP2001662

Homo sapiens clone 24615 mRNA sequence.

3.2e-94:485:95

AF055012

R-NT2RP2001755

Homo sapiens mRNA for KIAA0762 protein, partial cds.

1.3e-103:576:92

AB018305

R-NT2RP2001769

CIT-HSP-2376O23.TF CIT-HSP Homo sapiens genomic clone 2376023, genomic survey sequence.

1.5e-74:381:96

AQ111163

R-NT2RP2001817

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HS\_2037\_B2\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037  
Col=18 Row=B, genomic survey sequence.

3.9e-60:430:84

AQ243047

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R-NT2RP2001878

Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.

10

0.018:148:67

Z83821

R-NT2RP2001903

Human Not1 linking clone from chromosome 1q32.

15

0.99:160:63

U36769

R-NT2RP2001915

20

R-NT2RP2001921

Homo sapiens clone NH0332L11, complete sequence.

6.5e-86:295:98

AC005538

25

R-NT2RP2001948

Homo sapiens chromosome 19, cosmid R33590, complete sequence.

2.3e-79:440:91

AC005620

30

R-NT2RP2001956

R-NT2RP2002015

Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3'part of the DNA-binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.

35

1.1e-16:254:72

AL031277

R-NT2RP2002063

Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.

40

5.8e-105:550:95

AC004050

R-NT2RP2002188

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.

45

0.47:212:62

AL034555

R-NT2RP2002232

50

R-nnnnnnnnnnnnn

Human mRNA for KIAA0383 gene, partial cds.

2.5e-100:511:96

AB002381

55

R-NT2RP2002409

S.pombe chromosome I cosmid c17H9.

1.0:241:63

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Z98597

R-NT2RP2002510

Homo sapiens chromosome 19, cosmid F19847, complete sequence.  
1.6e-38:307:81

AC005952

R-NT2RP2002527

Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.

1.5e-18:165:83

AC004770

R-NT2RP2002533

Homo sapiens alpha 2 delta calcium channel subunit isoform II mRNA, complete cds.  
9.7e-116:580:96

AF042793

R-NT2RP2002564

Homo sapiens clone DJ0800G07, complete sequence.  
3.8e-110:580:94

AC004890

R-NT2RP2002674

Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.  
1.0:244:60

AE001374

R-NT2RP2002721

Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.  
1.2e-10:221:73

AC003962

R-NT2RP2002824

Human HepG2 3' region Mbol cDNA, clone hmd4f06m3.  
3.0e-07:108:77

D17237

R-NT2RP2002942

Human DNA sequence from clone 88D7 on chromosome Xq25-26.3 Contains F9 (coagulation factor IX (plasma thromboplastic component, Christmas disease, haemophilia B)), dbl oncogene. EST, STS, GSS, complete sequence.

2.0e-37:491:71

AL033403

R-NT2RP2002974

H.sapiens DMAHP gene.  
4.0e-118:585:97

X84813

R-NT2RP2002976

CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.  
8.4e-45:233:98

AQ059444

R-NT2RP2003042

R-NT2RP2003179

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R-NT2RP2003210

R-NT2RP2003302

Human DNA sequence from 4PTL, Huntington's Disease Region, chromosome 4p16.3.

1.5e-24:255:78

Z95704

R-NT2RP2003369

Homo sapiens chromosome 7q22 sequence, complete sequence.

3.1e-95:514:92

AF053356

R-NT2RP2003383

Homo sapiens mRNA for KIAA0458 protein, complete cds.

3.9e-111:549:97

AB007927

R-NT2RP2003390

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.

4.9e-102:413:99

AL024507

R-NT2RP2003469

Genomic sequence from Human 9q34, complete sequence.

1.4e-35:376:74

AC001644

R-NT2RP2003545

Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.

1.5e-09:503:61

AL034557

R-NT2RP2003593

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 971N18, WORKING DRAFT SEQUENCE.

7.8e-81:433:93

AL021396

R-NT2RP2003599

HS\_3240\_A1\_C04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3240 Col=7 Row=E, genomic survey sequence.

0.091:341:58

AQ206348

R-NT2RP2003655

Homo sapiens PAC clone DJ0015I23 from 22, complete sequence.

2.0e-08:249:69

AC004819

R-NT2RP2003664

Homo sapiens mRNA for leptin receptor gene-related protein.

1.7e-110:549:96

Y12670

R-NT2RP2003931

Human mRNA for KIAA0365 gene, partial cds.

5.4e-112:571:96

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AB002363

R-NT2RP2003940

Human Chromosome 11 pac pDJ1173a5, complete sequence.

2.4e-20:353:70

AC000378

R-NT2RP2003950

Homo sapiens clone 24778 unknown mRNA.

1.5e-96:494:95

AF070572

R-NT2RP2004069

Human DNA sequence from clone 618F1 on chromosome Xq25 Contains part of gene similar to DOC4, CA repeat, GSS, complete sequence.

2.6e-50:539:75

AL023878

R-NT2RP2004108

RPCII1-91F9.TV RPCI11 Homo sapiens genomic clone R-91F9, genomic survey sequence. 0.00013:281:63

AQ283338

R-NT2RP2004141

cSRL-115f11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-115f11, genomic survey sequence.

2.3e-05:239:64

B00539

R-NT2RP2004179

Genomic sequence from Human 9q34, complete sequence.

0.43:130:68

AC002322

R-NT2RP2004205

Homo sapiens chromosome 7q22 sequence, complete sequence.

1.4e-42:324:83

AF053356

R-NT2RP2004447

Homo sapiens Chromosome 11q13 BAC Clone 18h3, WORKING DRAFT SEQUENCE, 7 ordered pieces.

5.5e-35:285:84

AC000353

R-NT2RP2004495

transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].

3.4e-44:238:97

S77359

R-NT2RP2004524

Genomic sequence from Human 9q34, complete sequence.

7.4e-113:572:96

AC001644

R-NT2RP2004556

CIT-HSP-2306F6.TF CIT-HSP Homo sapiens genomic clone 2306F6, genomic survey sequence.

8.1e-99:514:95

AQ019229



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R-NT2RP2004606 cDNA encoding NIC(Natural Inhibitor of Collagenase).  
8.2e-116:576:96  
E00985

5 R-NT2RP2004648  
Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.  
0.98:369:57  
AC005828

10 R-NT2RP2004670  
Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.  
4.5e-43:592:69  
L22557

15 R-NT2RP2004794  
  
R-NT2RP2004837  
Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.  
1.2e-60:366:90  
20 AC001232

R-NT2RP2004847  
Homo sapiens full length insert cDNA clone YY87C09.  
1.0e-68:333:100  
25 AF086055

R-NT2RP2005027  
Human glucose transporter-like protein-III (GLUT3), complete cds.  
7.8e-103:508:97  
30 M20681

R-NT2RP2005069  
Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.  
3.8e-42:463:73  
35 U35245

R-NT2RP2005163  
CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.  
7.4e-44:233:96  
40 AQ059444

R-NT2RP2005181  
Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.  
7.6e-53:567:73  
45 AB000113

R-NT2RP2005247  
Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPC11-93D11 (from Roswell  
Park Cancer Center) complete sequence.  
50 5.8e-38:341:76  
AC002357

R-NT2RP2005378  
Homo sapiens full length insert cDNA clone YW25A12.  
55 0.13:152:66  
AF086029

R-NT2RP2005391

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HS\_3056\_A1\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone  
Plate=3056 Col=5 Row=E, genomic survey sequence.

1.1e-14:140:84

AQ134064

5

R-NT2RP2005425

Homo sapiens mRNA for KIAA0803 protein, partial cds.

8.2e-100:526:94

AB018346

10

R-NT2RP2005463

R-NT2RP2005514

15

R-NT2RP2005535

Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.

1.9e-11:488:62

AC003973

20

R-NT2RP2005541

CIT-HSP-2034G23.TF CIT-HSP Homo sapiens genomic clone 2034G23, genomic survey sequence.

2.7e-61:311:98

B74709

25

R-NT2RP2005597

R-nnnnnnnnnnnnn

{FRA16A, folate-sensitive fragile site} [human, Genomic, 160 nt].

0.92:104:65

30

S70397

R-NT2RP2005666

R-NT2RP2005774

35

Homo sapiens apoptosis-related mRNA, 3'UTR, partial sequence.

2.2e-94:440:96

AF035364

R-NT2RP2005878

40

Homo sapiens chromosome 19, cosmid F17987, complete sequence.

1.3e-32:340:76

AC004790

R-NT2RP2005883

45

Human DNA sequence from clone 248E1 on chromosome 6q23.1-23.3 Contains DOPAMINE-BETA-MONOOXY-GENASE PRECURSOR, EF-1-ALPHA-2 pseudogene EST GSS and CA repeat, complete sequence.

1.3e-117:581:97

AL023578

50

R-NT2RP2005887

Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces

2.5e-61:367:90

AC001232

55

R-nnnnnnnnnnnnn

Human paired box gene (PAX6) homologue, complete cds.

5.0e-115:578:96

M93650

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R-NT2RP2005994

Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.

2.4e-116:594:96

AC004050

5

R-NT2RP2006004

Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.

1.8e-45:264:93

U42975

10

R-NT2RP2006042

T31H24TF TAMU Arabidopsis thaliana genomic clone T31H24, genomic survey sequence.

0.42:111:70

B78148

15

R-NT2RP2006092

Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.

1.7e-73:385:95

AC005214

20

R-NT2RP2006099

Homo sapiens PAC clone DJ0903G02, complete sequence.

1.3e-27:335:74

AC004924

25

R-NT2RP2006134

Homo sapiens chromosome 4 clone B139M23 map 4q25, complete sequence.

1.0:143:63

AC004045

30

R-NT2RP2006269

Phreatamoeba balamuthi UBI3 sequence, putative polyubiquitin gene.

0.82:153:63

AJ000657

35

R-NT2RP2006512

Homo sapiens clone 23904 mRNA sequence.

4.6e-106:531:96

AF052129

40

R-NT2RP3000011

HS\_2196\_A2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196

Col=16 Row=I, genomic survey sequence.

1.3e-36:292:83

AQ210450

45

R-NT2RP3000022

Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-15, complete sequence.

0.28:248:60

Z98550

50

R-NT2RP3000059

Homo sapiens chick ovalbumin upstream promoter transcription factor II (COUP-TFII) mRNA, partial cds.

0.047:393:61

M62760

55

R-NT2RP3000063

HS\_3190\_B2\_D10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone

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Plate=3190 Col=20 Row=H, genomic survey sequence.  
0.88:232:63  
AQ172428

- 5 R-nnnnnnnnnnnnn  
RPCI11-35A1.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-35A1, genomic survey sequence.  
3.8e-29:159:99  
AQ045699
- 10 R-NT2RP3000148  
Homo sapiens full length insert cDNA clone ZE03A07.  
2.8e-112:574:95  
AF086510
- 15 R-NT2RP3000169  
Homo sapiens MRS1 mRNA, complete cds.  
4.4e-110:551:96  
AF093239
- 20 R-NT2RP3000171  
  
R-NT2RP3000172  
Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.  
1.3e-40:554:70
- 25 L22557  
  
R-NT2RP3000201  
Homo sapiens BAC clone NH0353P23 from 2, complete sequence.  
6.4e-96:478:97
- 30 AC005035  
  
R-NT2RP3000232  
Plasmodium falciparum MAL3P2, complete sequence.  
0.93:262:61
- 35 AL034558  
  
R-NT2RP3000304  
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.  
2.4e-109:546:97
- 40 AF074264  
  
R-NT2RP3000378  
Mus musculus mSin3A (sin3A) mRNA, complete cds.  
3.0e-27:411:72
- 45 U22394  
  
R-NT2RP3000436  
Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.  
1.1e-06:440:57
- 50 AE001398  
  
R-NT2RP3000444  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 889J22, WORKING DRAFT SEQUENCE.  
5.9e-105:543:95
- 55 AL031406  
  
R-NT2RP3000460  
Canis familiaris sec61 homologue mRNA, complete cds.

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2.8e-12:292:68  
M96629

5 R-NT2RP3000481  
WORKING DRAFT SEQUENCE, 8 unordered pieces.  
0.99:160:65  
AC005992

10 R-NT2RP3000616  
Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5  
unordered pieces.  
0.00087:412:57  
AC005308

15 R-NT2RP3000645

R-NT2RP3000652  
Homo sapiens DNA from chromosome 19, cosmid R32532, complete sequence.  
1.9e-44:539:74  
20 AC004004

R-NT2RP3000676  
Homo sapiens mRNA for KIAA0446 protein, complete cds.  
3.1e-103:542:94  
25 AB007915

R-NT2RP3000677  
Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 4/10.  
0.067:235:61  
30 AB020872

R-NT2RP3000721  
CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.  
4.0e-45:233:98  
35 AQ059444

R-NT2RP3000789

40 R-NT2RP3000818  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 94M16, WORKING DRAFT SEQUENCE.  
5.7e-95:510:93  
Z97201

45 R-NT2RP3000820  
RPC11-77B13.TJ RPC11 Homo sapiens genomic clone R-77B13, genomic survey sequence.  
2.1e-50:266:96  
AQ283547

50 R-NT2RP3000838  
Homo sapiens mRNA for KIAA0638 protein, partial cds.  
4.6e-99:522:94  
AB014538

55 R-NT2RP3000871  
Homo sapiens clone DJ0703P08, WORKING DRAFT SEQUENCE, 23 unordered pieces.  
0.68:249:61  
AC005481

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R-NT2RP3000907

X.laevis oocyte repetitive sequence (XLOREP) mRNA.

2.9e-30:386:69

X65290

5

R-NT2RP3000921

HS\_2026\_A1\_B06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026

Col=11 Row=C, genomic survey sequence.

2.2e-54:311:92

AQ232644

10

R-NT2RP3001012

Rattus norvegicus mRNA for TIP120, complete cds.

9.2e-63:456:83

D87671

15

R-NT2RP3001044

Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.

1.2e-60:366:90

AC001232

20

R-NT2RP3001061

Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.

0.17:357:61

AC005506

25

R-NT2RP3001159

Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.

8.8e-111:561:96

AC004228

30

R-NT2RP3001170

Homo sapiens mRNA for KIAA0784 protein, partial cds.

8.8e-117:561:98

AB018327

35

R-NT2RP3001195

Genomic sequence from Human 9q34, complete sequence.

1.4e-35:376:74

AC001644

40

R-NT2RP3001240

Canis familiaris sec61 homologue mRNA, complete cds.

2.8e-12:292:68

M96629

45

R-NT2RP3001271

Homo sapiens chromosome 19, BAC CIT-B-470f8 (BC330812), complete sequence.

7.9e-17:260:71

AC006115

50

R-NT2RP3001322

Human DNA sequence from PAC 128N22 on chromosome Xq25-Xq26.3. contains STS.

0.035:451:60

Z97629

55

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R-NT2RP3001542

Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.

4.1e-08:500:61

AC004153

R-NT2RP3001560

Mouse mRNA for thymic epithelial cell surface antigen, complete cds.

1.0e-30:523:65

D67067

R-NT2RP3001592

R-NT2RP3001685

Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.

2.4e-30:147:85

AL024474

R-NT2RP3001738

Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.

9.2e-107:553:95

AC004228

R-NT2RP3001754

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.

2.0e-67:345:97

AL034380

R-NT2RP3001858

R-NT2RP3001976

Homo sapiens chromosome 9, clone hRPK.467\_F\_21, complete sequence.

4.4e-14:302:62

AC006239

R-NT2RP3002015

Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.

6.2e-65:492:82

AC004832

R-NT2RP3002160

Genomic sequence from Human 9q34, complete sequence.

2.1e-82:431:95

AC001643

R-NT2RP3002281

Homo sapiens mRNA for KIAA0765 protein, partial cds.

1.1e-81:446:93

AB018308

R-NT2RP3002286

Mus musculus EGF repeat transmembrane protein mRNA, complete cds.

1.0e-80:378:90

U57368

R-NT2RP3002311

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Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.  
0.57:366:58  
AC005828

5 R-NT2RP3002324  
H.sapiens gene for nitric oxide synthase (promoter region).  
1.6e-30:337:72  
Z49251

10 R-NT2RP3002342  
transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].  
6.5e-45:238:98  
S77359

15 R-NT2RP3002353  
Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence. 0.00015:164:70  
AC002044

NNNNNNNNNNNNNNNN  
20 Homo sapiens mRNA for KIAA0788 protein, partial cds.  
4.5e-98:493:96  
AB018331

NNNNNNNNNNNNNNNN

25 R-NT2RP3002448  
S.cerevisiae DNA for ori 2.  
0.52:91:71  
X59535

30 /  
R-NT2RP3002571

R-NT2RP3002664  
Homo sapiens full length insert cDNA clone ZC48G09.  
35 9.9e-103:522:96  
AF086209

R-NT2RP3002721

40 R-NT2RP3002737

R-NT2RP3002738  
Sequence 4 from patent US 5541109.  
2.9e-22:171:74  
45 I24014

R-NT2RP3002790

R-NT2RP3002836  
50 Bos taurus retina specific RGS protein (RET-RGS1) mRNA, complete cds.  
2.3e-34:384:75  
U89254

R-NT2RP3002887  
55 Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.  
1.6e-05:435:62  
AF051726



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R-NT2RP3002900

Homo sapiens mRNA from chromosome 5q21-22, clone:A3-B.

1.3e-116:569:97

AB002451

R-NT2RP3002958

Homo sapiens clone 23851 mRNA sequence.

2.0e-117:575:98

AF035313

R-NT2RP3002983

Homo sapiens genomic DNA, chromosome 21q11.1, segment 17/28, WORKING DRAFT SEQUENCE.

5.1e-59:295:99

AP000046

**R-NT2RP3003000**

Homo sapiens clone 24597 mRNA sequence.

6. |e-109:562:95

AF070604

R-NT2RP3003076

R-NT2RP3003354

Human protocadherin 42 mRNA, complete cds for abbreviated PC42.

0.87:208:61

L11370

R-NT2RP3003448

High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.

1.3e-41:287:80

AC005840

R-NT2RP3003469

Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3' part of the DNA-binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.

2.1e-18:223:77

AL031277

R-NT2RP3003473

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING DRAFT SE-  
QUENCE.

1.5e-54:294:96

Z99716

R-NT2RP3003527

Homo sapiens mRNA for protein kinase Dyrk1B.

5.1e-91:445:97

Y17999

R-NT2RP3003532

Mus musculus cell surface molecule OX-2 mRNA, complete cds.

1.2e-30:529:67

AF004023

R-oooooooooooo

Homo sapiens PAC clone DJ0531G15 from 7p21, complete sequence.

0.13:294:61

AC004739

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5 R-NT2RP3003559  
CIT-HSP-2307F17.TR CIT-HSP Homo sapiens genomic clone 2307F17, genomic survey sequence.  
1.4e-15:342:68  
AQ016972

10 R-NT2RP3003614  
Homo sapiens chromosome 19, cosmid F21967, complete sequence.  
0.013:174:64  
AC005256

15 R-NT2RP3003729

R-NT2RP3003849  
Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 6 unordered pieces.  
8.9e-106:557:94  
AC002320

20 R-NT2RP3003874  
Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c.  
1.6e-55:302:94  
AJ001381

25 R-NT2RP3003963  
cSRL-66f9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-66f9, genomic survey sequence.  
0.028:78:76  
B05608

30 R-NT2RP3004000  
Tapa-1=integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 861 nt, segment 7 of 7].  
0.87:212:62  
S45012

35 R-NT2RP3004025  
Homo sapiens chromosome 19, cosmid F17987, complete sequence.  
0.71:197:62  
AC004790

40 R-NT2RP3004075

R-NT2RP3004083  
Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 5.  
0.27:375:59  
Z97340

45 R-NT2RP3004090  
CIT-HSP-2172H20.TR CIT-HSP Homo sapiens genomic clone 2172H20, genomic survey sequence.  
2.2e-40:243:91  
B99962

50 R-NT2RP3004119  
Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.  
8.3e-42:475:73  
AC004953

55 R-NT2RP3004130

R-NT2RP3004133

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CIT-HSP-2306G15.TR CIT-HSP Homo sapiens genomic clone 2306G15, genomic survey sequence.  
0.00037:194:64  
AQ022229

5 R-NT2RP3004202  
Homo sapiens BAC clone GS285F21 from 7q21-q22, complete sequence.  
0.65:209:62  
AC004012

10 R-NT2RP3004294

R-NT2RP3004309  
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.  
15 7.4e-99:500:96  
AC004228

R-NT2RP3004321  
Human chromosome 11 168h3 cosmid, complete sequence.  
20 1.7e-105:540:96  
U73637

R-NT2RP3004345  
Human BAC clone RG016J04 from 7q21, complete sequence.  
25 0.00033:348:61  
AC002064

R-NT2RP3004355  
Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.  
30 0.0029:180:66  
AC004709

R-NT2RP3004374  
Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3' part of the DNA-binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.  
35 4.3e-18:223:77  
AL031277

40 R-NT2RP3004406  
Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-70, complete sequence.  
1.0:201:62  
AL010239

45 R-NT2RP3004481

R-NT2RP3004552  
Human germline immunoglobulin lambda light chain pseudogene (VII.1).  
1.0:165:63  
50 X57825

R-NT2RP3004625  
Homo sapiens I-1 receptor candidate protein mRNA, complete cds.  
8.2e-49:352:84  
55 AF082516

R-NT2RP3004640  
Homo sapiens full length insert cDNA clone ZC45E05.

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1.2e-96:471:98  
AF086205

5 R-NT2RP3004647  
Homo sapiens mRNA for KIAA0446 protein, complete cds.  
1.5e-109:555:96  
AB007915

10 R-NT2RP4000108  
Mouse neurofilament protein (NF-L) gene, 3' flank.  
1.0e-09:344:63  
M55424

15 R-NT2RP4000634  
Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.  
1.6e-16:267:71  
AC003037

20 R-NT2RP4000962  
Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a BAC end-sequence (GSS).  
0.026:176:67  
AL021069

25 R-NT2RP4001001  
Drosophila melanogaster Oregon-R mitochondrial A+T region.  
0.00026:354:61  
U11584

30 R-NT2RP4001009  
Homo sapiens mRNA for Hs Ste24p, complete cds.  
1.6e-82:408:98  
AB016068

35 R-NT2RP4001467  
Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).  
1.8e-111:545:97  
X55740

40 R-NT2RP4001877  
Yeast (S.cerevisiae) mitochondrial cob gene, intron 4.  
0.19:384:59  
J01469

45 R-NT2RP4001879  
Homo sapiens full length insert cDNA clone ZD76G10.  
4.4e-107:548:94  
AF086408

50 R-NT2RP4002187  
RPCI11-69F22.TK RPCI11 Homo sapiens genomic clone R-69F22, genomic survey sequence.  
7.1e-37:240:89  
AQ238297

55 R-NT2RP4002451  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING DRAFT SEQUENCE.  
5.8e-111:575:96  
Z98200

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R-NT2RP4002715

Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.

2.5e-61:367:90

AC001232

5

R-NT2RP4002750

Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.

1.2e-52:527:74

AB000113

10

R-OVARC1000003

Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.

2.3e-10:140:77

AC004909

15

R-OVARC1000090

Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SE-  
QUENCE.

2.8e-59:323:78

20

DB4394

R-OVARC1000105

H.sapiens gene for ribosomal protein L38.

2.7e-12:83:100

25

Z26876

R-OVARC1000137

R-OVARC1000208

30

Homo sapiens PAC clone DJ0817I18 from 7p11.2p13, complete sequence.

2.7e-52:464:79

AC004901

R-OVARC1000255

35

H.sapiens syk mRNA for protein-tyrosine kinase.

1.9e-105:511:98

Z29630

R-OVARC1000275

40

R-OVARC1000298

Plasmodium falciparum carbamoyl phosphate synthetase II gene, complete cds.

0.66:364:59

L32150

45

R-OVARC1000307

R-OVARC1000313

Homo sapiens mRNA for KIAA0573 protein, partial cds.

50

1.6e-96:534:93

AB011145

R-OVARC1000331

Sequence 2 from patent US 5763589.

55

8.1e-66:335:97

AR012692

R-OVARC1000410

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Homo sapiens clone 23767 and 23782 mRNA sequences.

1.0e-88:462:94

AF007150

5

R-OVARC1000439

E.coli fanG and fanH genes.

0.99:424:58

Y00531

10

R-OVARC1000467

HS\_3235\_A2\_A12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=24 Row=A, genomic survey sequence.

9.2e-09:125:76

AQ206826

15

R-OVARC1000529

R-OVARC1000553

Homo sapiens chromosome 19, cosmid R26894, complete sequence.

20

2.0e-84:437:96

AC005594

R-OVARC1000775

CIT-HSP-2060P5.TF CIT-HSP Homo sapiens genomic clone 2060P5, genomic survey sequence. 0.29:223:63

25

B70025

R-OVARC1000811

Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.

2.8e-89:438:98

30

AC004235

R-OVARC1000853

RPCI11-16C11.TV RPCI-11 Homo sapiens genomic clone RPCI-11-16C11, genomic survey sequence.

5.3e-53:317:92

35

B76661

R-OVARC1000873

Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.

40

1.2e-102:511:97

AL034418

R-OVARC1000916

H.sapiens PISSLRE mRNA.

45

5.8e-111:588:94

X78342

R-OVARC1000956

Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains polymorphic VNTR pYNZ32.

50

2.7e-89:478:94

Z69708

R-OVARC1000995

Human DNA sequence from clone 885E17 on chromosome 1p33-34.1. Contains STSs and GSSs and genomic marker D1S1302, complete sequence.

55

9.5e-46:325:84

AL031294

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- 5 R-OVARC1001030  
Homo sapiens neuroendocrine-specific protein C (NSP) mRNA, complete cds.  
1.2e-05:197:63  
L10335
- 10 R-OVARC1001049  
  
R-OVARC1001086  
Homo sapiens cyclin T2a mRNA, complete cds.  
4.3e-105:569:94  
AF048731
- 15 R-OVARC1001132  
Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.  
2.2e- 111:569:96  
AP000038
- 20 R-OVARC1001163  
Sus scrofa MHC SLA class III steroid 21-hydroxylase (CYP21) gene, complete cds, ORF human-like gene, last 5  
exons.  
0.010:349:60  
M83939
- 25 R-OVARC1001222  
Spiroplasma citri orfa and orff genes, partial cds, orfb, orfc, and orfe genes and Spiroplasma virus SpV1-derived  
ORF1 and ORF3 genes, complete cds, and SpV1-derived ORF14 gene, partial cds.  
0.58:184:60  
U28972
- 30 R-OVARC1001260  
Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.  
1.1e-10:140:78  
AC004909
- 35 R-OVARC1001336  
Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.  
2.3e-10:140:77  
AC004909
- 40 R-OVARC1001338  
  
R-OVARC1001569  
  
R-OVARC1001570
- 45 R-OVARC1001596  
Homo sapiens chromosome 17, clone hRPK.372\_K\_20, complete sequence.  
5.9e-47:361:83  
AC005951
- 50 R-OVARC1001607  
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.  
3.3e-112:559:96  
U15128
- 55 R-OVARC1001725  
Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.  
3.9e-56:318:95

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AF064800

R-OVARC1001727

Human DNA sequence from clone 48A11 on chromosome 20p12 Contains EST, STS, GSS, complete sequence.  
6.1e-101:533:94  
AL031132

R-OVARC1001807

Human TR3 orphan receptor mRNA, complete cds.  
2.8e-87:426:97  
L13740

R-OVARC1001833

Mouse fork head related protein (HNF-3beta) mRNA, complete cds.  
1.1e-21:263:76  
L10409

R-OVARC1001991

H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 301e3, reverse read 301e3.r.  
0.90:151:59  
Z79826

R-OVARC1002058

Homo sapiens full length insert cDNA clone ZD58C02.  
1.9e-105:547:95  
AF088043

R-OVARC1002178

Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.  
0.26:429:58  
AL031053

R-PLACE1000033

Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.  
0.098:467:59  
AC004688

R-PLACE1000231

Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.  
0.91:141:64  
AC003083

R-PLACE1000258

Human DNA sequence from clone 710L4 on chromosome Xq11.2-12 Contains part of a gene similar to myotubularin-related protein, EST, STS and GSS, complete sequence.  
3.8e-53:524:75  
AL034408

R-PLACE1000442

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22F20, complete sequence.  
3.0e-07:413:62  
AB016873

R-PLACE1000560

Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.  
6.3e-59:323:94



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AC005368

R-PLACE1000740  
H.sapiens PEX gene.  
0.0065:202:63  
Y10196

R-PLACE1000912

R-PLACE1000914  
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.  
3.4e-68:452:86  
AC002093

R-PLACE1000927  
Cowpox virus strain GRI-90 DNA (49 kb fragment).  
1.8e-46:432:76  
Y15035

R-PLACE1000986  
HS\_2037\_A2\_B06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037  
Col=12 Row=C, genomic survey sequence.  
0.087:48:89  
AQ232754

R-PLACE1001016  
M.fascicularis gene for apolipoprotein A-IV.  
0.016:226:61  
X68361

R-PLACE1001100  
Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear in-  
hibitor of protein phosphatase-1, ESTs, and a CA repeat.  
3.4e-37:320:80  
AL020997

R-PLACE1001114  
RPC111-5C23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-5C23, genomic survey sequence.  
9.2e-44:173:85  
B49180

R-PLACE1001123

R-PLACE1001183  
Plasmodium falciparum MAL3P8, complete sequence.  
0.47:217:63  
AL034560

R-PLACE1001229  
Mitochondrion Culex torrentium A+T rich mitochondrial control region.  
3.3e-09:356:63  
U69573

R-PLACE1001231  
Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.  
1.2e-09:186:72  
AF026554

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R-PLACE1001340

Homo sapiens mRNA for KIAA0719 protein, complete cds.

2.0e-51:265:98

AB018262

5

R-PLACE1001401

Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence.

0.0073:203:60

AF033929

10

R-PLACE1001407

Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.

5.8e-70:360:96

AL023582

15

R-PLACE1001464

Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).

3.1e-90:457:96

X55740

20

R-PLACE1001500

Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.

1.0:232:62

AC004929

25

R-PLACE1001516

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.

1.9e-26:168:88

AC002425

30

R-PLACE1001536

Human Chromosome X clone bWXD187, complete sequence.

6.5e-61:310:98

AC004383

35

R-PLACE1001564

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SE-  
QUENCE.

2.9e-100:504:97

AL033377

40

R-PLACE1001655

Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds.

3.8e-1 17:578:97

AF043472

45

R-PLACE1001788

Sequence 9 from Patent WO9722695.

1.9e-05:91:82

A63556

50

R-PLACE1001795

R-PLACE1001836

, complete sequence.

4.1e-14:269:69

AC005406

55

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R-PLACE1001918

Human HepG2 3' region Mbol cDNA, clone hmd4f06m3.

7.3e-25:151:95

D17237

5

R-PLACE1001949

Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR1S1). Contains ESTs, an STS and GSSs, complete sequence.

10

0.54:165:63

Z94056

R-PLACE1002080

Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.

15

3.7e-60:289:95

AC004150

R-PLACE1002095

Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-52, complete sequence.

20

0.00052:422:59

AL008982

R-PLACE1002153

Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.

25

4.6e-100:514:95

AF095791

R-PLACE1002329

Homo sapiens chromosome 19, cosmid R31855, complete sequence.

30

1.3e-46:257:95

AC005782

R-PLACE1002355

HS\_2057\_B1\_D01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2057 Col=1 Row=H, genomic survey sequence.

35

0.089:132:65

AQ245227

R-PLACE1002374

Human mRNA for pro-cathepsin L (major excreted protein MEP).

40

2.6e-101:501:97

X12451

R-PLACE1002518

HS\_2176\_A2\_D04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2176 Col=8 Row=G, genomic survey sequence.

45

1.7e-43:221:100

AQ014851

R-PLACE1002547

Homo sapiens mRNA for KIAA0719 protein, complete cds.

50

2.0e-53:276:97

AB018262

R-PLACE1002726

Human DNA-binding protein ABP/ZF mRNA, complete cds.

55

1.1e-37:212:94

U82613

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R-PLACE1002905

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SE-  
QUENCE.

1.2e-42:302:86

AL034417

R-PLACE1002911

R-PLACE1002967

Homo sapiens chromosome 16, BAC clone 461A8, complete sequence.

2.3e-39:310:82

AC006111

R-PLACE1003135

Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SE-  
QUENCE.

2.2e-07:418:60

AL034557

R-PLACE1003163

Homo sapiens DBI-related protein mRNA, complete cds.

4.7e-110:547:96

AF069301

R-PLACE1003407

Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.

1.7e-47:287:91

AF068227

R-PLACE1003428

Human DNA sequence from clone 55C23 on chromosome 6q22.3-23.3 contains vanin-like genes VNN1 and VNN2,  
ESTs, GSSs,, complete sequence.

1.1e-75:268:98

AL032821

R-PLACE1003438

R-PLACE1003460

HS\_3026\_B1\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026  
Col=15 Row=B, genomic survey sequence.

0.30:100:69

AQ093523

R-nnnnnnnnnnnnn

Homo sapiens clone DJ0981007, complete sequence.

3.3e-46:135:98

AC006017

R-PLACE1003573

HS\_3079\_B2\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079  
Col=4 Row=B, genomic survey sequence.

1.1e-49:261:96

AQ121751

R-PLACE1003598

R-PLACE1003644

Caenorhabditis elegans cosmid F52H3, complete sequence.

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0.38:345:62  
Z66512

R-PLACE1003737

5 Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.  
1.9e-77:406:96  
AC005859

R-PLACE1003772

10 Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.  
2.2e-29:454:70  
AL020997

R-PLACE1003839

15 Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.  
3.0e-52:272:97  
AC004131

R-PLACE1003845

20 HS\_3219\_A1\_A10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=19 Row=A, genomic survey sequence.  
1.5e-13:231:70  
AQ181482

R-PLACE1003852

25 Homo sapiens mRNA for KIAA0758 protein, partial cds.  
6.8e-86:439:96  
AB018301

R-PLACE1004028

R-PLACE1004078

35 Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.  
5.0e-36:310:80  
AC006064

R-PLACE1004166

40 Petromyzon marinus neurofilament subunit NF-180 mRNA, complete cds.  
0.95:224:62  
U19361

R-nnnnnnnnnnnnn

45 Fugu rubripes GSS sequence, clone 076D01bH10, genomic survey sequence.  
3.0e-08:107:77  
AL026605

R-PLACE1004199

50 Human prostaglandin D2 synthase gene, exons 2 through 6 and complete cds.  
0.0028:157:67  
M98538

R-PLACE1004279

55 Human DNA sequence from PAC 193B12 on chromosome 6p21.3-22.3. Contains histone H2A/d, H2B/d, H2A.i, H1.5, H3.F, H4.k, H3/j genes, histone pH2b.i and hypothetical protein A4 pseudogenes, histone H2A.1 and H2B.2 duplicate genes, Glycine (GGC) tRNA gene, olfactory receptor OL1 like gene, ESTs STSs and predicted CpG islands.

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0.00065:228:58  
Z98744

R-PLACE1004282

R-PLACE1004305  
Homo sapiens mRNA for KIAA0740 protein, complete cds.  
2.0e-77:377:99  
AB018283

R-PLACE1004441  
RPCI11-76P13.TV RPCI11 Homo sapiens genomic clone R-76P13, genomic survey sequence.  
1.8e-73:370:97  
AQ281810

R-PLACE1004450  
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.  
0.87:269:59  
AB012242

R-PLACE1004482  
Mus musculus hematopoietic lineage switch 2 (HLS2) mRNA, complete cds.  
5.2e-33:356:75  
AF009513

R-PLACE1004492  
Mus musculus mRNA for Doc2, partial cds.  
4.1e-28:268:77  
D50000

R-PLACE1004519  
Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.  
1.8e-14:330:67  
AL021808

R-PLACE1004520  
Human pregnancy specific beta-1-glycoprotein 1 (PSG1) gene.  
1.4e-73:397:93  
M93705

R-PLACE1004630

R-PLACE1004637  
Human Chromosome 11 Cosmid cSRL16b6, complete sequence.  
5.5e-108:625:91  
U73638

R-PLACE1004648

R-PLACE1004816  
Homo sapiens mRNA for Hakata antigen, complete cds.  
5.6e-103:586:90  
D88587

R-PLACE1004887  
CIT-HSP-2172H20.TR CIT-HSP Homo sapiens genomic clone 2172H20, genomic survey sequence.

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1.2e-31:177:97  
B99962

5 R-PLACE1005003  
Mus musculus clone OST13719, genomic survey sequence.  
0.0043:159:64  
AF046703

10 R-PLACE1005005  
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.  
2.1e-56:299:95  
AF032456

15 R-PLACE1005031  
Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.  
1.0:155:65  
AC005821

20 R-PLACE1005239  
Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, pH4-17).  
4.4e-85:450:93  
AJ223351

25 R-PLACE1005250  
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.  
7.7e-19:232:73  
U50734

30 R-PLACE1005383  
Homo sapiens UP50 mRNA, complete cds.  
2.0e-77:471:88  
AF093118

35 R-PLACE1005410  
Canis familiaris sec61 homologue mRNA, complete cds.  
6.4e-12:132:82  
M96629

40 R-PLACE1005426  
Human pregnancy specific beta-1-glycoprotein 4 (PSG4) mRNA, complete cds.  
2.3e-109:574:94  
M94891

45 R-PLACE1005519  
Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SE-  
QUENCE.  
4.1e-08:426:61  
AL034557

50 R-PLACE1005539

R-PLACE1005544  
Homo sapiens chromosome 19, cosmid F20887, complete sequence.  
1.0e-17:202:73  
55 AC005578

R-PLACE1005569  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.

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3.8e-89:470:95  
AL034397

R-PLACE 1005601  
Homo Sapiens angiotensin II receptor gene, complete cds.  
8.0e-52:301:90  
L48211

R-PLACE1005660

R-PLACE1005669  
Mitochondrion Culex torrentium A+T rich mitochondrial control region.  
9.5e-09:338:63  
U69573

R-PLACE1005682  
Caenorhabditis elegans cosmid M70.  
0.012:226:62  
AF047661

R-PLACE1005725  
Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y48E1, WORKING DRAFT SE-  
QUENCE.  
0.42:435:59  
Z92856

R-PLACE1005736  
Rattus norvegicus DD6A4-1 mRNA, partial sequence.  
9.0e-21:282:73  
AF034237

R-PLACE1005745  
RPC11-88L20.TJ RPC11 Homo sapiens genomic clone R-88L20, genomic survey sequence.  
2.4e-62:310:99  
AQ281511

R-PLACE1005768  
Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.  
5.6e-94:511:93  
Z82185

R-PLACE1005815  
Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.  
9.0e-55:586:73  
AC002310

R-PLACE1005878

R-PLACE1005927

R-PLACE1006071  
CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.  
1.6e-76:410:95  
AQ022149

R-PLACE1006073  
Homo sapiens mRNA for glucuronyltransferase I, complete cds.  
2.2e-97:513:93



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AB009598

R-PLACE1006079

Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.

5.4e-57:333:91

AF028233

R-PLACE1006093

R-nnnnnnnnnnnnn

Caenorhabditis elegans mRNA for GAP-2-7, partial cds.

1.9e-08:251:60

AB011283

R-PLACE1006219

HS\_3219\_A1\_A10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219

Col=19 Row=A, genomic survey sequence.

3.1e-12:228:69

AQ181482

R-PLACE1006277

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.

7.8e-96:557:91

AL034397

R-PLACE1006290

Bacillus whitei clone pWH/Cugl satellite DNA.

0.37:209:62

U90159

R-PLACE1006443

Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.

8.9e-76:451:91

AC002093

R-PLACE1006515

Homo sapiens mRNA for KIAA0576 protein, partial cds.

2.1e-76:413:94

AB011148

R-PLACE1006716

M.musculus gene encoding prostaglandin D synthase, putative.

1.0:199:59

Y10138

R-PLACE1006786

HS\_2037\_A2\_B06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037

Col=12 Row=C, genomic survey sequence.

0.33:47:91

AQ232754

R-PLACE1006809

Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene.

0.67:241:59

U52112

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R-PLACE1006959

R-PLACE1007028

5 R-PLACE1007040  
Rabbit angiotensin-converting enzyme (ACE-P) gene, 5' end.  
0.0037:208:65  
M58579

10 R-PLACE1007077  
CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.  
3.0e-76:411:94  
AQ022149

15 R-PLACE1007081  
RPCI11-31D7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-31D7, genomic survey sequence.  
1.9e-06:88:84  
AQ016433

20 R-PLACE1007096  
H.sapiens DMD gene microsatellite (147-200bp).  
1.0:142:59  
X77677

25 R-PLACE1007296

R-PLACE1007591  
Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.  
30 1.6e-11:203:66  
AL023574

R-PLACE1007626  
Homo sapiens unknown mRNA, complete cds.  
35 4.9e-29:183:91  
AF047439

R-PLACE1007702  
Homo sapiens chromosome 17, clone 363G12, WORKING DRAFT SEQUENCE, 11 unordered pieces.  
40 2.3e-75:445:90  
AC002348

R-PLACE1007845  
CIT-HSP-2306G15.TR CIT-HSP Homo sapiens genomic clone 2306G15, genomic survey sequence.  
45 0.00045:194:64  
AQ022229

R-PLACE1007881  
CITBI-E1-2503C21.TF CITBI-E1 Homo sapiens genomic clone 2503C21, genomic survey sequence.  
50 0.43:104:69  
AQ263355

R-PLACE1007971

55 R-PLACE1008282  
Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.  
7.7e-73:396:94  
AC005995

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R-PLACE1008297

N.frontalis enolase gene, promotor region.

1.2e-08:457:57

X81451

R-PLACE1008359

Plasmodium falciparum MAL3P1, complete sequence.

0.00044:443:56

Z97348

R-PLACE1008469

Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.

4.4e-78:536:84

AC002093

R-PLACE1008549

Mus musculus E74-like factor 5 (Elf5) mRNA, complete cds.

3.4e-30:256:75

AF049702

R-PLACE1008657

Homo sapiens BAC clone GS067A24 from 7q21.q21.2, complete sequence.

1.9e-40:320:82

AC005009

R-PLACE1008716

Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.

8.2e-118:591:96

U15128

R-PLACE1008744

Sequence 1 from patent US 5691147.

3.1e-108:559:94

I76197

R-PLACE1008984

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SEQUENCE.

1.6e-102:503:96

AL031427

R-PLACE1008985

Mus musculus synaptotagmin VIII mRNA, partial cds.

9.7e-29:255:77

U20107

R-PLACE1009067

R-PLACE1009196

Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y48A6, WORKING DRAFT SEQUENCE.

0.0094:206:65

Z92854

R-PLACE1009279

Homo sapiens serine protease (PRSS11) mRNA, partial cds.

2.4e-26:553:62

AF097709

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R-PLACE1009527

Human DNA-binding protein ABP/ZF mRNA, complete cds.

7.9e-91:497:91

U82613

R-PLACE1009546

Human PAC clone DJ218B13 from Xq23, complete sequence.

0.29:147:64

AC002072

R-PLACE1009600

Mouse mRNA for tetracycline transporter-like protein, complete cds.

6.1e-81:466:90

D88315

R-PLACE1009735

Homo sapiens clone NH0523H20, complete sequence.

2.0e-74:268:99

AC005041

R-nnnnnnnnnnnnn

Homo sapiens DNA sequence from PAC 833B2 on chromosome Xq26.1-27.2. Contains an EST, complete sequence.

1.9e-05:255:65

AL023800

R-PLACE1010011

, complete sequence.

2.9e-77:174:100

AC005409

R-PLACE1010078

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 209H1, WORKING DRAFT SEQUENCE.

1.0:108:65

Z84465

R-PLACE1010081

Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.

9.2e-105:560:93

AF027706

R-PLACE1010251

Plasmodium falciparum MAL3P4, complete sequence.

5.0e-07:468:58

AL008970

R-PLACE1010445

Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence.

1.2e-49:303:90

AF077058

R-PLACE1010713

RPCI11-69F22.TK RPCI11 Homo sapiens genomic clone R-69F22, genomic survey sequence.

7.4e-11:114:80

AQ238297

R-PLACE1010784

Capra hircus strain Saanen, genomic survey sequence.

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7.4e-24:182:87  
AF083406

R-PLACE1010827

5 nbxb0026K23f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0026K23f, genomic survey sequence.  
1.0:252:61  
AQ271546

R-PLACE1010968

10 Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5  
unordered pieces.  
0.0038:295:57  
AC005308

R-PLACE1011045

15 Homo sapiens E1-like protein mRNA, complete cds.  
1.6e-90:453:96  
AF094516

R-PLACE1011116

20 Homo sapiens embryonic lung protein (HUEL) mRNA, complete cds.  
4.6e-72:385:94  
AF006621

R-PLACE1011236

25 \*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0289H06; HTGS phase 1,  
WORKING DRAFT SEQUENCE, 4 unordered pieces.  
0.98:142:65  
AC004580

R-PLACE1011364

R-PLACE1011407

35 Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some  
similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1).  
Contains GSSs, complete sequence.  
9.1e-27:293:74  
AL031575

R-PLACE1011516

40 Fugu rubripes GSS sequence, clone 190N14aC12, genomic survey sequence.  
1.0:96:68  
AL030602

R-PLACE1011708

45 Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.  
2.4e-91:521:91  
AF034611

R-PLACE1011824

50 Figure 6. DNA sequence of three 3'apoB VNTR alleles.  
2.2e-06:264:65  
M23046

R-PLACE1011978

55 Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.  
4.8e-50:553:69  
M27877

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R-PLACE2000118

Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence), complete sequence.

3.9e-107:567:94

AL022578

R-PLACE2000219

Homo sapiens clone RG132J19, complete sequence.

4.7e-39:317:82

AC005163

R-PLACE3000181

Human protocadherin 42 mRNA, 3' end of cds for alternative splicing PC42-8.

3.9e-81:441:94

L11369

R-PLACE3000213

Sequence 1 from patent US 5691147.

1.5e-109:559:95

I76197

R-PLACE4000354

Sequence 1 from patent US 5691147.

2.7e-106:548:95

I76197

R-PLACE4000455

Arabidopsis thaliana genomic DNA chromosome 3, P1 clone: MEBS, complete sequence.

9.3e-07:357:60

AB019230

R-THYRO1000036

Sequence 11 from patent US 5773248.

4.0e-99:527:93

AR014074

R-THYRO1000061

Homo sapiens chromosome 19, cosmid R34382, complete sequence.

7.3e-90:460:96

AC005329

R-THYRO1000099

R-THYRO1000196

Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.

1.1e-104:530:96

AF016272

R-THYRO1000400

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.

1.0:308:61

AC004685

R-THYRO1000580

Human Kox26 mRNA for zinc finger protein, partial.

0.11:105:67

X52357

R-THYRO1000584

\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1, WORKING DRAFT SEQUENCE, 15 unordered pieces.

1.4e-14:241:68

AC004480

R-THYRO1000678

Belonogaster petiolata 16S ribosomal RNA gene, mitochondrial gene for mitochondrial rRNA, partial sequence.

0.049:150:64

AF066910

R-THYRO1000776

CITBI-E1-2505N5.TF.1 CITBI-E1 Homo sapiens genomic clone 2505N5, genomic survey sequence.

0.38:179:63

AQ241670

R-THYRO1000795

R-THYRO1000846

Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.

3.6e-06:425:61

AF029779

R-THYRO1000866

Homo sapiens SKB1Hs mRNA, complete cds.

4.0e-42:251:92

AF015913

R-THYRO1000956

R-THYRO1000964

Human Chromosome 11 Cosmid cSRL186g7, complete sequence.

0.18:292:61

U73627

R-THYRO1000999

CIT-HSP-2288E24.TR CIT-HSP Homo sapiens genomic clone 2288E24, genomic survey sequence.

3.6e-18:292:71

AQ002356

R-THYRO1001063

Homo sapiens chromosome 16 BAC clone CIT987SK-381E11 complete sequence.

1.5e-27:292:76

AF001552

R-THYRO1001071

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 37E16, WORKING DRAFT SEQUENCE.

1.7e-105:513:98

Z83844

R-THYRO1001102

Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.

3.2e-62:429:86

AC004832

R-THYRO1001113

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Caenorhabditis elegans cosmid C25F9, complete sequence.

0.026:338:58

Z81476

5 R-THYRO1001128

Homo sapiens chromosome 9q34, clone 63G10, complete sequence.

5.3e-12:132:79

AC002096

10 R-THYRO1001205

Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5 unordered pieces.

1.9e-60:251:85

AC004987

15 R-THYRO1001237

R-THYRO1001242

Mouse mRNA for thymic epithelial cell surface antigen, complete cds.

1.5e-45:525:75

20 D67067

R-THYRO1001266

H.sapiens DNA containing a polymorphic (CA)<sub>n</sub> repeat (436bp).

6.0e-05:258:67

25 X65457

R-THYRO1001327

Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

30 2.8e-104:541:95

AL021578

R-THYRO1001456

35

R-THYRO1001457

H.sapiens mRNA for protein kinase C mu.

2.9e-23:391:66

X75756

40

R-THYRO1001471

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete sequence.

0.39:271:61

AC004787

45

R-THYRO1001478

R-THYRO1001495

Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.

50 2.8e-88:446:88

AC006006

R-THYRO1001523

CIT-HSP-2333F9.TF CIT-HSP Homo sapiens genomic clone 2333F9, genomic survey sequence.

55 1.4e-05:126:71

AQ039390

R-THYRO1001529



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R-THYRO1001593

Homo sapiens chromosome 19, cosmid R33632, complete sequence.

3.7e-100:514:96

AC005781

R-THYRO1001608

Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.

2.3e-40:369:79

AC004845

R-THYRO1001641

Homo sapiens clone 24448 unknown mRNA, partial cds.

3.4e-110:562:96

AF070638

R-THYRO1001700

R-THYRO1001702

Mus musculus mRNA for myeloid associated differentiation protein.

1.1e-11:367:66

AJ001616

R-THYRO1001725

Homo sapiens, clone hRPK.1\_A\_1, complete sequence.

9.1e-12:329:65

AC006196

R-THYRO1001770

Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence..

0.12:339:59

AC004879

R-THYRO1001803

R-Y79AA1000030

Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.

2.0e-98:515:95

AC005214

R-Y79AA1000127

Homo sapiens genomic DNA, chromosome 21q11.1, segment 5/28, WORKING DRAFT SEQUENCE.

3.2e-115:551:99

AP000034

R-Y79AA1000207

Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.

1.8e-38:282:85

AC005562

R-Y79AA1000226

Homo sapiens full length insert cDNA YN52F10.

4.8e-09:104:85

AF075033

R-Y79AA1000270

Human mRNA for ORF, Xq terminal portion.

1.0e-105:564:93

D16469

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- 5 R-Y79AA1000426  
Rattus norvegicus activin beta E mRNA, complete cds.  
6.1e-50:562:72  
AF089825
- 10 R-Y79AA1000521  
Rattus norvegicus steroid sulfatase (Sts) mRNA, complete cds.  
0.48:233:62  
U37138
- 15 R-Y79AA1000750  
Human DNA from cosmid f23280 from chromosome 19q13.2, genomic sequence.  
6.8e-07:320:60  
L47334
- 20 R-Y79AA1000776  
R-Y79AA1000777  
Homo sapiens full length insert cDNA clone ZD93D10.  
2.9e-110:574:95  
AF088072
- 25 R-Y79AA1000876  
Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete cds.  
0.0096:105:71  
U73520
- 30 R-Y79AA1000959  
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.  
1.0e-78:453:92  
AF093420
- 35 R-Y79AA1000967  
Rattus norvegicus vesicle-associated calmodulin-binding protein mRNA, complete cds.  
2.3e-43:263:84  
L22557
- 40 R-Y79AA1001013  
R-Y79AA1001056  
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.  
1.5e-22:269:73  
U50734
- 45 R-Y79AA1001062  
D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & tRNA-Val.  
1.1e-07:494:57  
X54011
- 50 R-Y79AA1001090  
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.  
1.2e-26:269:77  
AC002300
- 55 R-Y79AA1001212  
Homo sapiens SL15 protein mRNA, complete cds.  
5.7e-82:407:97  
AF038961

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R-Y79AA1001264

HS\_2195\_A2\_A07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195  
Col=14 Row=A, genomic survey sequence.

3.4e-07:101:82

AQ191092

R-Y79AA1001272

Hansenula wingei mitochondrial DNA, complete sequence.

2.1e-05:435:60

D31785

R-Y79AA1001328

Rattus norvegicus Delta 3 mRNA, complete cds.

1.0e-29:356:72

AF084576

R-Y79AA1001426

R-Y79AA1001430

Homo sapiens mRNA for KIAA0469 protein, complete cds.

6.2e-111:555:96

AB007938

R-Y79AA1001523

Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.

3.7e-71:259:90

Z84480

R-Y79AA1001530

Human beta-tubulin gene (5-beta) with ten Alu family members.

2.6e-56:301:96

X00734

R-Y79AA1001592

HS\_2175\_A2\_B11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175  
Col=22 Row=C, genomic survey sequence.

1.0:237:59

AQ307634

R-Y79AA1001727

R-Y79AA1001787

Homo sapiens mRNA for putative ATPase, partial.

7.2e-80:405:97

AJ009947

R-Y79AA1001795

Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BINGS gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and GSSs, complete sequence.

4.2e-110:555:97

AL031228

R-Y79AA1001799

R-Y79AA1001803

Rattus norvegicus secretogranin III (SgIII) mRNA, complete cds.  
6.2e-60:499:77

U02983

R-Y79AA1001863

Human DNA sequence from PAC 365E2 on chromosome 6p22.3-24.1. Contains EST and STS.  
1.4e-45:261:75

AL009177

R-Y79AA1002022

H.sapiens mRNA for basement membrane heparan sulfate proteoglycan.  
1.0:311:61

X62515

R-nnnnnnnnnnnnn

Plasmodium falciparum chromosome 2, section 18 of 73 of the complete sequence.

1.0:208:62

AE001381

R-nnnnnnnnnnnnn

Homo sapiens DNA, trinucleotide repeats region, clone CAG83.

0.17:132:67

AB018494

R-Y79AA1002213

Human DNA sequence from PAC 340G1 on chromosome 6 contains STS.

5.6e-46:490:73

Z84719

R-Y79AA1002334

Japanese Quail (C.coturnix) troponin T isoform mRNA, clone cC501.

0.96:210:63

M26599

R-Y79AA1002373

Human BAC clone RG126M09 from 7q21-q22, complete sequence.

9.7e-82:544:85

AC002067

R-Y79AA1002376

Human mitochondrial DNA, fragment M1, encoding transfer RNAs, cytochrome oxidase I, and 2 URFs.

1.9e-111:546:97

M10546

R-Y79AA1002378

Mus musculus mRNA for zinc finger protein, complete cds, clone:CTfin51.

1.5e-33:244:74

D10630

R-Y79AA1002381

Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.

0.0046:177:68

Z95152

## Homology search result 8.

**[0300]** The result of the homology search in the Human Unigene(<http://www.ncbi.nlm.nih.gov/UniGene>) using the clone sequences of the 5'-ends.

5 Indicated are from the top,  
the name of the clone sequence,  
title of the top hit data,  
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),  
10 the Accession No. of the top hit data.

**[0301]** Data were not shown for the clones in which the P-value was higher than 1.

15 F-BNGH41000020  
ESTs  
6.6e-72:412:92  
Hs.153375:AI287812

20 F-BNGH41000087  
Homo sapiens mRNA for MIFR-1, complete cds  
0.027:499:57  
Hs.58269:AB010962

25 F-BNGH41000091  
Homo sapiens voltage-gated potassium channel eag (EAG) mRNA, complete cds  
5.2e-81:687:76  
Hs.158305:AJ001366

30 F-HEMBA1000006  
ESTs, Weakly similar to HYPOTHETICAL 51.2 KD PROTEIN IN LAG1-RPL14B INTERGENIC REGION [S.cere-  
visiae]  
2.0e-25:167:91  
Hs.9252:R53360

35 F-HEMBA1000121  
ESTs, Moderately similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis  
elegans]  
3.0e-34:180:98  
Hs.149509:N24022

40 F-HEMBA1000128  
EST  
0.00069:177:62  
Hs.158854:AI377837

45 F-HEMBA1000275  
Human modulator recognition factor I (MRF-1) mRNA, 3'end  
0.012:508:58  
Hs.920:M62324

50 F-HEMBA1000300  
Human mRNA for KIAA0355 gene, complete cds  
1.6e-46:402:78  
Hs.153014:AB002353

55 F-HEMBA1000349  
EST  
6.7e-08:65:95

	Hs.54372:N80032
	F-HEMBA1000443
	ESTs
5	6.1e-23:278:76
	Hs.69492:AA116026
	F-HEMBA1000462
10	F-HEMBA1000477
	ESTs
	6.9e-78:414:94
	Hs.152861:AA287444
15	F-HEMBA1000590
	Homo sapiens mRNA for matrilin-4, partial
	7.3e-95:482:96
	Hs.129361:AJ007581
20	F-HEMBA1000634
	ESTs
	1.3e-38:246:86
	Hs.6145:W26640
25	F-HEMBA1000671
	Zinc finger protein 140 (clone pHZ-39)
	2.4e-53:469:68
	Hs.154205:U09368
30	F-HEMBA1000713
	Homo sapiens 10kD protein (BC10) mRNA, complete cds
	2.1e-127:442:97
	Hs.5300:AF053470
35	F-HEMBA1000732
	Homo sapiens latent transforming growth factor-beta binding protein 4S mRNA, complete cds
	1.0e-45:258:94
	Hs.85087:AF051344
40	F-HEMBA1000745
	Human cardiotrophin-1 (CTF1) mRNA, complete cds
	1.1e-07:316:61
	Hs.25537:U43030
45	F-HEMBA1000835
	ESTs
	4.2e-11:188:72
	Hs.116265:AI184988
50	F-HEMBA1000875
	Zinc finger protein 133 (clone pHZ-13)
	1.5e-27:169:93
	Hs.78434:U09366
55	F-HEMBA1000907
	Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
	1.3e-06:545:60
	Hs.143551:AF048693

F-HEMBA1000940

Homo sapiens connexin46.6 (Cx46.6) gene, complete cds

4.1e-18:307:66

Hs.100072:AF014643

5

F-HEMBA1000962

Homo sapiens mRNA for MEGF8, partial cds

0.0018:391:62

Hs.158200:AB011541

10

F-HEMBA1001184

Homo sapiens SH3 domain binding glutamic acid-rich-like protein (SH3BGRL) mRNA, complete cds

2.7e-24:404:67

Hs.14368:AF042081

15

F-HEMBA1001221

Human transmembrane protein mRNA, complete cds

7.7e-44:858:63

Hs.78531:U19878

20

F-HEMBA1001228

Human germline oligomeric matrix protein (COMP) mRNA, complete cds

2.2e-85:463:93

Hs.1584:AC003107

25

F-HEMBA1001272

Antidiuretic hormone receptor

0.064:616:57

Hs.2524:L22206

30

F-HEMBA1001296

Homo sapiens delta-catenin mRNA, complete cds

0.031:410:59

Hs.80220:U96136

35

F-HEMBA1001297

Homo sapiens putative transcription factor CA150 mRNA, complete cds

3.0e-15:143:81

Hs.13063:AF017789

40

F-HEMBA1001390

ESTs, Highly similar to polymerase I-transcript release factor [M.musculus]

1.6e-49:297:91

Hs.25581:AI246284

45

F-HEMBA1001563

ESTs

4.9e-12:160:74

Hs.162813:AA524616

50

F-HEMBA1001621

Human P2U nucleotide receptor mRNA, complete cds

0.00098:314:61

Hs.339:U07225

55

F-HEMBA1001878

Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds

3.4e-172:810:98

Hs.10290:AF090988

F-HEMBA1001886

Human repressor transcriptional factor (ZNF85) mRNA, complete cds

1.1e-115:849:80

Hs.37138:U35376

F-HEMBA1002048

Homo sapiens mRNA for APC 2 protein, complete cds

0.96:266:62

Hs.20912:AB012162

F-HEMBA1002131

Homo sapiens mRNA for KIAA0584 protein, partial cds

1.1e-45:709:66

Hs.106794:AB011156

F-HEMBA1002163

ASPARTYL-TRNA SYNTHETASE

0.026:568:58

Hs.80758:J05032

F-HEMBA1002164

Pregnancy-associated plasma protein A

0.0049:274:60

Hs.158229:U28727

F-HEMBA1002167

F-HEMBA1002178

Homo sapiens mRNA for KIAA0584 protein, partial cds

8.3e-48:794:65

Hs.106794:AB011156

F-HEMBA1002195

EST

2.0e-05:177:70

Hs.145935:AI275921

F-HEMBA1002227

Myristoylated alanine-rich C-kinase substrate

1.2e-138:382:95

Hs.75607:D10522

F-HEMBA1002239

Homo sapiens mRNA, chromosome I specific transcript KIAA0488

1.2e-47:570:71

Hs.67619:AB007957

F-HEMBA1002316

EST

1.8e-28:246:79

Hs.136950:AA825638

F-HEMBA1002420

Homo sapiens GABA-B receptor mRNA, complete cds

1.7e-05:303:63

Hs.12307:AF056085



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F-HEMBA1002421  
Syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)  
4.3e-167:778:98  
Hs.1501:J04621

5

F-HEMBA1002524  
Human MHC Class I region proline rich protein mRNA, complete cds  
8.5e-128:751:89  
Hs.41548:U63336

10

F-HEMBA1002551  
ESTs  
2.4e-25:207:84  
Hs.158172:N24325

15

F-HEMBA1002767  
Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds  
4.4e-170:798:98  
Hs.19154:AF038660

20

F-HEMBA1002985  
ESTs  
2.6e-09:124:76  
Hs.118620:T60326

25

F-HEMBA1002992  
ESTs  
2.4e-21:121:97  
Hs.143571:AI089396

30

F-HEMBA1003047  
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds  
1.5e-188:873:99  
Hs.148318:AF034611

35

F-HEMBA1003072  
ESTs  
1.2e-33:387:71  
Hs.59628:W91959

40

F-HEMBA1003101  
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds  
1.7e-140:671:98  
Hs.26350:AF049891

45

F-HEMBA1003120  
Zinc finger protein 91 (HPF7, HTF10)  
1.0e-24:143:76  
Hs.8597:L11672

50

F-HEMBA1003230  
Homo sapiens UP50 mRNA, complete cds  
1.8e-184:856:98  
Hs.11494:AF093118

55

F-HEMBA1003294  
Human antisecretory factor-1 mRNA, complete cds  
5.1e-45:324:83

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Hs.148495:AF050199

F-HEMBA1003315

Homo sapiens mRNA for TIP49, complete cds

4.2e-19:377:64

Hs.155541:AF070735

F-HEMBA1003392

Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds

9.2e-185:851:99

Hs.23672:AF074264

F-HEMBA1003399

H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase

0.00042:297:61

Hs.118929:X79568

F-HEMBA1003487

Homo sapiens receptor for viral semaphorin protein (VESPR) mRNA, complete cds

0.0011:237:63

Hs.88145:AF030339

F-HEMBA1003497

ESTs, Weakly similar to similar to zinc finger 5 protein from Gallus gallus, U51640 [H.sapiens]

2.5e-09:303:63

Hs.143723:H86048

F-HEMBA1003530

Homo sapiens mRNA for ephrin-A2

0.024:396:60

Hs.158306:AJ007292

F-HEMBA1003602

Homo sapiens DNA from chromosome 19, cosmid R29144

0.0072:663:57

Hs.155647:AC004221

F-HEMBA1003732

ESTs

1.0e-106:494:100

Hs.157568:AI356515

F-HEMBA1003945

Homo sapiens clone 638 unknown nRNA, complete sequence

5.9e-78:310:93

Hs.159515:AF091085

F-HEMBA1004007

PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC

0.56:165:64

Hs.115742:AF077754

F-HEMBA1004067

Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]

0.048:581:58

Hs.83190:U29344

F-HEMBA1004085

ESTs

1.7e-15:92:98

Hs.98138:AI183561

- 5 F-HEMBA1004110  
Homo sapiens intersectin short form mRNA, complete cds  
1.2e-159:779:96  
Hs.66392:AF064244
- 10 F-HEMBA1004250  
Human mRNA for KIAA0327 protein, complete cds  
2.1e-23:676:59  
Hs.149323:AB002325
- 15 F-HEMBA1004391  
NEURAL CELL ADHESION MOLECULE L1 PRECURSOR  
0.43:157:63  
Hs.1757:U52112
- 20 F-HEMBA1004444  
H.sapiens mRNA for gp25L2 protein  
1.5e-54:544:73  
Hs.159569:X90872
- 25 F-HEMBA1004454  
Homo sapiens tetraspan NET-4 mRNA, complete cds  
1.1e-05:230:62  
Hs.20709:AF065389
- 30 F-HEMBA1004505  
ESTs  
9.1e-61:345:93  
Hs.4814:AA631254
- 35 F-HEMBA1004785  
Homo sapiens Polycomb 2 homolog (hPc2) mRNA, complete cds  
3.7e-18:294:65  
Hs.123085:AF013956
- 40 F-HEMBA1004797  
ESTs  
3.9e-06:107:73  
Hs.42302:AI032142
- 45 F-HEMBA1004952  
Human cardiotrophin-1 (CTF1) mRNA, complete cds  
0.00021:175:68  
Hs.25537:U43030
- 50 F-HEMBA1004971  
  
F-HEMBA1004982  
Human metabotropic glutamate receptor 8 mRNA, complete cds  
0.31:288:60
- 55 Hs.86204:U92459  
  
F-HEMBA1005070  
Human mRNA for KIAA0310 gene, complete cds

7.9e-67:370:93  
Hs.5716:AB002308

5 F-HEMBA1005084  
Homo sapiens mRNA for KIAA0612 protein, partial cds  
0.00022:400:59  
Hs.112499:AB014512

10 F-HEMBA1005145  
Lymphocyte-activation gene 3  
3.4e-05:480:59  
Hs.74011:X51985

15 F-HEMBA1005230  
ESTs  
2.3e-103:481:99  
Hs.135112:AI090827

20 F-HEMBA1005246  
Homo sapiens ALR mRNA, complete cds  
2.0e-05:220:62  
Hs.153638:AF010403

25 F-HEMBA1005267  
ESTs  
5.6e-16:305:64  
Hs.125699:AA868017

30 F-HEMBA1005337  
EST  
2.1e-59:304:97  
Hs.48956:N64339

35 F-HEMBA1005430  
ESTs  
6.9e-19:333:65  
Hs.116567:AI332643

40 F-HEMBA1005449  
Human plectin (PLEC1) mRNA, complete cds  
0.026:576:56  
Hs.79706:U53204

45 F-HEMBA1005489  
Homo sapiens mRNA for KIAA0291 gene, partial cds  
0.14:551:59  
Hs.104717:AB006629

50 F-HEMBA1005522  
COAGULATION FACTOR VII PRECURSOR  
1.8e-12:298:64  
Hs.36989:M13232

55 F-HEMBA1005545  
MUSCARINIC ACETYLCHOLINE RECEPTOR M3  
2.6e-143:672:98  
Hs.7138:U29589

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F-HEMBA1005698  
 ESTs  
 1.8e-124:611:97  
 Hs.144441:AI338335  
 5 F-HEMBA1005913  
  
 F-HEMBA1005929  
 H.sapiens mRNA for serine/threonine protein kinase EMK  
 10 1.5e-86:847:72  
 Hs.157199:X97630  
  
 F-HEMBA1005945  
 ESTs, Weakly similar to F17E5.2 [C.elegans]  
 15 4.2e-26:159:92  
 Hs.126571:AI038963  
  
 F-HEMBA1006016  
 ESTs  
 20 1.3e-22:145:93  
 Hs.33728:H97503  
  
 F-HEMBA1006171  
  
 25 F-HEMBA1006276  
 Homo sapiens KIAA0412 mRNA, partial cds  
 5.1e-19:371:65  
 Hs.6200:AB007872  
  
 30 F-HEMBA1006299  
  
 F-HEMBA1006311  
  
 F-HEMBA1006335  
 35 ESTs  
 0.00021:327:62  
 Hs.146044:AI089998  
  
 F-HEMBA1006357  
 40 Homo sapiens secretory carrier mernbrane protein (SCAMP2) mRNA, complete cds  
 7.4e-28:389:67  
 Hs.10761:AF005038  
  
 F-HEMBA1006430  
 45 ESTs  
 9.7e-92:463:95  
 Hs.143702:AI084062  
  
 F-HEMBA1006482  
 50 Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds  
 6.2e-146:575:98  
 Hs.14511:AF026852  
  
 F-HEMBA1006517  
 55 ESTs  
 3.6e-63:381:87  
 Hs.11611:W21919

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F-HEMBA1006544

Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds

2.0e-50:503:76

Hs.43543:AF042800

5

F-HEMBA1006572

Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit

0.031:611:57

Hs.96253:U79666

10

F-HEMBA1006658

Homo sapiens mRNA for KIAA0687 protein, partial cds

1.2e-128:646:95

Hs.3628:AB014587

15

F-HEMBA1006707

Homo sapiens mRNA for matrilin-4, partial

1.7e-101:476:98

Hs.129361:AJ007581

20

F-HEMBA1006724

ESTs

8.3e-86:450:95

Hs.10056:AA210796

25

F-HEMBA1006749

Homo sapiens mRNA for matrilin-4, partial

6.1e-97:457:98

Hs.129361:AJ007581

30

F-HEMBA1006770

ESTs, Highly similar to BRAIN PROTEIN F41 [Mus musculus]

1.6e-31:237:85

Hs.31612:H41366

35

F-HEMBA1006902

Homo sapiens mRNA for matrilin-4, partial

9.4e-113:541:97

Hs.129361:AJ007581

40

F-HEMBA1006912

ESTs

1.4e-94:460:97

Hs.88672:AA279956

45

F-HEMBA1006916

Homo sapiens Grb14 mRNA, complete cds

5.2e-120:651:92

Hs.83070:L76687

50

F-HEMBA1006960

Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds

0.011:628:57

Hs.159234:U89995

55

F-HEMBA1007013

ESTs

2.6e-05:139:69

Hs.113817:AA702497

F-HEMBA1007057

Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds

5 7.5e-12:389:64  
Hs.143641:AB009462

F-HEMBA1007063

10 F-HEMBA1007226

ESTs

1.8e-35:202:94

Hs.105140:N32669

15 F-HEMBA1007241

ESTs, Weakly similar to No definition line found [C.elegans]

4.1e-27:361:67

Hs.114062:AI421699

20 F-HEMBA1007291

ESTs

0.96:114:69

Hs.121411:AA770241

25 F-HEMBA1007332

ESTs, Weakly similar to hTAFII100 [H.sapiens]

2.5e-81:405:97

Hs.3727:AA205887

30 F-HEMBA1000106

ESTs

2.2e-76:393:96

Hs.151874:AI023405

35 F-HEMBA1000276

EST

0.81:239:63

Hs.149811:AI286277

40 F-HEMBA1000309

Homo sapiens zinc finger protein (MBLL) mRNA, complete cds

2.4e-35:180:100

Hs.44806:AF061261

45 F-HEMBA1000407

Cyclin-dependent kinase inhibitor 1C (p57, Kip2)

0.026:218:65

Hs.106070:U22398

50 F-HEMBA1000447

Homo sapiens JWA protein mRNA, complete cds

4.6e-160:750:98

Hs.92384:AF070523

55 F-HEMBA1000542

ESTs, Weakly similar to C01H6.7 [C.elegans]

6.8e-07:130:77

Hs.18171:AA524327

5 F-HEMBB1000567  
ESTs  
8.8e-13:271:71  
Hs.19934:AA455673

F-HEMBB1000642

10 F-HEMBB1000668  
EST  
0.83:192:58  
Hs.126372:AA912193

15 F-HEMBB1000679  
H.sapiens mRNA for TRAMP protein  
4.1e-96:727:80  
Hs.4147:X63679

20 F-HEMBB1000881  
Homo sapiens chromosome 4p homeobox mRNA sequence  
2.2e-06:512:60  
Hs.104134:M99587

25 F-HEMBB1000905  
Homo sapiens mRNA for voltage gated potassium channel  
0.93:337:58  
Hs.4975:Y15065

30 F-HEMBB1001026  
Human p76 mRNA, complete cds  
6.1e-08:410:61  
Hs.28757:U81006

35 F-HEMBB1001048  
Human Hpast (HPAST) mRNA, complete cds  
2.1e-56:524:75  
Hs.155119:AF001434

40 F-HEMBB 1001200  
EST  
0.10:300:61  
Hs.161647:AA133367

45 F-HEMBB1001407  
Homo sapiens PRKY exon 1 and joined CDS  
2.6e-40:271:81  
Hs.56336:Y15801

50 F-HEMBB1001530  
ESTs  
1.2e-98:477:98  
Hs.135208:AI093908

55 F-HEMBB1001547  
F-HEMBB1001573  
EST  
2.2e-06:115:75  
Hs.138275:R43976



F-HEMBB1001847

ESTs

5.3e-79:389:98

Hs.16141:W56079

5

F-HEMBB1001959

Homo sapiens clone 24781 mRNA sequence

1.0e-58:322:93

Hs.108112:AF070640

10

F-HEMBB1001978

EST

4.7e-23:245:74

Hs.136356:AA493225

15

F-HEMBB1002039

EST

2.3e-25:345:70

Hs.128248:AA972858

20

F-HEMBB1002041

Human plectin (PLEC1) mRNA, complete cds

2.2e-08:477:60

Hs.79706:U53204

25

F-HEMBB1002051

Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds

9.9e-97:454:99

Hs.159267:AF049703

30

F-HEMBB1002120

ESTs

7.6e-10:68:100

Hs.146335:AI262660

35

F-HEMBB1002162

Homo sapiens genethonin 1 mRNA, complete cds

2.2e-68:328:99

Hs.109590:AF062534

40

F-HEMBB1002228

Homo sapiens unknown mRNA, complete cds

5.3e-41:208:98

Hs.11441:AF047439

45

F-HEMBB1002245

Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds

5.6e-05:299:63

Hs.92614:M62302

50

F-HEMBB1002302

F-HEMBB1002427

Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds

55

0.84:108:68

Hs.8786:AB014680

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5	F-HEMBB1002465 ESTs, Highly similar to ACYL-COA DEHYDROGENASE [Bacillus subtilis] 3.2e-18:159:84 Hs.14791:AA741056
10	F-HEMBB1002661 ESTs 0.023:424:55 Hs.154029:AI380603
	F-HEMBB1002663  F-HEMBB1002693
15	F-MAMMA1000046 Human mRNA for tryptophan hydroxylase (EC 1.14.16.4) 3.2e-43:454:74 Hs.144563:AF057280
20	F-MAMMA1000102 Homo sapiens mRNA for cathepsin V, complete cds 0.70:222:65 Hs.87417:AB001928
25	F-MAMMA1000106 Homo sapiens mRNA for KIAA0754 protein, partial cds 0.00076:331:61 Hs.159183:AB018297
30	F-MAMMA1000118 B94 PROTEIN 1.5e-07:511:61 Hs.75522:M92357
35	F-MAMMA1000141 ESTs 2.3e-18:268:73 Hs.155334:AA827904
40	F-MAMMA1000204 Homo sapiens dysferlin mRNA, complete cds 2.5e-167:781:98 Hs.143897:AF075575
45	F-MAMMA1000226 Human involucrin mRNA 0.0010:414:61 Hs.157091:M13903
50	F-MAMMA1000403 ESTs 2.0e-24:163:90 Hs.44281:AI342377
55	F-MAMMA1000449 ESTs 0.99:211:60 Hs.143715:AI167929

5 F-MAMMA1000457  
NADH-CYTOCHROME B5 REDUCTASE  
7.7e-37:551:66  
Hs.75666:M28713

10 F-MAMMA1000473  
  
F-MAMMA1000496  
Homo sapiens PAC clone DJ130H16 from 22q12.1-qter  
1.1e-107:543:96  
Hs.8003:AC004997

15 F-MAMMA1000528  
EST  
0.22:227:59  
Hs.161400:AI423879

20 F-MAMMA1000591  
H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase  
3.3e-23:470:62  
Hs.55823:X92689

25 F-MAMMA1000614  
H.sapiens mRNA for CCAAT/enhancer binding protein alpha  
1.9e-06:492:61  
Hs.76171:Y11525

30 F-MAMMA1000652  
Homo sapiens mRNA, chromosome I specific transcript KIAA0487  
1.5e-61:449:75  
Hs.92381:AB007956

35 F-MAMMA1000681  
Homo sapiens mRNA for putative G-protein coupled receptor, EDG6  
4.0e-34:636:65  
Hs.159543:AJ000479

40 F-MAMMA1000706  
COAGULATION FACTOR VII PRECURSOR  
9.7e-16:378:65  
Hs.36989:M13232

45 F-MAMMA1000788  
ESTs, Weakly similar to M01E11.2 [C.elegans]  
3.4e-118:571:97  
Hs.78389:AI191127

50 F-MAMMA1000810  
EST  
0.065:211:61  
Hs.116798:AA633813

55 F-MAMMA1000814  
EST  
3.1e-08:224:66  
Hs.141620:N63316

F-MAMMA1000881

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- Homo sapiens sgk gene  
3.5e-08:165:69  
Hs.159640:AJ000512
- 5 F-MAMMA1000986  
Homo sapiens clone 24796 mRNA sequence  
2.3e-115:320:99  
Hs.27191:AF070596
- 10 F-MAMMA1000994  
Human HOX4C mRNA for a homeobox protein  
0.050:178:64  
Hs.74061:X59372
- 15 F-MAMMA1001043  
Latent transforming growth factor beta binding protein 2  
0.0013:376:60  
Hs.83337:Z37976
- 20 F-MAMMA1001066  
ESTs  
1.1e-18:128:77  
Hs.114031:AA700958
- 25 F-MAMMA1001094  
Homo sapiens clone 243 unknown mRNA, complete sequence  
2.0e-182:844:99  
Hs.20423:AF091094
- 30 F-MAMMA1001141  
Homo sapiens achaete scute homologous protein (ASH1) mRNA, complete cds  
6.1e-07:492:58  
Hs.1619:L08424
- 35 F-MAMMA1001150  
Protein kinase C, mu  
8.3e-51:691:67  
Hs.2891:X75756
- 40 F-MAMMA1001237  
Homo sapiens monocarboxylate transporter (MCT3) mRNA, complete cds  
8.2e-08:386:60  
Hs.85838:U81800
- 45 F-MAMMA1001284  
ESTs  
1.1e-91:452:97  
Hs.114756:AI279440
- 50 F-MAMMA1001310  
Homo sapiens mRNA for KIAA0708 protein, partial cds  
0.014:512:57  
Hs.117177:AB014608
- 55 F-MAMMA1001344  
ESTs, Weakly similar to No definition line found [C.elegans]  
8.3e-80:406:96  
Hs.121619:AI188389

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F-MAMMA1001418  
Human Na<sup>+</sup>/nucleoside cotransporter (hCNT1a) mRNA, complete cds  
1.9e-36:622:63  
Hs.97207:U62966

5

F-MAMMA1001532  
Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds  
2.1e-33:282:68  
Hs.158174:U66561

10

F-MAMMA1001609  
Insulin-like growth factor-binding protein 4  
0.00026:596:57  
Hs.1516:U20982

15

F-MAMMA1001615  
Homo sapiens DNA from chromosome 19, cosmid R29144  
1.1e-05:504:59  
Hs.155647:AC004221

20

F-MAMMA1001623  
Excision repair protein ERCC6  
1.2e-38:274:86  
Hs.99924:L04791

25

F-MAMMA1001634  
ESTs  
1.5e-26:176:90  
Hs.16187:AI139901

30

F-MAMMA1001893  
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)  
0.00030:170:68  
Hs.106070:U22398

35

F-MAMMA1001901  
ESTs  
1.5e-36:201:76  
Hs.161660:AA167744

40

F-MAMMA1001957  
Prostaglandin I<sub>2</sub> (prostacyclin) receptor (IP)  
0.041:277:61  
Hs.393:D38128

45

F-MAMMA1001978  
EST  
4.0e-43:359:81  
Hs.136494:AA587773

50

F-MAMMA1002070  
Human PAC clone DJ515N1 from 22q11.2-q22  
5.1e-135:652:97  
Hs.26670:AC002073

55

F-MAMMA1002080  
Calcium channel, voltage-dependent, L type, alpha 1C subunit  
0.0019:574:57

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Hs.89925:L04569

F-MAMMA1002087

Human mRNA for KIAA0009 gene, complete cds

0.71:228:63

Hs.79972:D13634

F-MAMMA1002091

Homo sapiens CD39L2 (CD39L2) mRNA, complete cds

5.2e-158:743:98

Hs.12330:AF039916

F-MAMMA1002095

Homo sapiens mRNA for KIAA0703 protein, complete cds

4.9e-55:657:68

Hs.6168:AB014603

F-MAMMA1002128

Human leucine zipper on the D14S46E locus mRNA, complete cds

0.77:449:59

Hs.89606:M95925

F-MAMMA1002142

F-MAMMA1002165

Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds

1.2e-35:182:98

Hs.139340:AF083500

F-MAMMA1002205

ESTs

4.7e-32:385:71

Hs.46158:AI160121

F-MAMMA1002224

TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT

1.3e-34:248:85

Hs.3006:X63468

F-MAMMA1002234

ESTs

1.1e-100:501:97

Hs.158161:AA312511

F-MAMMA1002586

Human mRNA for KIAA0183 gene, partial cds

0.00041:388:61

Hs.76666:D80005

F-MAMMA1002633

Landsteiner-Wiener blood group glycoprotein

1.1e-37:477:71

Hs.108287:L27670

F-MAMMA1003126

Human Hpast (HPAST) mRNA, complete cds

4.1e-84:801:74

Hs.155119:AF001434

5 F-NT2RM1000407  
ESTs  
4.1e-19:132:92  
Hs.133484:D80522

10 F-NT2RM1000462

10 F-NT2RM1000542  
Beta-galactosidase (GLB1)  
1.3e-17:436:61  
Hs.79222:M34423

15 F-NT2RM1000580  
ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]  
6.2e-51:254:98  
Hs.132096:AA314601

20 F-NT2RM1000789  
Homo sapiens mRNA for hTCF-4  
3.5e-96:299:92  
Hs.154485:Y11306

25 F-NT2RM1000855  
Hydroxysteroid (11-beta) dehydrogenase 2  
0.021:178:67  
Hs.1376:U26726

30 F-NT2RM1000858

30 F-NT2RM1000899  
Homo sapiens BAC clone RG119C02 from 7p15  
0.037:222:63  
Hs.22900:AC004520

35 F-NT2RM2000241  
ESTs  
2.9e-31:166:97  
Hs.156175:AI334328

40 F-NT2RM2000306

45 F-NT2RM2000410  
ESTs  
3.2e-12:81:97  
Hs.72116:AA151564

50 F-NT2RM2000423  
Beta-galactosidase (GLB1)  
0.074:163:63  
Hs.79222:M34423

55 F-NT2RM2000497  
ESTs, Weakly similar to CHL1 protein [H.sapiens]  
3.7e-21:121:97  
Hs.97515:AA435715

F-NT2RM2000514

F-NT2RM2000565

F-NT2RM2000582

EST

1.7e-42:218:98

Hs.160262:AI146610

F-NT2RM2000589

F-NT2RM2000622

Androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)

0.00018:409:62

Hs.99915:M23263

F-NT2RM2000632

Homo sapiens TBP-associated factor 172 (TAF-172) mRNA, complete cds

0.00017:331:59

Hs.14244:AF038362

F-NT2RM2000773

Human zinc finger protein (MAZ) mRNA

7.2e-47:274:91

Hs.7647:M94046

F-NT2RM2001126

Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds

5.1e-163:663:99

Hs.21301:AF093419

F-NT2RM2001558

Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds

3.9e-166:770:98

Hs.98397:AF093408

F-NT2RM2001626

Human mRNA for KIAA0231 gene, partial cds

2.8e-40:562:67

Hs.7938:D86984

F-NT2RM2001643

ESTs

7.9e-112:548:97

Hs.12610:W56112

F-NT2RM2001738

FACTOR VIII INTRON 22 PROTEIN

0.32:452:59

Hs.83363:M34677

F-NT2RM2001767

Homo sapiens mRNA for B120, complete cds

5.0e-24:131:100

Hs.123090:AB001895

F-NT2RM2001792

Homo sapiens mRNA for serum lectin P35, complete cds

8.2e-14:244:67



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Hs.54517:D63160

F-NT2RM2001818

EST

5 0.051:152:61

Hs.157619:AI357718

F-NT2RM2001902

Human p21-activated protein kinase (Pak1) gene, complete cds

10 4.4e-39:568:66

Hs.62402:U24152

F-NT2RM2001939

Human G protein-coupled receptor GPR-NGA gene, complete cds

15 4.2e-141:664:98

Hs.92458:U55312

F-NT2RM2001941

Dopamine receptor D4

20 1.3e-14:547:61

Hs.99922:L12398

F-NT2RM4000100

Human involucrin mRNA

25 1.1e-09:487:62

Hs.157091:M13903

F-NT2RM4000115

30 F-NT2RM4000198

ESTs

9.3e-101:496:98

Hs.128676:AA464413

35 F-NT2RM4000284

Human IgG Fc receptor hFcRn mRNA, complete cds

2.4e-38: 194:98

Hs.110804:U12255

40 F-NT2RM4000295

Homo sapiens SOX22 protein (SOX22) mRNA, complete cds

1.7e-06:479:60

Hs.43627:U35612

45 F-NT2RM4000326

Phosphorylase kinase, gamma 2 (testis)

0.95:204:63

Hs.87452:M31606

50 F-NT2RM4000417

H.sapiens Syt V gene (genomic and cDNA sequence)

0.97:143:67

Hs.23179:X96783

55 F-NT2RM4000444

Eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)

0.45:194:64

Hs.90319:Z21507

F-NT2RM4000587  
 Human proto-oncogene (FRAT1) gene, complete cds  
 3.8e-05:495:60  
 Hs.143005:U58975  
 5 F-NT2RM4000593  
  
 F-NT2RM4000648  
 Homo sapiens glypican-4 (GPC4) mRNA, complete cds  
 10 1.0e-50:610:70  
 Hs.58367:AF030186  
  
 F-NT2RM4000761  
 EST  
 15 0.89:53:79  
 Hs.161967:AA494423  
  
 F-NT2RM4000965  
 H.sapiens mRNA for PHAPI2b protein  
 20 0.18:148:68  
 Hs.84264:U70439  
  
 F-NT2RM4000997  
  
 25 F-NT2RM4001321  
 ESTs  
 1.8e-94:467:97  
 Hs.12610:W56112  
  
 30 F-NT2RM4001325  
 Homo sapiens mRNA for chondroitin 6-sulfotransferase, complete cds  
 2.1e-13:384:64  
 Hs.158304:AB012192  
  
 35 F-NT2RM4001377  
 Homo sapiens mRNA for KIAA0638 protein, partial cds  
 3.1e-156:719:99  
 Hs.77864:AB014538  
  
 40 F-NT2RM4001735  
  
 F-NT2RM4001768  
 ESTs  
 0.00012:123:68  
 45 Hs.128045:AA970231  
  
 F-NT2RM4001843  
  
 F-NT2RM4002352  
 50 Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds  
 4.4e-157:761:97  
 Hs.143641:AB009462  
  
 F-NT2RP1000002  
 55 EST  
 0.00023:170:68  
 Hs.135504:AI091717

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F-NT2RP1000050  
 Histidine-rich calcium binding protein  
 0.0047:257:61  
 Hs.1480:M60052  
 5

F-NT2RP1000181  
 Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene  
 6.9e-99:510:94  
 Hs.132898:AC004770  
 10

F-NT2RP1000239  
 ESTs  
 1.7e-34:240:67  
 Hs.33020:N31946  
 15

F-NT2RP1000261  
 ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]  
 9.1e-92:484:94  
 Hs.7870:AI078137  
 20

F-NT2RP1000271  
 Homo sapiens DNA-binding protein mRNA, complete cds  
 1.4e-140:678:97  
 Hs.137582:AF038951  
 25

F-NT2RP1000300  
 Human endosome-associated protein (EEA1) mRNA, complete cds  
 1.0:205:61  
 Hs.2864:L40157  
 30

F-NT2RP1000325  
 Phosphate carrier, mitochondrial  
 7.7e-84:444:93  
 Hs.78713:X60036  
 35

F-NT2RP1000448  
 ESTs  
 9.5e-73:405:93  
 Hs.24054:N46499  
 40

F-NT2RP1000465  
 ESTs  
 8.5e-10:81:87  
 Hs.18619:AI202769  
 45

F-NT2RP1000468  
 Homo sapiens clone 24781 mRNA sequence  
 2.1e-20:133:92  
 Hs.108112:AF070640  
 50

F-NT2RP1000551  
 Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds  
 2.4e-140:742:93  
 Hs.75402:U09585  
 55

F-NT2RP1000579  
 SUCCINATE DEHYDROGENASE

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1.1e-141:798:91  
Hs.469:L21936

5 F-NT2RP1000613  
Homo sapiens carbonic anhydrase precursor (CA 12) mRNA, complete cds  
5.5e-11:468:58  
Hs.5338:AF037335

10 F-NT2RP1000679  
ESTs  
0.79:127:65  
Hs.146093:AA100242

15 F-NT2RP1000740  
Homo sapiens Trio isoform mRNA, complete cds  
0.24:160:66  
Hs.150625:AF091395

20 F-NT2RP1000903  
F-NT2RP1000981

F-NT2RP1001004  
Human mRNA for Doc2 beta, complete cds  
25 0.00072:520:57  
Hs.54402:D70830

F-NT2RP1001020  
ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]  
30 2.1e-73:392:94  
Hs.4789:AI418298

F-NT2RP1001031  
Miller-Dieker syndrome chromosome region  
35 4.5e-07:383:61  
Hs.77318:L13385

F-NT2RP1001563  
Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds  
40 0.086:398:59  
Hs.57783:U78525

F-NT2RP2000092  
Zinc finger protein 136 (clone pHZ-20)  
45 5.5e-56:652:70  
Hs.69740:U09367

F-NT2RP2000178  
Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence  
50 0.14:231:62  
Hs.159402:AC005609

F-NT2RP2000240  
Homo sapiens KIAA0415 mRNA, complete cds  
55 3.0e-61:554:76  
Hs.7289:AB007875

F-NT2RP2000394

ESTs

0.0063:210:63

Hs.134272:AI220363

- 5 F-NT2RP2000447  
Human (clone SY11) golgin-95 mRNA, complete cds  
3.8e-22:498:65  
Hs.24049:L06147
- 10 F-NT2RP2000479  
ESTs  
1.3e-46:298:90  
Hs.15641:W63676
- 15 F-NT2RP2000514  
Homo sapiens roundabout 1 (robo1) mRNA, complete cds  
1.2e-37:543:67  
Hs.36702:AF040990
- 20 F-NT2RP2000533  
ESTs, Highly similar to HYPOTHETICAL 16.3 KD PROTEIN IN DUR1,2-NGR1 INTERGENIC REGION [Saccha-  
romyces cerevisiae]  
5.4e-132:647:96  
Hs.18120:AA913148
- 25 F-NT2RP2000610  
Homo sapiens antigen NY-CO-16 mRNA, complete cds  
0.00027:182:66  
Hs.132206:AF039694
- 30 F-NT2RP2000616  
ESTs  
0.44:235:60  
Hs.31714:AA514389
- 35 F-NT2RP2000649  
Homo sapiens mRNA for Hs Ste24p, complete cds  
6.2e-167:802:97  
Hs.25846:AB016068
- 40 F-NT2RP2000663  
Homo sapiens mRNA for KIAA0512 protein, complete cds  
4.8e-15:305:64  
Hs.48924:AB011084
- 45 F-NT2RP2000694  
H.sapiens 5T4 gene for 5T4 Oncofetal antigen  
1.0e-113:558:96  
Hs.82128:AJ012159
- 50 F-NT2RP2000712  
ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]  
1.5e-83:442:93  
Hs.154226:AA468767
- 55 F-NT2RP2000739  
Human mRNA for KIAA0326 gene, partial cds  
2.1e-25:574:62

Hs.6833:AB002324

F-NT2RP2000818

5 F-NT2RP2000903  
H.sapiens 5T4 gene for 5T4 Oncofetal antigen  
3.5e-112:539:97  
Hs.82128:AJ012159

10 F-NT2RP2001200  
Homo sapiens mRNA for KIAA0676 protein, partial cds  
1.1e-111:540:96  
Hs.115763:AB014576

15 F-NT2RP2001223  
ESTs  
5.9e-91:461:95  
Hs.103733:AA436929

20 F-NT2RP2001276  
Homo sapiens mRNA for KIAA0634 protein, partial cds  
2.4e-11:382:62  
Hs.30898:AB014534

25 F-NT2RP2001388

F-NT2RP2001469  
ESTs  
7.3e-39:213:95

30 Hs.151001:AA564706

F-NT2RP2001480  
Homo sapiens thrombospondin 3 (THBS3) gene, complete cds  
2.9e-141:686:96

35 Hs.82165:L38969

F-NT2RP2001495  
Human transporter protein (g17) mRNA, complete cds  
6.0e-37:581:64

40 Hs.76460:U49082

F-NT2RP2001514

F-NT2RP2001529  
Homo sapiens mRNA for ZIP-kinase, complete cds  
1.5e-153:757:96  
Hs.25619:AB007144

45 F-NT2RP2001538  
ESTs, Highly similar to co-repressor protein [M.musculus]  
4.4e-63:329:94  
Hs.22583:AA188168

50 F-NT2RP2001562  
Homo sapiens GLE1 (GLE1) mRNA, complete cds  
7.5e-119:572:97  
Hs.81449:AF058922

55

5 F-NT2RP2001662  
H.sapiens mRNA for TGIF protein  
2.6e-29:448:67  
Hs.90077:X89750

10 F-NT2RP2001755  
ESTs, Highly similar to F-SPONDIN PRECURSOR [Rattus norvegicus]  
1.0e-47:275:92  
Hs.153657:H37929

15 F-NT2RP2001769  
Human protein kinase C-L (PRKCL) mRNA, complete cds  
1.9e-09:399:59  
Hs.89616:M55284

20 F-NT2RP2001817  
EST  
0.97:133:63  
Hs.145274:AI249468

25 F-NT2RP2001878  
Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds  
3.6e-05:491:60  
Hs.159234:U89995

30 F-NT2RP2001903  
Human mRNA for apolipoprotein E receptor 2, complete cds  
0.0023:270:60  
Hs.54481:D86407

35 F-NT2RP2001915  
Homo sapiens Pig3 (PIG3) mRNA complete cds  
3.2e-05:493:60  
Hs.50649:AF010309

40 F-NT2RP2001921  
F-NT2RP2001948  
ESTs  
0.55:213:61  
Hs.147805:AI221717

45 F-NT2RP2001956  
ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]  
8.1e-45:510:70  
Hs.13144:T67556

50 F-NT2RP2002015  
ESTs  
4.3e-20:127:92  
Hs.12610:W56112

55 F-NT2RP2002063  
ESTs  
1.0e-08:73:91  
Hs.19814:T81721

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F-NT2RP2002188

F-NT2RP2002232

EST

5 0.82:99:67  
Hs.148596:AI202232

F-NT2RP2002304

Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds

10 0.031:107:71  
Hs.82210:U47742

F-NT2RP2002409

Homo sapiens lymphocyte secreted C-type lectin precursor, mRNA, complete cds

15 0.00063:302:65  
Hs.105927:AF020044

F-NT2RP2002510

ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)

20 4.4e-09:298:64  
Hs.144023:U15197

F-NT2RP2002527

Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene

25 5.2e-65:327:96  
Hs.132898:AC004770

F-NT2RP2002533

Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds

30 2.1e-142:726:95  
Hs.127436:AF040709

F-NT2RP2002564

Homo sapiens mRNA for repressor protein, partial cds

35 3.5e-55:594:74  
Hs.58167:D30612

F-NT2RP2002674

Epoxide hydrolase 2, cytoplasmic

40 2.5e-07:332:62  
Hs.113:L05779

F-NT2RP2002721

F-NT2RP2002824

ESTs, Weakly similar to ZK858.6 [C.elegans]

50 5.2e-28:190:90  
Hs.120416:AA057428

F-NT2RP2002942

Homo sapiens mRNA for KIAA0806 protein, complete cds

55 2.0e-146:758:94  
Hs.24279:AB018349

F-NT2RP2002974

ESTs



4.9e-51:475:77  
Hs.137840:AI123378

5 F-NT2RP2002976  
ESTs, Weakly similar to No definition line found [C.elegans]  
7.8e-50:315:89  
Hs.159604:AI380827

10 F-NT2RP2003042  
Lecithin-cholesterol acyltransferase  
2.4e-25:454:65  
Hs.112125:M12625

15 F-NT2RP2003138  
H.sapiens mRNA for TGIF protein  
2.0e-05:121:75  
Hs.90077:X89750

20 F-NT2RP2003179  
Homo sapiens mRNA for KIAA0537 protein, complete cds  
1.0e-43:587:70  
Hs.12836:AB011109

25 F-NT2RP2003210  
F-NT2RP2003302  
Zinc finger protein 136 (clone pHZ-20)  
1.8e-64:691:69  
Hs.69740:U09367

30 F-NT2RP2003369  
Homo sapiens chromosome 7q22 sequence  
5.1e-109:539:96  
Hs.125742:AF053356

35 F-NT2RP2003383  
Homo sapiens mRNA for KIAA0458 protein, complete cds  
1.6e-159:801:95  
Hs.7414:AB007927

40 F-NT2RP2003390  
Homo sapiens SEC63 (SEC63) mRNA, complete cds  
2.2e-116:554:98  
Hs.31575:AF100141

45 F-NT2RP2003469  
ESTs  
0.26:127:69  
Hs.62649:AA115328

50 F-NT2RP2003545  
ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]  
4.2e-111:550:96  
Hs.85768:W16504

55 F-NT2RP2003593  
EST  
8.7e-43:213:99

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Hs.130657:AI005473

F-NT2RP2003599

ESTs

5 7.8e-14:84:98

Hs.107171:H53973

F-NT2RP2003655

10 F-NT2RP2003664

Homo sapiens mRNA for leptin receptor gene-related protein

5.4e-134:630:98

Hs.23581:Y12670

15 F-NT2RP2003931

Human mRNA for KIAA0365 gene, partial cds

4.3e-14:101:92

Hs.84123:AB002363

20 F-NT2RP2003940

Zinc finger protein 43 (HTF6)

4.6e-99:693:82

Hs.74107:X59244

25 F-NT2RP2003950

Cell division cycle 25A

0.00041:419:59

Hs.1634:M81933

30 F-NT2RP2004069

ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II [C.elegans]

1.3e-75:390:94

Hs.13322:AA151730

35 F-NT2RP2004108

Zinc finger protein 136 (clone pHZ-20)

4.9e-69:548:78

Hs.69740:U09367

40 F-NT2RP2004141

TRICHOHYALIN

4.8e-11:435:63

Hs.82276:L09190

45 F-NT2RP2004179

ESTs

0.0054:180:66

Hs.134917:AI092952

50 F-NT2RP2004205

Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds

0.27:474:56

Hs.112049:U93181

55 F-NT2RP2004447

Homo sapiens LDL receptor member LR3 mRNA, complete cds

0.016:456:57

Hs.6347:AF077820

F-NT2RP2004495

Human transporter protein (g17) mRNA, complete cds

1.2e-26:497:61

Hs.76460:U49082

5

F-NT2RP2004524

Human bone morphogenetic protein-3b

0.0016:259:64

Hs.2171:D49493

10

F-NT2RP2004556

ESTs

1.1e-34:181:97

Hs.27160:AA421991

15

F-NT2RP2004606

Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)

5.7e-107:587:92

Hs.148726:X03124

20

F-NT2RP2004648

TUBULIN ALPHA-4 CHAIN

0.59:186:61

Hs.75318:X06956

25

F-NT2RP2004670

Human mRNA for KIAA0369 gene, complete cds

0.097:309:61

Hs.21355:AB002367

30

F-NT2RP2004794

ESTs

1.3e-60:310:96

Hs.84926:N50073

35

F-NT2RP2004837

F-NT2RP2004847

Zinc finger protein 42 (myeloid-specific retinoic acid-responsive)

1.4e-05:396:60

Hs.78247:M58297

40

F-NT2RP2005027

GLUCOSE TRANSPORTER TYPE 3, BRAIN

7.2e-147:713:96

Hs.7594:M20681

45

F-NT2RP2005069

Human mRNA for KIAA0355 gene, complete cds

0.14:303:61

Hs.153014:AB002353

50

F-NT2RP2005163

ESTs, Weakly similar to No definition line found [C.elegans]

1.4e-23:334:70

Hs.159604:AI380827

55

F-NT2RP2005181

- Ecotropic retroviral receptor  
8.3e-45:501:70  
Hs.2928:X57303
- 5 F-NT2RP2005247  
Oxysterol binding protein  
4.2e-08:356:62  
Hs.143065:M86917
- 10 F-NT2RP2005378  
ESTs  
1.7e-100:485:97  
Hs.151572:AA588083
- 15 F-NT2RP2005391  
EST  
1.0:264:62  
Hs.148259:AA905706
- 20 F-NT2RP2005425  
Homo sapiens mRNA for KIAA0803 protein, partial cds  
3.3e-118:566:97  
Hs.58103:AB018346
- 25 F-NT2RP2005463
- F-NT2RP2005514  
ESTs  
3.6e-18:193:77
- 30 Hs.153344:R26293
- F-NT2RP2005535  
Homo sapiens DNA-binding protein mRNA, complete cds  
7.5e-127:726:90
- 35 Hs.137582:AF038951
- F-NT2RP2005541  
Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)  
1.2e-06:225:64
- 40 Hs.2703:Z12173
- F-NT2RP2005597
- F-NT2RP2005632  
ESTs  
5.6e-67:344:96
- 45 Hs.112011:AA987961
- F-NT2RP2005666  
ESTs  
5.8e-71:453:87
- 50 Hs.122698:AI042484
- F-NT2RP2005774  
Zinc finger protein 136 (clone pHZ-20)  
1.3e-45:451:74
- 55 Hs.69740:U09367

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F-NT2RP2005878  
 ESTs, Highly similar to ESTRADIOL 17 BETA-DEHYDROGENASE 3 [Homo sapiens]  
 5.9e-10:67:100  
 Hs.104523:AA584520  
 5 F-NT2RP2005883  
 F-NT2RP2005887  
 10 F-NT2RP2005941  
 Human novel homeobox mRNA for a DNA binding protein  
 6.2e-11:464:61  
 Hs.37035:U07664  
 15 F-NT2RP2005994  
 F-NT2RP2006004  
 Homo sapiens KIAA0405 mRNA, complete cds  
 1.2e-13:273:63  
 20 Hs.48998:AB007865  
 F-NT2RP2006042  
 Human mRNA for KIAA0144 gene, complete cds  
 5.6e-12:220:69  
 25 Hs.8127:D63478  
 F-NT2RP2006092  
 Human FE65-like protein (hFE65L) mRNA, partial cds  
 2.6e-23:353:65  
 30 Hs.24957:U62325  
 F-NT2RP2006099  
 EST  
 2.5e-28:180:90  
 35 Hs.160878:A1361890  
 F-NT2RP2006134  
 Neogenin (chicken) homolog 1  
 0.035:219:60  
 40 Hs.90408:U61262  
 F-NT2RP2006269  
 Homo sapiens mRNA for matrilin-3  
 1.0:147:65  
 45 Hs.119534:AJ224741  
 F-NT2RP2006512  
 ESTs  
 1.6e-09:70:95  
 50 Hs.118981:AA282396  
 F-NT2RP3000011  
 F-NT2RP3000022  
 55 EST  
 0.016:293:60  
 Hs.127706:AA961478

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F-NT2RP3000059  
Human SH3 domain-containing proline-rich kinase (sprk) mRNA, complete cds  
0.0041:608:59  
Hs.89449:L32976

F-NT2RP3000063  
Excision repair protein ERCC6  
1.0:264:59  
Hs.99924:L04791

F-NT2RP3000125  
Human mRNA for KIAA0314 gene, partial cds  
6.9e-08:379:59  
Hs.155045:AB002312

F-NT2RP3000148  
Human Chromosome 16 BAC clone CIT987SK-A-635H12  
4.5e-40:349:73  
Hs.108604:AC002310

F-NT2RP3000169  
Homo sapiens MRS1 mRNA, complete cds  
1.1e-107:501:99  
Hs.30985:AF093239

F-NT2RP3000171  
Homo sapiens methionine synthase reductase (MTRR) mRNA, complete cds  
1.0:279:64  
Hs.153792:AF025794

F-NT2RP3000172  
Homo sapiens mRNA for ZIP-kinase, complete cds  
7.4e-09:463:59  
Hs.25619:AB007144

F-NT2RP3000201  
Homo sapiens mRNA for KIAA0687 protein, partial cds  
3.0e-171:792:98  
Hs.3628:AB014587

F-NT2RP3000232  
ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]  
8.6e-24:304:70  
Hs.112094:AA447558

F-NT2RP3000304  
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds  
1.1e-172:797:98  
Hs.23672:AF074264

F-NT2RP3000378  
Homo sapiens mRNA for KIAA0700 protein, partial cds  
4.3e-45:585:66  
Hs.13999:AB014600

F-NT2RP3000427  
Protein kinase, cAMP-dependent, catalytic, beta  
1.2e-15:97:98

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Hs.87773:M34181

F-NT2RP3000436

Human protein disulfide isomerase-related protein P5 mRNA, partial cds

5 4.1e-06:353:59

Hs.85200:D49489

F-NT2RP3000444

Homo sapiens mRNA for KIAA0445 protein, complete cds

10 1.2e-08:542:60

Hs.154139:AB007914

F-NT2RP3000460

ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]

15 1.3e-17:181:75

Hs.131840:AI016073

F-NT2RP3000481

Homo sapiens RanBP7/importin 7 mRNA, complete cds

20 5.4e-164:770:98

Hs.5151:AF098799

F-NT2RP3000616

Homo sapiens KIAA0405 mRNA, complete cds

25 1.5e-32:579:62

Hs.48998:AB007865

F-NT2RP3000645

Human KH type splicing regulatory protein KSRP mRNA, complete cds

30 4.6e-06:245:64

Hs.91142:U94832

F-NT2RP3000652

Homo sapiens DNA from chromosome 19, BAC 33152

35 2.6e-135:853:84

Hs.55452:AC003973

F-NT2RP3000676

Homo sapiens mRNA for KIAA0446 protein, complete cds

40 8.8e-88:420:98

Hs.158286:AB007915

F-NT2RP3000677

ESTs

45 3.9e-09:67:97

Hs.98819:AA778727

F-NT2RP3000721

ESTs, Weakly similar to No definition line found [C.elegans]

50 1.2e-57:395:86

Hs.159604:AI380827

F-NT2RP3000789

Homo sapiens putative RNA binding protein KOC (koc) mRNA, complete cds

55 4.8e-75:833:69

Hs.79440:U97188

F-NT2RP3000818

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Homo sapiens chromosome 19, fosmid 39554  
5.9e-08:313:63  
Hs.129906:AC004410

5 F-NT2RP3000820  
ESTs, Moderately similar to WSB-1 [M.musculus]  
8.8e-127:613:97  
Hs.24630:AI365246

10 F-NT2RP3000838  
Homo sapiens mRNA for KIAA0638 protein, partial cds  
8.3e-79:682:79  
Hs.77864:AB014538

15 F-NT2RP3000871  
Homo sapiens retinoblastoma-interacting protein (RBBP8) mRNA, complete cds  
1.9e-08:350:60  
Hs.29287:U72066

20 F-NT2RP3000907  
Human Ini1 mRNA, complete cds  
0.91:345:59  
Hs.155626:U04847

25 F-NT2RP3000921  
Homo sapiens mRNA for KIAA0806 protein, complete cds  
2.0e-65:798:68  
Hs.24279:AB018349

30 F-NT2RP3001012  
Homo sapiens mRNA for KIAA0667 protein, partial cds  
1.3e-21:383:64  
Hs.154740:AB014567

35 F-NT2RP3001044

F-NT2RP3001061  
KERATIN, TYPE II CYTOSKELETAL 7  
3.4e-05:256:62

40 Hs.23881:M99063

F-NT2RP3001159  
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene  
1.8e-81:527:70

45 Hs.132874:AC004770

F-NT2RP3001170  
Homo sapiens mRNA for KIAA0784 protein, partial cds  
7.3e-183:859:98

50 Hs.3657:AB018327

F-NT2RP3001 195  
ESTs

3.5e-08:282:62

55 Hs.135168:AI394026

F-NT2RP3001240  
ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]



2.8e-64:344:95  
Hs.14038:R06800

F-NT2RP3001271  
Centromere protein B (80kD)  
7.6e-08:288:64  
Hs.85004:X05299

F-NT2RP3001322  
ESTs, Weakly similar to W09D10.2 [C.elegans]  
1.2e-86:422:98  
Hs.26107:R60661

F-NT2RP3001388

F-NT2RP3001542

F-NT2RP3001560  
Protein phosphatase 2C alpha [human, teratocarcinoma, mRNA, 2346 nt]  
0.016:190:63  
Hs.57764:S87759

F-NT2RP3001592  
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)  
2.3e-13:188:71  
Hs.106070:U22398

F-NT2RP3001650  
Homo sapiens KIAA0415 mRNA, complete cds  
1.6e-17:394:66  
Hs.7289:AB007875

F-NT2RP3001685

F-NT2RP3001738  
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene  
1.9e-54:776:65  
Hs.132898:AC004770

F-NT2RP3001754  
Homo sapiens mRNA for B120, complete cds  
2.4e-18:106:100  
Hs.123090:AB001895

F-NT2RP3001858  
Homo sapiens mRNA for KIAA0584 protein, partial cds  
1.9e-40:770:63  
Hs.106794:AB011156

F-NT2RP3001976  
Zinc finger protein 140 (clone pHZ-39)  
7.3e-33:493:68  
Hs.154205:U09368

F-NT2RP3002015  
Homo sapiens OPA-containing protein mRNA, complete cds  
0.018:329:62  
Hs.85313:AF071309

F-NT2RP3002160  
Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds  
0.53:182:64  
Hs.113259:AF023456

5

F-NT2RP3002281  
Homo sapiens mRNA for KIAA0765 protein, partial cds  
5.2e-151:713:98  
Hs.62318:AB018308

10

F-NT2RP3002286  
ESTs  
0.034:48:95  
Hs.124692:AA777421

15

F-NT2RP3002311  
Beta-galactosidase (GEB1)  
2.3e-28:633:61  
Hs.79222:M34423

20

F-NT2RP3002324  
ESTs  
2.5e-28:296:75  
Hs.22822:H06408

25

F-NT2RP3002342  
Human transporter protein (g17) mRNA, complete cds  
3.2e-37:565:65  
Hs.76460:U49082

30

F-NT2RP3002353  
Homo sapiens mRNA for KIAA0790 protein, partial cds  
0.0055:271:60  
Hs.12002:AB018333

35

F-NT2RP3002409  
Homo sapiens mRNA for KIAA0719 protein, complete cds  
6.4e-191:897:98  
Hs.21198:AB018262

40

F-NT2RP3002411  
Hydroxysteroid (17-beta) dehydrogenase 3  
2.9e-28:604:62  
Hs.477:U05659

45

F-NT2RP3002448  
Human mRNA for KIAA0233 gene, complete cds  
1.6e-08:721:57  
Hs.79077:D87071

50

F-NT2RP3002571  
Homo sapiens mRNA for KIAA0603 protein, complete cds  
9.7e-67:707:71  
Hs.16909:AB011175

55

F-NT2RP3002664  
Homo sapiens Trio isoform mRNA, complete cds  
0.26:160:66

Hs.150625:AF091395

F-NT2RP3002721

Homo sapiens citrate synthase mRNA, complete cds

2.4e-180:873:96

Hs.132991:AF047042

F-NT2RP3002737

Homo sapiens mRNA for voltage gated potassium channel

7.1e-43:409:75

Hs.4975:Y15065

F-NT2RP3002738

Human BMK1 alpha kinase mRNA, complete cds

0.0070:722:57

Hs.3080:U29725

F-NT2RP3002790

Cyclin-dependent kinase inhibitor 1C (p57, Kip2)

7.2e-17:626:62

Hs.106070:U22398

F-NT2RP3002836

Homo sapiens mRNA for KIAA0463 protein, partial cds

2.2e-153:717:99

Hs.77738:AB007932

F-NT2RP3002887

Human plectin (PLEC1) mRNA, complete cds

2.5e-06:605:59

Hs.79706:U53204

F-NT2RP3002900

H.sapiens mRNA for transmembrane protein rnp24

3.1e-09:346:64

Hs.75914:X92098

F-NT2RP3002958

ESTs

8.3e-117:765:86

Hs.107119:AI198794

F-NT2RP3002983

ESTs

1.4e-07:270:67

Hs.160271:AI149075

F-NT2RP3003000

Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds

2.5e-89:555:88

Hs.122359:AF051946

F-NT2RP3003076

Homo sapiens mRNA for APC 2 protein, complete cds

0.00016:522:60

Hs.20912:AB012162

F-NT2RP3003354

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Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds  
4.0e-36:625:64  
Hs.10761:AF005038

- 5 F-NT2RP3003448  
Arginine vasopressin receptor 1B  
0.77:149:69  
Hs.1372:L37112
- 10 F-NT2RP3003469  
ESTs  
1.4e-42:239:93  
Hs.12610:W56112
- 15 F-NT2RP3003473  
ESTs, Highly similar to transcription factor ARF6 chain B [M.musculus]  
8.7e-46:281:89  
Hs.136172:W28257
- 20 F-NT2RP3003527  
Homo sapiens mRNA for protein kinase Dyrk1B  
4.6e-162:769:98  
Hs.130988:Y17999
- 25 F-NT2RP3003532  
OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR  
1.5e-146:682:98  
Hs.79015:M17229
- 30 F-NT2RP3003535  
EST  
6.7e-10:330:60  
Hs.133239:AI052508
- 35 F-NT2RP3003559  
Breakpoint cluster region protein BCR  
1.0:143:66  
Hs.2557:Y00661
- 40 F-NT2RP3003614  
ESTs  
3.7e-50:327:88  
Hs.148873:T33582
- 45 F-NT2RP3003729  
ESTs, Weakly similar to unknown [S.cerevisiae]  
1.9e-96:449:99  
Hs.100843:W28953
- 50 F-NT2RP3003849  
ESTs, Weakly similar to rhophilin [M.musculus]  
1.7e-32:197:92  
Hs.118457:AA019161
- 55 F-NT2RP3003874  
Homo sapiens incomplete cDNA for a myosin class I, myh-1c  
8.5e-84:494:90  
Hs.109805:AJ001381

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F-NT2RP3003939

Peroxisomal biogenesis factor 6

1.5e-05:236:62

Hs.30729:D83703

5

F-NT2RP3003963

F-NT2RP3004000

Homo sapiens mRNA for APC 2 protein, complete cds

10

4.8e-06:669:59

Hs.20912:AB012162

F-NT2RP3004025

ESTs

15

0.0015:68:86

Hs.154835:AI289188

F-NT2RP3004067

ESTs, Weakly similar to HYPOTHETICAL 51.2 KD PROTEIN IN LAG1-RPL14B INTERGENIC REGION [S.cerevisiae]

20

2.1e-76:416:94

Hs.9252:R53360

F-NT2RP3004075

ESTs

25

1.1e-54:298:94

Hs.124051:T15786

F-NT2RP3004083

30

F-NT2RP3004090

Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds

2.4e-06:486:62

Hs.135639:U77629

35

F-NT2RP3004119

Human mRNA for KIAA0215 gene, complete cds

4.1e-74:640:75

Hs.82292:D86969

40

F-NT2RP3004130

F-NT2RP3004133

ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]

45

4.6e-52:259:98

Hs.132096:AA314601

F-NT2RP3004202

ALPHA-2C-1 ADRENERGIC RECEPTOR

50

1.0:229:62

Hs.123022:J03853

F-NT2RP3004294

Homo sapiens mRNA for KIAA0741 protein, complete cds

55

2.4e-05:404:59

Hs.3615:AB018284

F-NT2RP3004309

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Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene  
3.4e-71:756:71  
Hs.132874:AC004770

- 5 F-NT2RP3004321  
Homo sapiens (clone MG2-5-12) mucin (MG2) mRNA, complete polyA site  
0.015:263:60  
Hs.103944:L13283
- 10 F-NT2RP3004345  
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)  
2.3e-13:188:71  
Hs.106070:U22398
- 15 F-NT2RP3004355  
EST  
0.25:130:59  
Hs.149436:AI274484
- 20 F-NT2RP3004374  
ESTs  
1.4e-95:480:96  
Hs.12610:W56112
- 25 F-NT2RP3004406  
Human breast cancer, estrogen regulated LIV-1 protein (LIV-1) mRNA, partial cds  
3.4e-45:505:70  
Hs.79136:U41060
- 30 F-NT2RP3004481  
Homo sapiens mRNA for KIAA0476 protein, complete cds  
0.00065:594:58  
Hs.6684:AB007945
- 35 F-NT2RP3004552  
Biglycan  
0.92:347:57  
Hs.821:J04599
- 40 F-NT2RP3004557  
Human Ki nuclear autoantigen mRNA, complete cds  
2.6e-121:626:94  
Hs.152978:U11292
- 45 F-NT2RP3004625  
Homo sapiens I-1 receptor candidate protein mRNA, complete cds  
3.1e-152:710:98  
Hs.26285:AF082516
- 50 F-NT2RP3004640  
ESTs, Moderately similar to unknown [H.sapiens]  
0.76:195:64  
Hs.6487:T65302
- 55 F-NT2RP3004647  
Homo sapiens mRNA for KIAA0446 protein, complete cds  
6.6e-111:524:98  
Hs.158286:AB007915

F-NT2RP4000108  
NEUROFILAMENT TRIPLET L PROTEIN  
5.3e-159:862:93  
Hs.159540:X05608

5

F-NT2RP4000634  
Human MEK kinase 3 mRNA, complete cds  
2.3e-54:370:71  
Hs.86201:U78876

10

F-NT2RP4000962  
ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [*Saccharomyces cerevisiae*]  
2.3e-95:479:96  
Hs.4789:AI418298

15

F-NT2RP4001001  
EST  
0.98:93:64  
Hs.147598:AI217868

20

F-NT2RP4001009  
Homo sapiens mRNA for Hs Ste24p, complete cds  
3.1e-176:828:98  
Hs.25846:AB016068

25

F-NT2RP4001467  
5' nucleotidase (CD73)  
1.1e-160:742:98  
Hs.153952:X55740

30

F-NT2RP4001877  
ESTs, Weakly similar to siah binding protein 1 [*H.sapiens*]  
3.3e-103:495:98  
Hs.65648:AA600816

35

F-NT2RP4001879  
EST  
0.78:171:61  
Hs.112790:AA609949

40

F-NT2RP4002187  
Hydroxysteroid (17-beta) dehydrogenase 3  
9.9e-27:534:63  
Hs.477:U05659

45

F-NT2RP4002451  
ESTs  
1.5e-11:106:86  
Hs.163724:AA017689

50

F-NT2RP4002715  
EST  
4.2e-07:64:93  
Hs.160901:AI366910

55

F-NT2RP4002750  
Ecotropic retroviral receptor  
6.6e-51:581:68

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Hs.2928:X57303

F-OVARC1000003

Solute carrier family 17 (sodium phosphate), member 2

6.9e-65:587:73

Hs.936:L13258

F-OVARC1000090

ESTs

4.8e-07:214:65

Hs.87456:AA434484

F-OVARC1000105

Human novel homeobox mRNA for a DNA binding protein

0.00095:204:64

Hs.37035:U07664

F-OVARC1000137

Human SNARE protein Ykt6 (YKT6) mRNA, complete cds

4.0e-35:184:98

Hs.31531:U95735

F-OVARC1000208

Human calcium-dependent group X phospholipase A2 mRNA, complete cds

1.5e-61:365:90

Hs.136004:U95301

F-OVARC1000255

Spleen tyrosine kinase

2.2e-88:615:84

Hs.74101:L28824

F-OVARC1000275

ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]

4.7e-85:424:97

Hs.55165:AA573499

F-OVARC1000298

Homo sapiens GABA-B receptor mRNA, complete cds

0.00021:285:61

Hs.12307:AF056085

F-OVARC1000307

ESTs

0.00016:226:63

Hs.162935:AI393970

F-OVARC1000313

Homo sapiens mRNA for KIAA0573 protein, partial cds

5.5e-121:585:97

Hs.154023:AB011145

F-OVARC1000331

Glucose-6-phosphate dehydrogenase

5.3e-18:213:71

Hs.1435:M24470

F-OVARC1000410



Homo sapiens mRNA for angiopoietin-like factor  
1.5e-27:538:62  
Hs.146559:Y16132

5 F-OVARC1000439

F-OVARC1000467  
ESTs  
2.5e-26:173:90  
10 Hs.105040:AA292817

F-OVARC1000529  
Homo sapiens mRNA for C8FW phosphoprotein  
1.1e-12:391:59  
15 Hs.143513:AJ000480

F-OVARC1000553  
Homo sapiens chromosome 19, cosmid R26894  
9.0e-111:425:99  
20 Hs.157732:AC005594

F-OVARC1000775  
Human chromosome 3p21.1 gene sequence  
2.2e-70:380:95  
25 Hs.82837:L13435

F-OVARC1000811  
HEPATOCTE GROWTH FACTOR ACTIVATOR PRECURSOR  
1.2e-06:446:61  
30 Hs.104:D14012

F-OVARC1000853  
ESTs  
7.9e-09:268:63  
35 Hs.92700:W37903

F-OVARC1000873  
Homo sapiens mRNA for MIFR-1, complete cds  
0.038:343:60  
40 Hs.58269:AB010962

F-OVARC1000916  
H.sapiens PISSLRE mRNA  
1.3e-56:435:82  
45 Hs.77313:X78342

F-OVARC1000956  
Human TBP-associated factor (hTAFII130) mRNA, partial cds  
7.7e-05:511:59  
50 Hs.24644:U75308

F-OVARC1000995  
ESTs  
2.4e-39:205:98  
55 Hs.163662:AA514348

F-OVARC1001030  
EST

- 1.1e-44:232:96  
Hs.135504:AI091717
- 5 F-OVARC1001049  
ESTs  
6.1e-78:373:98  
Hs.135022:AI417283
- 10 F-OVARC1001086  
Homo sapiens cyclin T2a mRNA, complete cds  
6.0e-166:761:99  
Hs.155478:AF048731
- 15 F-OVARC1001132  
ESTs, Weakly similar to GC-RICH SEQUENCE DNA-BINDING FACTOR [Homo sapiens]  
7.9e-121:610:96  
Hs.26461:AI341685
- 20 F-OVARC1001163  
ESTs  
5.9e-39:215:94  
Hs.126067:AI344351
- 25 F-OVARC1001222  
ESTs  
2.7e-93:467:95  
Hs.10267:W27845
- 30 F-OVARC1001260  
Pregnancy-zone protein  
1.0:251:58  
Hs.74094:X54380
- 35 F-OVARC1001336  
Solute carrier family 17 (sodium phosphate), member 2  
1.2e-31:304:74  
Hs.936:L13258
- 40 F-OVARC1001338  
Homo sapiens cam kinase I mRNA, complete cds  
3.7e-17:570:60  
Hs.118414:L41816
- 45 F-OVARC1001569  
Human novel homeobox mRNA for a DNA binding protein  
0.038:178:63  
Hs.37035:U07664
- 50 F-OVARC1001570  
ESTs  
4.5e-10:75:93  
Hs.120928:AA703165
- 55 F-OVARC1001596  
Matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase)  
0.0092:287:63  
Hs.111301:M55593

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F-OVARC1001607

Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds

5.5e-41:323:80

Hs.154844:U15128

5

F-OVARC 1001725

F-OVARC1001727

EST

10

3.2e-05:237:61

Hs.119508:AA485732

F-OVARC1001807

Hormone receptor (growth factor-inducible nuclear protein N10)

15

3.4e-91:564:88

Hs.1119:D49728

F-OVARC1001833

ESTs

20

1.2e-94:444:97

Hs.155256:AA707750

F-OVARC1001952

Myristoylated alanine-rich C-kinase substrate

25

2.9e-10:364:64

Hs.75607:D10522

F-OVARC1001991

Human mRNA for KIAA0176 gene, partial cds

30

0.0019:224:62

Hs.4935:D79998

F-OVARC1002058

Human mRNA for KIAA0149 gene, complete cds

35

5.0e-48:674:67

Hs.57735:D86864

F-OVARC1002178

Homo sapiens zinc-finger protein of the cerebellum 3 (ZIC3) mRNA, complete cds

40

0.010:310:61

Hs.111227:AF028706

F-PLACE1000033

45

F-PLACE1000231

Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)

0.00021:235:63

Hs.1686:M69013

50

F-PLACE1000258

KRAB zinc finger protein {alternative products}

1.2e-14:241:70

Hs.22556:U37251

55

F-PLACE1000442

Zinc finger protein 136 (clone pHZ-20)

7.3e-89:774:76

Hs.69740:U09367

F-PLACE1000560  
ESTs  
1.5e-36:200:96  
Hs.86541:AA214554

5

F-PLACE1000740  
Homo sapiens secreted apoptosis related protein 3 (SARP3) mRNA, complete cds  
6.5e-05:283:62  
Hs.113285:AF017988

10

F-PLACE1000907  
ESTs, Moderately similar to zinc finger protein [H.sapiens]  
8.1e-38:237:89  
Hs.139115:AA325104

15

F-PLACE1000912  
ESTs  
4.6e-61:331:95  
Hs.17558:AA155762

20

F-PLACE1000914  
Homo sapiens PB39 mRNA, complete cds  
3.1e-45:500:69  
Hs.18910:AF045584

25

F-PLACE1000927  
ESTs, Weakly similar to N-methyl-D-aspartate receptor-associated protein [D.melanogaster]  
1.4e-123:655:94  
Hs.8661:AI189791

30

F-PLACE1000986  
ESTs  
1.2e-105:494:99  
Hs.19207:AA039595

35

F-PLACE1001016  
Calcium channel, voltage-dependent, L type, alpha 1S subunit  
0.011:432:59  
Hs.1294:L33798

40

F-PLACE1001100  
Human clone 23839 mRNA sequence  
0.38:342:60  
Hs.78362:U79249

45

F-PLACE1001114  
Human mRNA for KIAA0303 gene, partial cds  
0.085:339:59  
Hs.54985:AB002301

50

F-PLACE1041123  
ESTs  
5.0e-14:505:61  
Hs.99272:AI147740

55

F-PLACE1001183  
ESTs, Weakly similar to gene pp21 protein [H.sapiens]  
0.66:361:58

Hs.15984:A,l085974

F-PLACE1001229

ESTs, Weakly similar to D9481.15 gene product [S.cerevisiae]

9.3e-110:561:96

Hs.125155:W52093

F-PLACE1001231

ESTs, Weakly similar to sodium iodide symporter [H.sapiens]

1.0e-17:120:91

Hs.5167:AA053914

F-PLACE1001340

Homo sapiens mRNA for KIAA0719 protein, complete cds

4.1e-132:636:97

Hs.21198:AB018262

F-PLACE1001401

ESTs, Weakly similar to IgE receptor beta subunit [H.sapiens]

3.1e-100:516:95

Hs.43900:AA418443

F-PLACE 1001407

H.sapiens mRNA for B-HLH DNA binding protein

0.00015:244:66

Hs.66744:X99268

F-PLACE1001464

5' nucleotidase (CD73)

1.6e-152:742:96

Hs.153952:X55740

F-PLACE1001500

Bloom syndrome

5.7e-05:450:58

Hs.36820:U39817

F-PLACE1001516

Homo sapiens Rigui (RIGUI) mRNA, complete cds

2.3e-07:663:58

Hs.8114:AF022991

F-PLACE1001536

ESTs

4.6e-60:318:97

Hs.13026:H04491

F-PLACE1001564

H.sapiens mRNA for HE6 Tm7 receptor

8.8e-41:499:70

Hs.155681:X81892

F-PLACE1001655

Homo sapiens Shab-related delayed-rectifier K<sup>+</sup> channel alpha subunit (KCNS3) mRNA, complete cds

4.3e-125:585:98

Hs.47584:AF043472

F-PLACE1001788

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Homo sapiens mRNA for HYA22, complete cds  
3.2e-22:234:75  
Hs.147189:D88153

5 F-PLACE1001795

F-PLACE1001836  
ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]  
1.1e-18:162:80  
10 Hs.157223:AA309318

F-PLACE1001918  
Human p76 mRNA, complete cds  
1.3e-22:693:60  
15 Hs.28757:U81006

F-PLACE1001949  
ESTs  
0.97:243:63  
20 Hs.151143:AA576926

F-PLACE1002080  
Homo sapiens mRNA for KIAA0600 protein, partial cds  
2.4e-130:622:98  
25 Hs.9028:AF039691

F-PLACE1002095

F-PLACE1002153  
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds  
2.7e-162:764:98  
30 Hs.90415:AF095791

F-PLACE1002329  
ESTs  
1.5e-107:556:95  
35 Hs.28907:AI343292

F-PLACE1002355  
Homo sapiens protease-activated receptor 4 mRNA, complete cds  
9.0e-19:190:77  
40 Hs.137574:AF055917

F-PLACE1002374  
Cathepsin L  
2.0e-163:716:94  
45 Hs.78056:X12451

F-PLACE1002518  
Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds  
7.0e-19:396:64  
50 Hs.28285:AF064801

F-PLACE1002547  
Homo sapiens mRNA for KIAA0719 protein, complete cds  
8.3e-173:819:98  
55 Hs.21198:AB018262

F-PLACE1002726

Human mRNA for KIAA0362 gene, partial cds

1.0:310:59

Hs.25515:AB002360

5

F-PLACE1002905

ESTs

2.4e-74:415:92

Hs.110298:AA621807

10

F-PLACE1002911

ESTs, Weakly similar to Y53C12A.3 [C.elegans]

0.030:279:58

Hs.107747:AI357868

15

F-PLACE1002967

ESTs

3.3e-120:574:98

Hs.11090:W37646

20

F-PLACE1003135

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds

1.5e-50:450:75

Hs.72292:AF024636

25

F-PLACE1003163

Homo sapiens DBI-related protein mRNA, complete cds

1.5e-153:722:98

Hs.15250:AF069301

30

F-PLACE1003407

Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds

2.0e-142:682:97

Hs.30213:AF068227

35

F-PLACE1003428

Biotinidase

8.2e-06:265:62

Hs.78885:AF018631

40

F-PLACE1003438

ESTs

0.018:470:60

Hs.119482:AI361002

45

F-PLACE1003460

ESTs

0.019:211:60

Hs.92700:W37903

50

F-PLACE1003529

130 KD LEUCINE-RICH PROTEIN

0.53:208:63

Hs.87157:M92439

55

F-PLACE1003573

F-PLACE1003598

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Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit  
0.00064:302:64  
Hs.96253:U79666

5 F-PLACE1003644  
ESTs  
1.3e-06:265:63  
Hs.163564:R43678

10 F-PLACE1003737

F-PLACE1003772  
Human p300/CBP-associated factor (P/CAF) mRNA, complete cds  
7.0e-09:448:61  
15 Hs.155302:U57317

F-PLACE1003839  
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12  
7.7e-109:521:97  
20 Hs.154050:AC004131

F-PLACE1003845  
ESTs, Moderately similar to similar to thymidine diphosphoglucose 4,6-dehydratase [C.elegans]  
1.2e-92:432:100  
25 Hs.153778:AI246000

F-PLACE1003852  
Homo sapiens mRNA for KIAA0758 protein, partial cds  
2.4e-172:814:98  
30 Hs.22039:AB018301

F-PLACE1004028

F-PLACE1004078  
35 GELSOLIN PRECURSOR, PLASMA  
3.1e-49:616:67  
Hs.80562:X04412

F-PLACE1004166  
40 ESTs  
7.6e-79:415:94  
Hs.163741:AA551077

45 F-PLACE1004168

F-PLACE1004199  
EST  
6.8e-15:147:80  
50 Hs.128205:AA972308

F-PLACE1004279  
Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds  
3.9e-20:456:62  
55 Hs.23965:AF057039

F-PLACE1004282

F-PLACE1004305



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Homo sapiens mRNA for KIAA0740 protein, complete cds  
8.7e-123:612:96  
Hs.15099:AB018283

5 F-PLACE1004441  
Human G protein-coupled receptor (GPR1) gene, complete cds  
8.6e-99:501:96  
Hs.159248:U13666

10 F-PLACE1004450  
AMINOPEPTIDASE N  
1.1e-09:587:57  
Hs.1239:M22324

15 F-PLACE1004482

F-PLACE1004492  
ESTs  
2.1e-25:134:100  
20 Hs.154475:AI199037

F-PLACE1004519  
ESTs  
1.0e-110:518:99  
25 Hs.128505:AA306435

F-PLACE1004520  
Pregnancy-specific beta 1-glycoprotein 7  
1.3e-110:606:92  
30 Hs.119662:M34715

F-PLACE1004630  
Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds  
2.0e-139:749:92  
35 Hs.82582:AB008375

F-PLACE1004637

40 F-PLACE1004648

F-PLACE1004816  
Homo sapiens mRNA for Hakata antigen, complete cds  
1.2e-99:590:90  
45 Hs.9225:D88587

F-PLACE1004887  
Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds  
5.1e-06:486:62  
50 Hs.135639:U77629

F-PLACE1005003  
Human SNC19 mRNA sequence  
1.5e-21:472:63  
55 Hs.56937:U20428

F-PLACE1005005  
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds  
4.7e-42:245:93

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Hs.151614:AF032456

F-PLACE1005031

ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]

2.9e-43:538:70

Hs.118991:AA675919

F-PLACE1005239

ESTs

2.4e-42:209:100

Hs.154475:AI199037

F-PLACE1005250

F-PLACE1005383

Homo sapiens UP50 mRNA, complete cds

8.5e-128:633:96

Hs.11494:AF093118

F-PLACE1005410

ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]

1.3e-17:181:75

Hs.131840:AI016073

F-PLACE1005426

Pregnancy-specific beta-1 glycoprotein 4

2.3e-109:596:93

Hs.108936:X17097

F-PLACE1005519

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds

3.3e-55:521:74

Hs.72292:AF024636

F-PLACE1005539

HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U

5.8e-05:277:63

Hs.103804:AF068846

F-PLACE1005544

F-PLACE1005569

EST

0.38:60:75

Hs.137086:AA912486

F-PLACE1005601

Homo Sapiens angiotensin II receptor gene, complete cds

0.016:72:84

Hs.20954:AI054441

F-PLACE1005660

F-PLACE1005669

Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds

3.5e-08:461:60

Hs.113286:U77783

F-PLACE1005682

F-PLACE1005725

Huntingtin (Huntington disease)

5 1.1e-06:401:61

Hs.79391:L12392

F-PLACE1005736

ESTs

10 3.6e-63:343:94

Hs.17757:AA875839

F-PLACE1005745

ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]

15 6.9e-66:351:94

Hs.7870:AI078137

F-PLACE1005768

ESTs

20 7.9e-60:318:95

Hs.143856:AI186351

F-PLACE1005815

Mutated in colorectal cancers

25 0.0029:199:62

Hs.1345:M62397

F-PLACE1005878

ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]

30 5.0e-38:464:70

Hs.118991:AA675919

F-PLACE1005927

INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR

35 0.010:511:59

Hs.839:M86826

F-PLACE1006071

EST

40 0.68:224:59

Hs.161788:AA371859

F-PLACE1006073

Homo sapiens mRNA for glucuronyltransferase I, complete cds

45 5.5e-96:464:98

Hs.26492:AB009598

F-PLACE1006079

Homo sapiens BAC clone RG300E22 from 7q21-q31.1

50 1.5e-18:402:65

Hs.99348:AC004774

F-PLACE1006093

Homo sapiens mRNA for protein phosphatase 1 (PPP1R6)

55 0.0022:306:59

Hs.106471:Y18206

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F-PLACE1006208

HOMEODOMAIN/POU DOMAIN PROTEIN RDC-1

0.022:425:57

Hs.74095:L20433

5

F-PLACE1006219

ESTs, Moderately similar to similar to thymidine diphosphoglucose 4,6-dehydratase [C.elegans]

1.7e-61:294:100

Hs.153778:AI246000

10

F-PLACE1006277

EST

0.42:60:75

Hs.137086:AA912486

15

F-PLACE1006290

ESTs, Weakly similar to similar to M. musculus MERS and other AHPC/TSA proteins [C.elegans]

1.3e-51:260:98

Hs.132096:AA314601

20

F-PLACE1006443

Homo sapiens PB39 mRNA, complete cds

1.2e-53:553:70

Hs.18910:AF045584

25

F-PLACE1006515

Homo sapiens mRNA for KIAA0576 protein, partial cds

1.3e-141:655:99

Hs.14687:AB011148

30

F-PLACE1006716

EST

7.2e-12:148:75

Hs.162969:AA677315

35

F-PLACE1006786

ESTs

0.0050:125:72

Hs.109156:AA193501

40

F-PLACE1006809

ESTs

4.5e-99:477:98

Hs.135208:AI093908

45

F-PLACE1006959

ESTs

7.4e-72:381:93

Hs.4963:W29030

50

F-PLACE1007028

Homo sapiens p17-Beckwith-Wiedemann region 1 C (BWR1C) mRNA, complete cds

1.8e-18:364:65

Hs.154036:AF035444

55

F-PLACE1007040

H.sapiens NF-H gene, exon 1 (and joined CDS)

1.4e-09:501:61

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Hs.75735:X15306

F-PLACE1007077

ESTs, Moderately similar to testis-specific TCP20 [H.sapiens]

0.88:192:62

Hs.85818:AI216525

F-PLACE1007081

Human plectin (PLEC1) mRNA, complete cds

0.079:403:60

Hs.79706:U53204

F-PLACE1007096

YY1 transcription factor

0.64:173:64

Hs.97496:M77698

F-PLACE1007296

ER LUMEN PROTEIN RETAINING RECEPTOR 1

4.2e-73:542:83

Hs.78040:X55885

F-PLACE1007591

EST

0.026:136:64

Hs.130897:AI014389

F-PLACE1007626

Homo sapiens unknown mRNA, complete cds

2.6e-105:516:97

Hs.11441:AF047439

F-PLACE1007702

Homo sapiens mRNA for UTF1, complete cds

0.033:297:62

Hs.158307:AB011076

F-PLACE1007845

ESTs

4.8e-22:158:89

Hs.23445:AA489015

F-PLACE1007881

F-PLACE1007971

ESTs, Weakly similar to K07F5.14 [C.elegans]

1.1e-128:599:99

Hs.157918:AA313781

F-PLACE1008282

ESTs, Highly similar to HEME-EGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE [Oryctolagus cuniculus]

2.4e-65:353:94

Hs.130830:W27380

F-PLACE1008297

F-PLACE1008359

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Human arginine-rich protein (ARP) gene, complete cds  
0.020:197:64  
Hs.75412:M83751

5 F-PLACE1008469  
Homo sapiens PB39 mRNA, complete: cds  
5.3e-20:620:60  
Hs.18910:AF045584

10 F-PLACE1008549  
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds  
1.8e-145:693:98  
Hs.159267:AF049703

15 F-PLACE1008657  
VILLIN  
2.3e-10:356:61  
Hs.3046:X12901

20 F-PLACE1008716  
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds  
1.5e-31:191:92  
Hs.154844:U15128

25 F-PLACE1008744

F-PLACE1008984  
Pregnancy-associated plasma protein A  
0.0085:268:60  
30 Hs.158229:U28727

F-PLACE1008985  
Signal transducer and activator of transcription 5A  
0.0047:249:64  
35 Hs.14203:U43185

F-PLACE1009067  
Human density enhanced phosphatase-1 mRNA, complete cds  
2.0e-06:453:60  
40 Hs.1177:U10886

F-PLACE1009196

F-PLACE1009279  
45 Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds  
1.9e-11:327:64  
Hs.75111:D87258

F-PLACE1009527  
50 Human DNA-binding protein ABP/ZF mRNA, complete cds  
6.8e-21:125:96  
Hs.86185:U82613

F-PLACE1009546  
55 TRANSCRIPTION FACTOR RELB  
0.051:248:61  
Hs.858:M83221

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F-PLACE1009600  
 ESTs  
 1.0:124:64  
 Hs.52794:W51887  
 5

F-PLACE1009735  
 ESTs  
 0.022:387:61  
 Hs.132253:AI027207  
 10

F-PLACE1009982  
 F-PLACE1010011  
 Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds  
 15  
 1.3e-09:330:66  
 Hs.143551:AF048693

F-PLACE1010078  
 ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]  
 20  
 8.3e-47:474:72  
 Hs.13144:T67556

F-PLACE1010081  
 Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds  
 25  
 2.2e-151:733:97  
 Hs.103755:AF027706

F-PLACE1010251  
 Homo sapiens Na<sup>+</sup>/H<sup>+</sup> exchanger regulatory factor 2 (NHERF-2) mRNA, complete cds  
 30  
 0.0037:405:60  
 Hs.101813:AB016243

F-PLACE1010445  
 ESTs  
 35  
 1.7e-45:235:97  
 Hs.144501:N39767

F-PLACE1010713  
 Hydroxysteroid (17-beta) dehydrogenase 3  
 40  
 2.8e-20:447:62  
 Hs.477:U05659

F-PLACE1010784  
 Human protease-activated receptor 3 (PAR3) mRNA, complete cds  
 45  
 0.56:199:59  
 Hs.159196:U92971

F-PLACE 1010827  
 H.sapiens mRNA for transmembrane protein rnp24  
 50  
 2.9e-09:346:64  
 Hs.75914:X92098

F-PLACE1010968  
 ESTs  
 55  
 0.00062:52:98  
 Hs.119408:T87544

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F-PLACE1011045

Homo sapiens E1-like protein mRNA, complete cds

6.0e-129:595:99

Hs.28190:AF094516

F-PLACE1011116

F-PLACE1011181

ESTs

1.0:301:58

Hs.80285:AI092519

F-PLACE1011236

Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds

1.1e-41:776:62

Hs.23965:AF057039

F-PLACE1011364

ESTs, Weakly similar to HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II [C.elegans]

3.7e-53:276:96

Hs.106499:W28299

F-PLACE1011407

ESTs, Moderately similar to ZINC FINGER PROTEIN 140 [H.sapiens]

3.2e-15:228:70

Hs.152174:AI199619

F-PLACE1011516

ESTs, Weakly similar to HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION [S.cerevisiae]

1.7e-85:444:95

Hs.110978:AA843431

F-PLACE1011708

Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds

5.9e-145:722:96

Hs.148318:AF034611

F-PLACE1011824

Human Ste20-like kinase (MST2) mRNA, complete cds

1.6e-101:561:92

Hs.92317:U26424

F-PLACE1011978

Homo sapiens DNA from chromosome 19, BAC 33152

3.8e-67:733:72

Hs.55452:AC003973

F-PLACE2000118

Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence)

7.8e-115:568:95

Hs.120856:AL022578

F-PLACE2000219

EST



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8.7e-11:137:75  
Hs.98191:AA417044

5 F-PLACE3000181  
Human protocadherin 42 mRNA, complete cds for abbreviated PC42  
1.5e-128:745:90  
Hs.79769:L11370

10 F-PLACE3000213  
EST  
1.0:219:63  
Hs.98452:AA426058

15 F-PLACE4000354  
ESTs  
1.4e-13:190:71  
Hs.138841:R94879

20 F-PLACE4000455  
F-SKNMC1000004  
Homo sapiens GABA-B receptor mRNA, complete cds  
0.00039:275:62  
Hs.12307:AF056085

25 F-SKNMC1000014  
ESTs  
3.3e-38:196:98  
Hs.113307:H16716

30 F-SKNMC1000082  
Complement component 4A  
0.98:324:63  
Hs.76682:K02403

35 F-THYRO1000036  
Homo sapiens mRNA for putative ATPase, partial  
0.98:199:60  
Hs.91471:AJ006268

40 F-THYRO1000061  
Human kinase Myt1 (Myt1) mRNA, complete cds  
1.0:210:62  
Hs.77783:AF014118

45 F-THYRO1000099  
ESTs  
2.5e-119:605:96  
Hs.11782:W07369

50 F-THYRO1000196  
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds  
1.6e-126:475:98  
Hs.115418:AF016272

55 F-THYRO1000400  
Human R kappa B mRNA, complete cds  
0.64:223:63

Hs.95262:U08191

F-THYRO1000580

ESTs, Weakly similar to ZINC FINGER PROTEIN 7 [H.sapiens]

5.4e-27:248:76

Hs.25465:AA528105

F-THYRO1000584

Alpha mannosidase II isozyme

2.2e-06:528:60

Hs.155961:L28821

F-THYRO1000678

Gap junction protein, beta 2, 26kD (connexin 26)

1.3e-33:266:80

Hs.81795:M86849

F-THYRO1000776

Human involucrin mRNA

0.0025:497:59

Hs.157091:M13903

F-THYRO1000795

MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN

4.1e-19:532:62

Hs.3816:AF070548

F-THYRO1000846

Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds

0.029:387:60

Hs.27910:AF049105

F-THYRO1000866

Homo sapiens SKB1Hs mRNA, complete cds

1.1e-92:529:89

Hs.12912:AF015913

F-THYRO1000956

Homo sapiens mRNA for G-protein coupled receptor

1.8e-15:474:64

Hs.155235:Y13583

F-THYRO1000964

Human OB binding protein-2 (OB-BP2) mRNA, complete cds

0.22:303:61

Hs.117005:U71383

F-THYRO1000999

EST

2.0e-05:198:63

Hs.146520:AI130948

F-THYRO1001063

Human mRNA for cerebroside sulfotransferase, complete cds

0.51:448:60

Hs.17958:D88667

F-THYRO1001071

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ESTs

2.1e-29:237:83

Hs.155582:AI125241

5 F-THYRO1001102  
ESTs, Weakly similar to growth arrest inducible gene product [H.sapiens]  
4.7e-32:208:88  
Hs.7854:W21970

10 F-THYRO1001113  
Homo sapiens dysferlin mRNA, complete cds  
3.2e-53:684:68  
Hs.143897:AF075575

15 F-THYRO1001128  
ESTs  
2.1e-120:589:97  
Hs.62595:AA306052

20 F-THYRO1001205

F-THYRO1001237  
ESTs  
0.66:326:60  
25 Hs.148352:U80757

F-THYRO1001242  
Protein phosphatase 2C alpha [human, teratocarcinoma, mRNA, 2346 nt]  
0.017:188:63  
30 Hs.57764:S87759

F-THYRO1001266  
Human sodium iodide symporter mRNA, complete cds  
8.6e-43:806:62  
35 Hs.103983:U66088

F-THYRO1001327  
ESTs  
2.8e-50:264:96  
40 Hs.154667:AI343524

F-THYRO1001456  
EST  
0.90:84:72  
45 Hs.130049:AA902650

F-THYRO1001457  
Protein kinase C, mu  
6.0e-53:705:67  
50 Hs.2891:X75756

F-THYRO1001471  
ESTs  
8.0e-52:278:94  
55 Hs.7604:W31115

F-THYRO1001478  
Human mRNA for KIAA0150 gene, partial cds

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0.79:150:66  
Hs.98508:D63484

5 F-THYRO1001495  
Homo sapiens KIAA0415 mRNA, complete cds  
9.5e-75:550:82  
Hs.7289:AB007875

10 F-THYRO1001523  
ESTs  
7.2e-19:142:86  
Hs.140588:H60533

15 F-THYRO1001529  
ESTs  
5.7e-24:141:95  
Hs.114172:AA703201

20 F-THYRO1001593  
H.sapiens mRNA for serine/threonine protein kinase EMK  
1.4e-70:643:74  
Hs.157199:X97630

25 F-THYRO1001608  
Human mRNA for KIAA0227 gene, partial cds  
2.6e-07:533:59  
Hs.79170:D86980

30 F-THYRO1001641  
ESTs  
0.87:269:59  
Hs.14599:AA522511

35 F-THYRO1001700  
Homo sapiens c-Jun N-terminal kinase kinase 2 (JNKK2) mRNA, complete cds  
3.3e-05:441:59  
Hs.110299:AF013589

40 F-THYRO1001702  
Human plectin (PLEC1) mRNA, complete cds  
0.00017:346:62  
Hs.79706:U53204

45 F-THYRO1001725  
Homo sapiens mRNA for procollagen I-N proteinase  
1.3e-06:275:64  
Hs.120330:AJ003125

50 F-THYRO1001770  
Homo sapiens mRNA for HsGAK, complete cds  
0.046:265:58  
Hs.153227:D88435

55 F-THYRO1001803  
EST  
0.0085:201:63  
Hs.158782:AI376601

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F-Y79AA1000030  
 ESTs  
 0.00051:276:60  
 Hs.111999:AA465020  
 5  
 F-Y79AA1000127  
 ESTs  
 1.3e-85:430:96  
 Hs.49932:W58552  
 10  
 F-Y79AA1000207  
 ESTs  
 4.5e-81:407:96  
 Hs.125308:A1376737  
 15  
 F-Y79AA1000226  
 ESTs, Highly similar to HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV [Caenorhabditis elegans]  
 0.00081:76:84  
 20 Hs.11221:A1192291  
 F-Y79AA1000270  
 Human mRNA for ORF, Xq terminal portion  
 9.9e-97:590:88  
 25 Hs.6551:D16469  
 F-Y79AA1000426  
 CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR  
 0.045:507:59  
 30 Hs.82914:X68264  
 F-Y79AA1000521  
 Homo sapiens mRNA for putative G-protein coupled receptor, EDG6  
 0.0029:489:58  
 35 Hs.159543:AJ000479  
 F-Y79AA1000750  
 ESTs  
 9.9e-12:252:65  
 40 Hs.52885:H29851  
 F-Y79AA1000776  
 ESTs  
 1.4e-50:340:87  
 45 Hs.144198:A1017555  
 F-Y79AA1000777  
 Homo sapiens mRNA for putative transcription factor, partial  
 3.9e-10:501:61  
 50 Hs.26782:AJ009770  
 F-Y79AA1000876  
 Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds  
 1.3e-11:323:66  
 55 Hs.30250:AF055376  
 F-Y79AA1000888  
 Homo sapiens mRNA for KIAA0469 protein, complete cds

1.5e-05:641:58  
Hs.7764:AB007938

F-Y79AA1000959

5 Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds  
5.3e-54:277:96  
Hs.53066:AF093420

F-Y79AA1000967

10 Human mRNA for KIAA0369 gene, complete cds  
8.1e-10:517:61  
Hs.21355:AB002367

F-Y79AA1001013

15 ESTs  
2.4e-44:259:93  
Hs.109468:W52074

F-Y79AA1001056

20 ESTs, Moderately similar to maternal transcript Maid [M.musculus]  
4.7e-07:90:87  
Hs.36794:AI038407

F-Y79AA1001062

25 ESTs, Weakly similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]  
1.6e-60:320:96  
Hs.13982:W27344

F-Y79AA1001090

30 H.sapiens DAP-kinase mRNA  
2.3e-06:465:59  
Hs.153924:X76104

F-Y79AA1001212

35 Homo sapiens SL15 protein mRNA, complete cds  
1.5e-163:763:98  
Hs.6710:AF038961

F-Y79AA1001264

40 Homo sapiens mRNA for MSJ-1, complete cds  
5.3e-15:367:64  
Hs.3845:AB014888

F-Y79AA1001272

45 Human plectin (PLEC1) mRNA, complete cds  
6.3e-05:325:63  
Hs.79706:U53204

F-Y79AA1001328

50 Homo sapiens Delta mRNA, complete cds  
1.8e-07:271:61  
Hs.144631:AF003522

F-Y79AA1001426

55 Aldehyde dehydrogenase 7  
0.94:485:56  
Hs.83155:U10868

5  
F-Y79AA1001427  
NADH-CYTOCHROME B5 REDUCTASE  
1.7e-56:649:69  
Hs.75666:M28713

10  
F-Y79AA1001430  
Homo sapiens mRNA for KIAA0469 protein, complete cds  
2.8e-124:577:99  
Hs.7764:AB007938

15  
F-Y79AA1001523  
Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds  
1.1e-92:496:93  
Hs.128763:AF009353

20  
F-Y79AA1001530  
Human beta-tubulin gene (5-beta) with ten Alu family members  
1.0e-131:669:95  
Hs.108014:X00734

25  
F-Y79AA1001592  
ESTs  
1.2e-88:212:97  
Hs.131180:AA594251

30  
F-Y79AA1001727  
  
F-Y79AA1001787  
Human mRNA for KIAA0315 gene, partial cds  
0.48:248:63  
Hs.3989:AB002313

35  
F-Y79AA1001793  
ESTs  
1.4e-67:192:98  
Hs.118559:AA887084

40  
F-Y79AA1001795  
Homo sapiens mRNA for GalT4 protein  
5.3e-89:431:98  
Hs.21495:AL031228

45  
F-Y79AA1001799  
NUCLEAR FACTOR RIP140  
0.54:182:62  
Hs.155017:X84373

50  
F-Y79AA1001803  
ESTs, Highly similar to MELANOMA-ASSOCIATED ANTIGEN XP [Homo sapiens]  
0.72:169:63  
Hs.94011:AA627644

55  
F-Y79AA1001863  
EST  
1.0:114:63  
Hs.152260:AA489703

F-Y79AA1002022

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B94 PROTEIN  
5.7e-13:469:65  
Hs.75522:M92357

5 F-Y79AA1002058  
Homo sapiens clone 24733 mRNA sequence  
1.7e-154:740:98  
Hs.21970:AF052149

10 F-Y79AA1002121  
EST  
0.14:104:66  
Hs.100070:M91493

15 F-Y79AA1002129  
ESTs  
5.1e-90:431:98  
Hs.40719:AI183452

20 F-Y79AA1002213

F-Y79AA1002334  
ESTs  
5.0e-20:187:80  
25 Hs.111900:AA397579

F-Y79AA1002373  
ESTs  
4.5e-37:192:98  
30 Hs.118559:AA887084

F-Y79AA1002376  
Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds  
1.2e-36:657:64  
35 Hs.65248:AF063228

F-Y79AA1002378  
Homo sapiens KIAA0426 mRNA, complete cds  
4.9e-38:424:72  
40 Hs.97476:AB007886

F-Y79AA1002381  
CELL DIVISION PROTEIN KINASE 3  
8.4e-17:580:61  
45 Hs.100009:X66357

Homology search result 9

50 **[0302]** The result of the homology search in the Human Unigene(<http://www.ncbi.nlm.nih.gov/UniGene>) using the clone sequences of the 3'-ends.

Indicated are from the top,  
the name of the clone sequence,  
title of the top hit data,  
55 the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),  
the Accession No. of the top hit data.

**[0303]** Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.



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[0304] Data were not shown for the clones in which the P-value was higher than 1.

5	R-HEMBA1000006 ESTs 1.0:85:71 Hs.130699:AA621478
10	R-HEMBA1000121 ESTs 1.3e-111:545:97 Hs.153432:AA098922
15	R-HEMBA1000128 ESTs, Weakly similar to HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-MRPL8 INTERGENIC REGION PRE-CURSOR [S.cerevisiae] 3.0e-98:532:93 Hs.7745:H92988
20	R-HEMBA1000275 ESTs 6.5e-11:81:81 Hs.163492:AI334460
25	R-HEMBA1000300 Homo sapiens mRNA for putative lipoic acid synthetase, partial 1.2e-39:309:81 Hs.53531:AJ224162
30	R-nnnnnnnnnnnnn ESTs 4.9e-95:455:98 Hs.154009:AI284184
35	R-HEMBA1000462 Homo sapiens clone 243 unknown mRNA, complete sequence 3.6e-91:313:94 Hs.20423:AF091094
40	R-HEMBA1000477 ESTs 4.7e-111:541:97 Hs.84526:AI341541
45	R-HEMBA1000590 Homo sapiens mRNA for matrilin-4, partial 2.6e-102:547:93 Hs.129361:AJ007581
50	R-HEMBA1000634 ESTs 0.85:189:62 Hs.131268:AA909162
55	R-HEMBA1000671 ESTs 6.5e-84:432:96 Hs.31991:T78668

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5 R-HEMBA1000713  
Homo sapiens 10kD protein (BC10) mRNA, complete cds  
4.0e-119:575:97  
Hs.5300:AF053470

10 R-HEMBA1000732  
EST  
3.9e-81:435:92  
Hs.146718:AI146722

15 R-HEMBA1000875  
EST  
0.023:207:62  
Hs.148275:AA907849

20 R-HEMBA1000940  
Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds  
7.4e-31:211:81  
Hs.97203:U83171

25 R-HEMBA1000962  
ESTs  
1.1e-104:515:97  
Hs.8978:W63573

30 R-HEMBA1001 184  
EST  
7.1e-07:382:62  
Hs.124559:AA847550

35 R-HEMBA1001221  
ESTs, Weakly similar to transmembrane protein [H.sapiens]  
1.2e-95:487:95  
Hs.22791:AI056665

40 R-HEMBA1001228  
Human germline oligomeric matrix protein (COMP) mRNA, complete cds  
4.0e-42:170:92  
Hs.1584:AC003107

45 R-HEMBA1001272  
ESTs  
5.7e-71:514:84  
Hs.26966:N74056

50 R-HEMBA1001296  
EST  
1.7e-93:494:95  
Hs.102465:N27272

55 R-HEMBA1001297  
Homo sapiens putative transcription factor CA150 mRNA, complete cds  
1.5e-93:466:96  
Hs.13063:AF017789

R-HEMBA1001390

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## ESTs

1.6e-42:181:89  
Hs.139190:N55515

- 5 R-HEMBA1001563  
Homo sapiens DEC-205 mRNA, complete cds  
8.4e-42:311:83  
Hs.153563:AF011333
- 10 R-HEMBA1001621  
ESTs, Highly similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [Homo sapiens]  
4.2e-56:386:86  
Hs.9305:W84893
- 15 R-HEMBA1001878  
Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds  
1.1e-80:433:93  
Hs.10290:AF090988
- 20 R-HEMBA1001886  
Zinc finger protein 141 (clone pHZ-44)  
5.9e-61:530:80  
Hs.159596:L15309
- 25 R-HEMBA1002048  
ESTs  
0.95:127:63  
Hs.98690:AA431162
- 30 R-HEMBA1002131  
  
R-HEMBA1002163  
ESTs, Weakly similar to K09E9.2 [C.elegans]  
5.9e-36:225:90  
35 Hs.26813:AI339473  
  
R-HEMBA1002167  
ESTs  
1.5e-35:325:80  
40 Hs.124171:N98933  
  
R-HEMBA1002178  
MICROSOMAL DIPEPTIDASE PRECURSOR  
0.99:243:61  
45 Hs.109:J05257  
  
R-HEMBA1002195  
Deoxyhypusine synthase  
1.9e-19:109:100  
50 Hs.79064:U79262  
  
R-HEMBA1002227  
Myristoylated alanine-rich C-kinase substrate  
2.0e-116:567:97  
55 Hs.75607:D10522  
  
R-HEMBA1002316  
Homo sapiens mRNA for putative GTP-binding protein

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8.2e-20:160:85  
Hs.101033:Y14391

5 R-HEMBA1002420  
ESTs, Weakly similar to T03G11.6 gene product [C.elegans]  
2.7e-78:402:97  
Hs.108354:W19984

10 R-HEMBA1002421  
Syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)  
1.9e-91:443:97  
Hs.1501:J04621

15 R-HEMBA1002524  
Human MHC Class I region proline rich protein mRNA, complete cds  
1.0e-111:551:96  
Hs.41548:U63336

20 R-HEMBA1002551  
ESTs  
3.4e-107:553:96  
Hs.92071:W80592

25 R-HEMBA1002767  
Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds  
5.5e-108:568:95  
Hs.19154:AF038660

30 R-HEMBA1002985  
ESTs  
4.4e-39:211:96  
Hs.126894:AA932538

35 R-HEMBA1003047  
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds  
1.6e-115:571:96  
Hs.148318:AF034611

40 R-HEMBA1003072  
EST  
0.044:220:61  
Hs.136349:AA490873

45 R-HEMBA1003101  
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds  
1.2e-117:575:97  
Hs.26350:AF049891

50 R-HEMBA1003120  
Zinc finger protein 10 (KOX 1)  
5.8e-41:412:73  
Hs.2479:X78933

55 R-HEMBA1003230  
Homo sapiens UP50 mRNA, complete cds  
4.2e-44:258:93  
Hs.11494:AF093118

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R-HEMBA1003294  
ESTs  
4.3e-84:410:98  
Hs.113517:AA418756

5

R-HEMBA1003315  
ESTs, Weakly similar to TIP49 [R.norvegicus]  
7.3e-73:476:87  
Hs.6455:AA515838

10

R-HEMBA1003392  
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds  
8.3e-117:557:98  
Hs.23672:AF074264

15

R-HEMBA1003399  
ESTs, Highly similar to MVP1 PROTEIN [Saccharomyces cerevisiae]  
8.0e-94:526:92  
Hs.12169:N38744

20

R-HEMBA1003487  
ESTs  
4.5e-84:417:96  
Hs.21835:AA458524

25

R-HEMBA1003497  
ESTs  
1.4e-72:346:99  
Hs.129837:AA778570

30

R-HEMBA1003530  
ESTs  
8.5e-82:459:91  
Hs.22140:R41751

35

R-HEMBA1003602  
ESTs  
1.0e-101:592:90  
Hs.124342:AA829829

40

R-HEMBA1003732  
ESTs  
2.1e-111:530:99  
Hs.101660:AA481200

45

R-HEMBA1003945  
Calcineurin B  
2.9e-83:410:97  
Hs.1335:M30773

50

R-HEMBA1004007  
Homo sapiens PYRIN (MEFV) mRNA, complete cds  
3.8e-57:382:77  
Hs.113283:AF018080

55

R-HEMBA1004085  
ESTs  
3.0e-59:396:87

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Hs.102480:AA520980

R-nnnnnnnnnnnnn

Homo sapiens intersectin short form mRNA, complete cds

5 2.0e-116:569:97  
Hs.66392:AF064244

R-HEMBA1004250

ESTs

10 1.6e-97:469:97  
Hs.125529:AA883986

R-HEMBA1004391

EST

15 0.085:113:63  
Hs.157582:AI356856

R-HEMBA1004444

ESTs

20 2.3e-88:430:98  
Hs.141680:N98441

R-HEMBA1004454

ESTs

25 1.7e-71:338:100  
Hs.103913:AA740543

R-HEMBA1004505

ESTs

30 2.2e-63:329:95  
Hs.4814:AA631254

R-HEMBA1004785

EST

35 1.0:77:67  
Hs.144066:AA905236

R-HEMBA1004797

ESTs

40 4.1e-11:71:100  
Hs.27206:AA626782

R-HEMBA1004952

ESTs

45 6.0e-93:435:99  
Hs.115120:AA935633

R-HEMBA1004971

ESTs

50 0.98:152:58  
Hs.112621:AA608964

R-HEMBA1004982

ESTs

55 2.3e-109:516:98  
Hs.14877:AA749081

R-HEMBA1005070

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Human mRNA for KIAA0310 gene, complete cds  
4.0e-96:381:91  
Hs.5716:AB002308

5 R-HEMBA1005084  
ESTs  
1.0:75:80  
Hs.62119:AA043299

10 R-HEMBA1005145  
Homo sapiens LIM protein mRNA, complete cds  
1.6e-58:278:84  
Hs.154103:AF061258

15 R-HEMBA1005230  
ESTs  
3.7e-65:336:95  
Hs.124946:AI026708

20 R-HEMBA1005246  
  
R-HEMBA1005267  
Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA, partial cds  
7.8e-75:536:81  
25 Hs.44566:U28831

R-HEMBA1005337  
EST  
8.7e-58:291:97  
30 Hs.48956:N64339

R-HEMBA1005430  
ESTs  
7.6e-83:388:100  
35 Hs.28968:AA524690

R-HEMBA1005449  
ESTs  
5.0e-47:317:86  
40 Hs.23650:H21144

R-HEMBA1005489  
ESTs  
1.8e-96:504:94  
45 Hs.8028:AA053817

R-HEMBA1005522  
EST  
1.0:98:64  
50 Hs.157385:AI364194

R-HEMBA1005545  
MUSCARINIC ACETYLCHOLINE RECEPTOR M3  
6.3e-117:579:96  
55 Hs.7138:U29589

R-HEMBA1005698  
ESTs

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- 1.6e-113:562:96  
Hs.12942:AI042353
- 5 R-HEMBA1005913  
ESTs  
2.8e-109:564:94  
Hs.28827:AI125541
- 10 R-HEMBA1005929  
Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds  
9.6e-63:497:77  
Hs.97203:U83171
- 15 R-HEMBA1005945  
ESTs  
1.1e-74:412:92  
Hs.32246:AA464020
- 20 R-HEMBA1006016  
ESTs  
1.4e-18:162:82  
Hs.149448:AI082465
- 25 R-HEMBA1006171  
EST  
0.049:94:69  
Hs.159919:AA961766
- 30 R-HEMBA1006276  
ESTs  
6.3e-22:257:75  
Hs.138847:N64493
- 35 R-HEMBA1006299  
ESTs, Weakly similar to R06B9.b [C.elegans]  
3.9e-107:596:91  
Hs.30432:W28988
- 40 R-HEMBA1006311  
Homo sapiens SALL1 gene, partial  
0.99:273:60  
Hs.123094:X98833
- 45 R-HEMBA1006335  
ESTs  
2.5e-72:447:89  
Hs.23579:W38893
- 50 R-HEMBA1006357  
ESTs  
6.3e-15:187:74  
Hs.161714:AA229078
- 55 R-HEMBA1006430  
Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds  
2.9e-47:303:88  
Hs.129708:AF064090



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R-HEMBA1006482

Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds

5.5e-107:537:96

Hs.14511:AF026852

5

R-HEMBA1006517

ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]

2.7e-43:173:86

Hs.141505:N30650

10

R-HEMBA1006544

Homo sapiens mRNA for small GTP-binding protein, complete cds

5.8e-60:329:80

Hs.115325:D84488

15

R-HEMBA1006572

ESTs

7.2e-94:450:99

Hs.123933:AA758566

20

R-HEMBA1006658

Homo sapiens mRNA for KIAA0687 protein, partial cds

2.3e-112:570:94

Hs.3628:AB014587

25

R-HEMBA1006707

Homo sapiens mRNA for matrilin-4, partial

1.7e-79:389:97

Hs.129361:AJ007581

30

R-HEMBA1006724

R-HEMBA1006749

Homo sapiens mRNA for matrilin-4, partial

1.0e-89:472:94

Hs.129361:AJ007581

35

R-HEMBA1006770

ESTs, Moderately similar to CAGH4 [H.sapiens]

2.0e-112:554:96

Hs.41641:AA428519

40

R-HEMBA1006902

Homo sapiens mRNA for matrilin-4, partial

3.0e-113:540:98

Hs.129361:AJ007581

45

R-HEMBA1006912

H.sapiens mRNA for phosphoinositide 3-kinase

5.9e-45:297:86

Hs.101238:Y11312

50

R-HEMBA1006916

Homo sapiens Grb14 mRNA, complete cds

5.8e-116:346:99

Hs.83070:L76687

55

R-HEMBA1006960

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ESTs  
1.7e-110:519:99  
Hs.22015:AI359551

5 R-HEMBA1007013  
ESTs  
0.53:280:59  
Hs.143532:AI087321

10 R-HEMBA1007057

R-HEMBA1007063  
EST  
3.2e-41:310:83  
15 Hs.163333:AA879053

R-HEMBA1007241  
ESTs  
1.8e-103:492:98  
20 Hs.127478:AI188768

R-HEMBA1007291  
Human mRNA for KIAA0266 gene, complete cds  
8.7e-46:283:89  
25 Hs.78878:D87455

R-HEMBA1007332  
ESTs, Weakly similar to hTAFII100 [H.sapiens]  
2.8e-17:161:80  
30 Hs.3727:AA205887

R-HEMBA1000106  
ESTs  
1.3e-100:491:97  
35 Hs.27774:AA576731

R-HEMBA1000276

R-HEMBA1000309  
EST  
1.0:150:64  
40 Hs.125409:AA879096

R-HEMBA1000407  
ESTs, Weakly similar to C47D12.2 [C.elegans]  
4.1e-110:535:97  
45 Hs.14328:AA503393

R-HEMBA1000447  
Homo sapiens JWA protein mRNA, complete cds  
5.6e-109:533:97  
50 Hs.92384:AF070523

R-HEMBA1000542  
ESTs, Weakly similar to C01H6.7 [C.elegans]  
1.6e-88:497:91  
55 Hs.18171:AA524327

R-HEMBB1000567

Insulin-like growth factor 2 (somatomedin A)

8.9e-61:369:88

Hs.155487:J03242

5

R-HEMBB1000642

ESTs

2.2e-44:308:84

Hs.141318:N71080

10

R-HEMBB1000668

ESTs, Weakly similar to hTAFII100 [H.sapiens]

2.5e-102:520:95

Hs.3830:AA167691

15

R-HEMBB1000679

ESTs

6.7e-36:188:97

Hs.154218:AA169554

20

R-HEMBB1000881

ESTs

8.4e-105:519:96

Hs.110967:AA570505

25

R-HEMBB1000905

ESTs

1.1e-94:454:98

Hs.52515:AA464314

30

R-HEMBB1001026

ESTs

0.22:93:69

Hs.119510:AA630235

35

R-HEMBB1001048

EST

0.42:127:66

Hs.147466:AI215091

40

R-HEMBB1001200

ESTs

3.7e-07:330:62

Hs.10109:AI148628

45

R-HEMBB1001407

MHC class II transactivator

3.8e-35:414:71

Hs.3076:U18259

50

R-HEMBB1001530

ESTs

2.4e-95:455:98

Hs.8956:AI146421

55

R-HEMBB1001547

ESTs

1.0e-111:533:98

Hs.33979:AI074147

R-HEMBB1001573

ESTs, Moderately similar to LL5 protein [R.norvegicus]

1.7e-06:64:95

Hs.131327:AI148746

R-HEMBB1001847

ESTs

1.4e-54:280:96

Hs.109755:AA180809

R-HEMBB1001959

Homo sapiens clone 24781 mRNA sequence

1.5e-104:504:97

Hs.108112:AF070640

R-HEMBB1001978

Homo sapiens mRNA for TRAF5, complete cds

7.0e-28:220:84

Hs.29736:AB000509

R-HEMBB1002039

ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]

1.5e-34:423:72

Hs.154912:N63897

R-HEMBB1002041

ESTs, Weakly similar to transmembrane protein [H.sapiens]

7.0e-122:575:98

Hs.22791:AI056665

R-HEMBB1002051

ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]

4.2e-43:298:84

Hs.141429:AA631915

R-HEMBB1002120

ESTs

1.4e-91:438:99

Hs.145014:AI218562

R-HEMBB1002162

ESTs

1.0e-34:238:86

Hs.164036:AA845659

R-HEMBB1002228

Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds

1.7e-59:583:77

Hs.129735:AF010144

R-HEMBB1002245

ESTs

9.1e-66:383:91

Hs.8989:R71365

5  
R-HEMBB1002302  
ESTs  
3.6e-54:329:89  
Hs.37706:AA005120

10  
R-HEMBB1002427  
ESTs  
4.2e-83:400:98  
Hs.130783:AI263114

15  
R-HEMBB1002465  
EST  
9.9e-38:231:90  
Hs.133443:AI061405

20  
R-HEMBB1002661  
ESTs  
2.5e-101:472:99  
Hs.26878:AI421289

25  
R-HEMBB1002663  
Small inducible cytokine A5 (RANTES)  
7.1e-43:268:88  
Hs.155464:AF088219

30  
R-HEMBB1002693  
ESTs  
4.6e-84:435:96  
Hs.155522:AA829725

35  
R-MAMMA1000046  
EST  
3.9e-06:196:65  
Hs.136664:AA707467

40  
R-MAMMA1000102  
Human G protein-coupled receptor (STRL22) mRNA, complete cds  
1.1e-31:237:83  
Hs.46468:U45984

45  
R-MAMMA1000106  
ESTs  
1.3e-65:333:95  
Hs.130749:AI284219

50  
R-MAMMA1000118  
ESTs  
7.3e-95:465:97  
Hs.119286:AA126730

55  
R-MAMMA1000141  
ESTs  
4.2e-94:515:93  
Hs.8116:H23508

R-MAMMA1000204  
Homo sapiens dysferlin mRNA, complete cds  
2.3e-108:542:96

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Hs.143897:AF075575

R-MAMMA1000226

ESTs

5 2.1e-112:535:98

Hs.105761:AA903862

R-MAMMA1000403

ESTs

10 1.5e-36:162:83

Hs.152413:AA780515

R-MAMMA1000449

EST

15 1.5e-40:347:78

Hs.163333:AA879053

R-MAMMA1000457

Homo sapiens clone 638 unknown mRNA, complete sequence

20 2.6e-117:570:97

Hs.5825:AF091084

R-MAMMA1000473

ESTs

25 1.3e-62:308:99

Hs.53565:W02102

R-MAMMA1000496

Phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1)

30 0.051:125:68

Hs.189:AC005759

R-MAMMA1000528

ESTs

35 2.4e-12:216:71

Hs.134105:AI078038

R-MAMMA1000591

ESTs

40 5.0e-104:509:98

Hs.151678:AA032243

R-MAMMA1000614

Homo sapiens mRNA for KIAA0665 protein, complete cds

45 0.57:251:62

Hs.119004:AB014565

R-MAMMA1000652

ESTs

50 0.93:49:87

Hs.13248:R54144

R-MAMMA1000681

ESTs

55 1.3e-87:434:97

Hs.46668:N47089

R-MAMMA1000706

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Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds  
3.7e-48:232:100  
Hs.18953:AF067223

5 R-MAMMA1000788  
ESTs  
3.7e-108:559:94  
Hs.38969:AA130220

10 R-MAMMA1000810  
ESTs  
1.2e-45:347:80  
Hs.146811:AA410788

15 R-MAMMA1000814  
ESTs  
1.1e-18:288:70  
Hs.140608:N53448

20 R-MAMMA1000881  
ESTs  
1.9e-107:557:96  
Hs.141602:N63562

25 R-MAMMA1000986  
ESTs  
3.8e-46:342:83  
Hs.132722:AA618531

30 R-MAMMA1000994  
Homo sapiens mRNA for ISLR, complete cds  
1.2e-109:552:96  
Hs.102171:AB003184

35 R-MAMMA1001043  
ESTs  
2.3e-88:445:96  
Hs.20450:AI094818

40 R-MAMMA1001066  
Homo sapiens KIAA0414 mRNA, partial cds  
1.5e-43:282:81  
Hs.127649:AB007874

45 R-MAMMA1001094  
Homo sapiens clone 243 unknown mRNA, complete sequence  
3.0e-116:566:97  
Hs.20423:AF091094

50 R-MAMMA1001141  
ESTs  
1.2e-104:496:98  
Hs.29669:AI285856

55 R-MAMMA1001150  
ESTs, Highly similar to MYOSIN LIGHT CHAIN KINASE [Dictyostelium discoideum]  
1.9e-59:284:100  
Hs.9915:AI300083

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5 R-MAMMA1001237  
 ESTs  
 0.45:206:62  
 Hs.121366:AA758653

10 R-MAMMA1001284  
 ESTs  
 6.3e-40:279:85  
 Hs.109765:AI096738

15 R-MAMMA1001310  
 ESTs, Moderately similar to !!!! ALU SUBFAMTLY J WARNING ENTRY !!!! [H.sapiens]  
 5.1e-98:498:96  
 Hs.27264:AA159597

20 R-MAMMA1001418  
 Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds  
 1.2e-41:302:85  
 Hs.86188:D87845

25 R-MAMMA1001532  
 ESTs  
 3.9e-22:331:71  
 Hs.141840:AA028117

30 R-MAMMA1001609  
 Small inducible cytokine A5 (RANTES)  
 1.5e-31:277:78  
 Hs.155464:AF088219

35 R-MAMMA1001615  
 ESTs  
 1.1e-72:376:95  
 Hs.135569:AA923461

40 R-MAMMA1001623  
 ESTs  
 7.9e-106:505:98  
 Hs.22908:AI224910

45 R-MAMMA1001634  
 Homo sapiens PYRIN (MEFV) mRNA, complete cds  
 1.9e-44:428:76  
 Hs.113283:AF018080

50 R-MAMMA1001893  
 ESTs  
 8.0e-67:367:92  
 Hs.19210:W26097

55 R-MAMMA1001901  
 Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492  
 4.7e-35:342:69  
 Hs.127338:AB007961

R-MAMMA1001957  
 Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2  
 5.5e-47:383:79



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	Hs.1361:M55053
	R-MAMMA1001978
	ESTs
5	6.6e-108:560:95
	Hs.8859:AA191552
	R-MAMMA1002070
10	R-MAMMA1002080
	ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]
	9.8e-105:542:94
	Hs.10092:AI189282
15	R-MAMMA1002087
	ESTs
	4.0e-19:153:84
	Hs.136678:AA730474
20	R-MAMMA1002095
	ESTs
	6.8e-34:196:93
	Hs.48119:AA454227
25	R-MAMMA1002128
	ESTs, Highly similar to ABC1 PROTEIN PRECURSOR [Saccharomyces cerevisiae]
	9.0e-96:503:94
	Hs.39088:AA194773
30	R-MAMMA1002142
	ESTs
	5.6e-21:145:90
	Hs.62119:AA043299
35	R-MAMMA1002165
	ESTs
	1.6e-35:351:76
	Hs.140413:N47721
40	R-MAMMA1002205
	Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds
	6.4e-42:217:79
	Hs.133089:AF064019
45	R-MAMMA1002224
	ESTs
	0.50:170:64
	Hs.144140:H04293
50	R-MAMMA1002234
	R-MAMMA1002586
	ESTs
	5.0e-105:529:96
55	Hs.4814:AA631254
	R-MAMMA1002633
	ESTs

7.3e-97:470:98  
Hs.38039:AI360128

5 R-MAMMA1003126  
ESTs  
6.1e-114:567:97  
Hs.20733:AI417917

10 R-NT2RM4000100  
ESTs  
3.6e-71:343:99  
Hs.92186:AI080282

15 R-NT2RM4000115  
ESTs  
1.5e-86:405:100  
Hs.129151:AA988192

20 R-NT2RM4000198  
ESTs  
8.4e-83:462:93  
Hs.96772:AI369496

25 R-NT2RM4000284  
Human IgG Fc receptor hFcRn mRNA, complete cds  
5.4e-95:440:100  
Hs.110804:U12255

30 R-NT2RM4000295  
ESTs  
1.1e-112:544:97  
Hs.21452:AA581881

35 R-NT2RM4000326  
EST  
4.0e-59:301:96  
Hs.86264:AA206496

40 R-NT2RM4000417  
ESTs  
2.0e-88:489:93  
Hs.29098:AA521439

45 R-NT2RM4000444  
ESTs  
6.4e-90:497:92  
Hs.6129:U66676

50 R-NT2RM4000587  
ESTs  
1.0e-97:473:98  
Hs.24947:AA039350

55 R-NT2RM4000593  
ESTs  
9.8e-109:554:95  
Hs.7579:AA775865

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R-NT2RM4000648  
 ESTs, Moderately similar to GLYPICAN-1 PRECURSOR [Homo sapiens]  
 7.6e-39:262:85  
 Hs.118407:AA001322  
 5

R-NT2RM4000761  
 ESTs  
 6.4e-86:433:95  
 Hs.153428:AI246519  
 10

R-NT2RM4000965  
 ESTs  
 2.8e-102:523:96  
 Hs.61790:AA421156  
 15

R-NT2RM4000997  
 R-NT2RM4001321  
 ESTs  
 2.4e-66:315:100  
 Hs.75425:AA149434  
 20

R-NT2RM4001325  
 ESTs  
 0.99:104:62  
 Hs.116257:AA628680  
 25

R-NT2RM4001377  
 Homo sapiens mRNA for KIAA0638 protein, partial cds  
 9.3e-113:553:96  
 Hs.77864:AB014538  
 30

R-NT2RM4001735  
 Homo sapiens clone 23904 mRNA sequence  
 1.5e-107:553:94  
 Hs.67364:AF052129  
 35

R-NT2RM4001768  
 EST  
 1.6e-14:82:85  
 Hs.140922:R51520  
 40

R-NT2RM4001843  
 ESTs  
 2.1e-123:579:98  
 Hs.3741:AI057614  
 45

R-NT2RM4002352  
 Homo sapiens hLRp105 mRNA for LIJL receptor related protein 105, complete cds  
 1.8e-109:557:95  
 Hs.143641:AB009462  
 50

R-NT2RP2000092  
 ESTs  
 3.3e-08:286:65  
 Hs.79881:AA401302  
 55

R-NT2RP2000178

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ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]  
2.3e-95:462:98  
Hs.47305:AA195153

5 R-NT2RP2000240  
ESTs  
1.3e-55:272:98  
Hs.125522:AI299693

10 R-NT2RP2000394  
ESTs  
2.4e-107:528:96  
Hs.28555:W55892

15 R-NT2RP2000447  
ESTs, Moderately similar to dynamin, internal form 2, short C-terminal form [H.sapiens]  
1.6e-67:357:94  
Hs.128788:AA424076

20 R-NT2RP2000479  
ESTs  
2.6e-48:312:86  
Hs.146811:AA410788

25 R-NT2RP2000514  
EST  
3.2e-63:348:93  
Hs.44542:N33966

30 R-NT2RP2000533  
ESTs  
0.017:307:57  
Hs.97873:AA402799

35 R-NT2RP2000616  
ESTs  
1.0e-91:475:95  
Hs.50344:AI300539

40 R-NT2RP2000649  
Homo sapiens mRNA for Hs Ste24p, complete cds  
1.4e-66:322:98  
Hs.25846:AB016068

45 R-NT2RP2000663  
ESTs  
8.2e-59:311:96  
Hs.9728:T98746

50 R-NT2RP2000712  
EST  
1.7e-27:239:76  
Hs.161561:W60681

55 R-NT2RP2000739  
ESTs, Weakly similar to zinc finger protein [H.sapiens]  
6.3e-86:462:93  
Hs.13323:AA897542

R-NT2RP2000818  
ESTs  
7.3e-99:485:97  
Hs.100525:AI310204

5

R-NT2RP2000903  
H.sapiens 5T4 gene for 5T4 Oncofetal antigen  
1.2e-100:505:96  
Hs.82128:AJ012159

10

R-NT2RP2001200  
Homo sapiens mRNA for KIAA0676 protein, partial cds  
6.6e-59:306:95  
Hs.115763:AB014576

15

R-NT2RP2001223  
ESTs  
1.2e-94:475:95  
Hs.27556:AA115361

20

R-NT2RP2001276  
ESTs, Moderately similar to regulatory protein [M.musculus]  
4.7e-65:354:92  
Hs.105547:AI361036

25

R-NT2RP2001388  
ESTs  
5.5e-83:459:93  
Hs.15713:AA485755

30

R-NT2RP2001469  
ESTs, Weakly similar to teg292 protein [M.musculus]  
2.0e-30:233:83  
Hs.68791:AA527270

35

R-NT2RP2001480  
Homo sapiens thrombospondin 3 (THBS3) gene, complete cds  
2.1e-84:426:95  
Hs.82165:L38969

40

R-NT2RP2001495  
ESTs, Weakly similar to transporter protein [H.sapiens]  
1.7e-14:130:84  
Hs.18272:N78499

45

R-NT2RP2001514  
ESTs, Weakly similar to PROBABLE CATION-TRANSPORTING ATPASE YEL031W [Saccharomyces cerevisiae]  
3.3e-45:242:95  
Hs.9275:AA973284

50

R-NT2RP2001538  
EST  
1.4e-05:111:73  
Hs.137268:T39311

55

R-NT2RP2001562  
EST  
0.50:35:91

Hs.140505:AA804211

R-NT2RP2001662

Homo sapiens clone 24615 mRNA sequence

1.0e-95:485:95

Hs.94785:AF055012

R-NT2RP2001755

Homo sapiens mRNA for KIAA0762 protein, partial cds

4.2e-105:576:92

Hs.5378:AB018305

R-NT2RP2001769

ESTs

4.2e-102:548:93

Hs.14014:AA745592

R-NT2RP2001817

ESTs

6.0e-97:472:97

Hs.31176:AI037953

R-NT2RP2001878

ESTs

3.3e-94:475:95

Hs.144655:AI279798

R-NT2RP2001903

ESTs

1.7e-88:461:95

Hs.112218:AI038601

R-NT2RP2001915

ESTs

7.8e-96:480:96

Hs.100890:AA779892

R-NT2RP2001921

ESTs

2.5e-88:466:94

Hs.104859:AA779101

R-NT2RP2001948

ESTs

1.9e-81:439:91

Hs.105463:AA583017

R-NT2RP2001956

ESTs

8.7e-85:477:91

Hs.12101:AA677423

R-NT2RP2002015

ESTs

3.5e-85:431:95

Hs.75425:AA149434

R-NT2RP2002063

EST  
0.0083:199:62  
Hs.48699:N63049

5 R-NT2RP2002188  
ESTs  
1.5e-108:559:94  
Hs.47320:AA057440

10 R-NT2RP2002232  
ESTs  
2.5e-113:576:95  
Hs.7099:AI089774

15 R-ntntntntntntntntntntnt  
Human mRNA for KIAA0383 gene, partial cds  
8.0e-102:511:96  
Hs.27590:AB002381

20 R-NT2RP2002409  
ESTs  
3.2e-84:432:95  
Hs.128443:AI281991

25 R-NT2RP2002510  
ESTs  
1.3e-42:303:82  
Hs.146811:AA410788

30 R-NT2RP2002527  
Thromboxane A2 receptor  
2.9e-23:164:88  
Hs.89887:D38081

35 R-NT2RP2002533  
Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds  
4.0e-117:580:96  
Hs.127436:AF040709

40 R-NT2RP2002564  
Human zinc-finger protein C2H2-150 mRNA, complete cds  
4.0e-111:569:94  
Hs.108139:U38864

45 R-NT2RP2002674  
ESTs, Weakly similar to putative p150 [H.sapiens]  
0.010:293:60  
Hs.140964:AI214400

50 R-NT2RP2002721  
ESTs  
5.6e-10:165:69  
Hs.108745:H95644

55 R-NT2RP2002824  
EST  
0.0055:209:58

Hs.136259:AA347883

R-NT2RP2002942  
ESTs  
5 9.2e-82:422:96  
Hs.140952:R59211

R-NT2RP2002974  
ESTs  
10 5.6e-99:507:96  
Hs.43314:AA160543

R-NT2RP2002976  
ESTs  
15 2.9e-78:397:91  
Hs.83575:N28730

R-NT2RP2003042  
ESTs  
20 2.7e-107:526:97  
Hs.6770:AA972732

R-NT2RP2003179  
ESTs  
25 2.9e-59:335:92  
Hs.87019:AA760977

R-NT2RP2003210  
ESTs  
30 2.1e-80:419:94  
Hs.25354:N28667

R-NT2RP2003302  
ESTs, Moderately similar to ZINC FINGER PROTEIN 7 [Homo sapiens]  
35 2.1e-92:443:98  
Hs.112508:AA599140

R-NT2RP2003369  
ESTs  
40 9.7e-84:462:92  
Hs.155116:C16874

R-NT2RP2003383  
Homo sapiens mRNA for KIAA0458 protein, complete cds  
45 1.3e-112:549:97  
Hs.7414:AB007927

R-NT2RP2003390  
Homo sapiens SEC63 (SEC63) mRNA, complete cds  
50 4.9e-56:286:96  
Hs.31575:AF100141

R-NT2RP2003469  
Human mRNA for KIAA0355 gene, complete cds  
55 6.6e-40:302:83  
Hs.153014:AB002353

R-NT2RP2003545



- ESTs  
8.0e-121:572:98  
Hs.23643:AI299952
- 5 R-NT2RP2003593  
EST  
1.0:124:62  
Hs.59890:AA001879
- 10 R-NT2RP2003599  
EST  
5.2e-06:319:60  
Hs.147887:AI223203
- 15 R-NT2RP2003655  
ESTs  
9.3e-107:519:97  
Hs.5831:AA176450
- 20 R-NT2RP2003664  
Homo sapiens mRNA for leptin receptor gene-related protein  
5.3e-112:549:96  
Hs.23581:Y12670
- 25 R-NT2RP2003931  
Human mRNA for KIAA0365 gene, partial cds  
1.7e-113:571:96  
Hs.84123:AB002363
- 30 R-NT2RP2003940  
EST  
3.0e-71:385:93  
Hs.162657:AA603590
- 35 R-NT2RP2003950  
Homo sapiens clone 24778 unknown mRNA  
5.0e-98:494:95  
Hs.25306:AF070572
- 40 R-NT2RP2004069  
Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end  
6.3e-54:556:74  
Hs.103948:K00627
- 45 R-NT2RP2004108  
ESTs, Moderately similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]  
6.9e-92:442:98  
Hs.14831:AI261191
- 50 R-NT2RP2004141  
ESTs  
8.3e-29:171:93  
Hs.25700:AI338437
- 55 R-NT2RP2004179  
ESTs  
3.1e-71:461:88  
Hs.6748:R68509

5 R-NT2RP2004205  
 ESTs  
 2.6e-44:397:78  
 Hs.95115:AA206594  
  
 10 R-NT2RP2004447  
 ESTs  
 4.0e-101:494:97  
 Hs.51655:AA523276  
  
 15 R-NT2RP2004495  
 ESTs, Weakly similar to transporter protein [H.sapiens]  
 6.1e-71:417:92  
 Hs.18272:N78499  
  
 20 R-NT2RP2004524  
 ESTs  
 1.8e-93:482:95  
 Hs.119285:AI225008  
  
 25 R-NT2RP2004556  
 Homo sapiens mRNA for KIAA0459 protein, partial cds  
 8.8e-48:353:82  
 Hs.28169:AB007928  
  
 30 R-NT2RP2004606  
 Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)  
 3.5e-116:576:96  
 Hs.148726:X03124  
  
 35 R-NT2RP2004648  
 ESTs  
 5.9e-114:600:93  
 Hs.3741:AI057614  
  
 40 R-NT2RP2004670  
 ESTs  
 1.7e-92:488:94  
 Hs.6262:T89093  
  
 45 R-NT2RP2004794  
 EST  
 0.44:205:57  
 Hs.147759:AI220726  
  
 50 R-NT2RP2004837  
 ESTs  
 6.9e-111:576:94  
 Hs.12305:AA166889  
  
 55 R-NT2RP2004847  
 ESTs  
 8.3e-94:445:99  
 Hs.53996:AI268861  
  
 R-NT2RP2005027  
 GLUCOSE TRANSPORTER TYPE 3, BRAIN  
 2.5e-104:508:97

Hs.7594:M20681

R-NT2RP2005069

ESTs, Highly similar to vacuolar protein sorting homolog r-vps33b [R.norvegicus]

5 4.7e-111:541:97

Hs.26510:AA700425

R-NT2RP2005163

ESTs

10 6.8e-64:327:89

Hs.83575:N28730

R-NT2RP2005181

ESTs, Moderately similar to HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 [H.sapiens]

15 1.6e-106:527:97

Hs.86362:AA205485

R-NT2RP2005247

MHC class II transactivator

20 7.9e-35:465:69

Hs.3076:U18259

R-NT2RP2005378

ESTs

25 3.4e-110:566:94

Hs.23060:N64748

R-NT2RP2005391

ESTs

30 5.5e-82:463:92

Hs.118793:AA192438

R-NT2RP2005425

Homo sapiens mRNA for KIAA0803 protein, partial cds

35 2.6e-101:526:94

Hs.58103:AB018346

R-NT2RP2005463

ESTs, Weakly similar to weakly similar to S. cerevisiae PTM1 precursor [C.elegans]

40 7.6e-111:554:97

Hs.16492:N95400

R-NT2RP2005514

ESTs

45 1.8e-97:490:95

Hs.109677:AA447864

R-NT2RP2005535

EST

50 5.1e-40:399:73

Hs.127142:AA937570

R-NT2RP2005541

ESTs

55 5.2e-114:573:96

Hs.70823:AI378619

R-NT2RP2005597

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ESTs, Weakly similar to rotated abdomen protein [D.melanogaster]  
3.7e-109:543:96  
Hs.99654:AA670164

5 R-nnnnnnnnnnnnn  
ESTs  
1.1 e-100:501:97  
Hs.112011:AA987961

10 R-NT2RP2005666  
ESTs  
2.7e-106:560:94  
Hs.42814:AA205754

15 R-NT2RP2005774  
Homo sapiens apoptosis-related mRNA, 3'UTR, partial sequence  
7.0e-96:440:96  
Hs.139345:AF035364

20 R-NT2RP2005878  
ESTs  
2.8e-89:479:93  
Hs.142305:R42591

25 R-NT2RP2005883  
ESTs  
1.0e-85:431:96  
Hs.6909:AA928115

30 R-NT2RP2005887  
ESTs  
5.5e-109:566:94  
Hs.12305:AA166889

35 R-nnnnnnnnnnnnn  
Paired box homeotic gene 6 (aniridia, keratitis)  
1.6e-116:578:96  
Hs.89506:M93650

40 R-NT2RP2005994  
EST  
0.0061:129:68  
Hs.160756:AI310589

45 R-NT2RP2006004  
ESTs, Weakly similar to KIAA0405 [H.sapiens]  
4.7e-45:303:86  
Hs.14146:W92235

50 R-NT2RP2006042  
EST  
0.64:84:71  
Hs.133275:AI053487

55 R-NT2RP2006092  
ESTs, Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]  
1.1e-75:384:95  
Hs.32822:AI194045



Hs.147759:AI220726

R-NT2RP3000172

ESTs

5 2.0e-89:494:93

Hs.6262:T89093

R-NT2RP3000201

Human mRNA for KIAA0355 gene, complete cds

10 1.1e-40:305:83

Hs.153014:AB002353

R-NT2RP3000232

ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]

15 5.7e-65:386:90

Hs.4841:AI279875

R-NT2RP3000304

Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds

20 1.1e-109:541:97

Hs.23672:AF074264

R-NT2RP3000378

EST

25 2.0e-05:112:74

Hs.137268:T39311

R-NT2RP3000436

EST

30 1.2e-08:347:62

Hs.158830:AI377454

R-NT2RP3000444

ESTs

35 3.3e-70:314:99

Hs.57973:AI263207

R-NT2RP3000460

EST

40 1.9e-50:294:92

Hs.7260:T23737

R-NT2RP3000481

PROBABLE G PROTEIN-COUPLED RECEPTOR GPR6

45 1.0:183:59

Hs.46332:U18549

R-NT2RP3000616

ESTs

50 3.0e-71:309:93

Hs.41296:N71923

R-NT2RP3000645

ESTs

55 1.5e-101:550:92

Hs.21910:AA020743

R-NT2RP3000652

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ESTs

6.6e-88:411:100

Hs.43134:AA766138

- 5 R-NT2RP3000676  
Homo sapiens mRNA for KIAA0446 protein, complete cds  
1.0e-104:542:94  
Hs.158286:AB007915
- 10 R-NT2RP3000677  
ESTs  
0.33:307:59  
Hs.133022:AI374739
- 15 R-NT2RP3000721  
ESTs  
1.6e-75:390:90  
Hs.83575:N28730
- 20 R-NT2RP3000789  
ESTs  
1.5e-71:340:99  
Hs.37776:H93038
- 25 R-NT2RP3000818  
ESTs  
1.9e-52:330:88  
Hs.111052:H80504
- 30 R-NT2RP3000820  
EST  
9.1e-05:82:74  
Hs.124352:AA830406
- 35 R-NT2RP3000838  
Homo sapiens mRNA for KIAA0638 protein, partial cds  
1.5e-100:522:94  
Hs.77864:AB014538
- 40 R-NT2RP3000871  
ESTs  
3.9e-76:424:91  
Hs.121642:AA772262
- 45 R-NT2RP3000907  
ESTs, Weakly similar to PROBABLE CATION-TRANSPORTING ATPASE YEL031W [Saccharomyces cerevisiae]  
4.5e-95:493:94  
Hs.9275:AA973284
- 50 R-NT2RP3000921  
ESTs  
4.1e-52:283:94  
Hs.49714:AA442453
- 55 R-NT2RP3001012  
Homo sapiens mRNA for CMP-sialic acid transporter, complete cds  
0.60:250:61  
Hs.82921:D87969

5  
R-NT2RP3001044  
ESTs  
3.5e-106:547:95  
Hs.12305:AA166889

10  
R-NT2RP3001061  
ESTs  
1.3e-96:453:99  
Hs.4916:AI149707

15  
R-NT2RP3001159  
ESTs, Weakly similar to T13F2.1 [C.elegans]  
3.8e-47:302:90  
Hs.6281:AA523081

20  
R-NT2RP3001170  
Homo sapiens mRNA for KIAA0784 protein, partial cds  
2.8e-118:561:98  
Hs.3657:AB018327

25  
R-NT2RP3001195  
ESTs  
1.5e-40:461:72  
Hs.152438:AI334078

30  
R-NT2RP3001240  
EST  
1.9e-50:294:92  
Hs.7260:T23737

35  
R-NT2RP3001271  
ESTs  
1.1e-77:432:92  
Hs.12211:AA908631

40  
R-NT2RP3001322  
ESTs  
0.25:331:60  
Hs.44330:N32264

45  
R-NT2RP3001542  
EST  
0.0032:432:58  
Hs.148107:AA693476

50  
R-NT2RP3001560  
EST  
3.5e-50:281:93  
Hs.101727:H16171

55  
R-NT2RP3001592  
ESTs  
3.2e-65:344:93  
Hs.28964:AA715101

R-NT2RP3001685  
EST  
3.0e-37:165:81



Hs.160895:AI365871

R-NT2RP3001738

ESTs, Weakly similar to T13F2.1 [C.elegans]

5 3.8e-47:302:90

Hs.6281 :AA523081

R-NT2RP3001754

EST

10 0.00043:104:69

Hs.148331:AA911426

R-NT2RP3001858

ESTs

15 7.6e-93:502:93

Hs.153524:AA533582

R-NT2RP3001976

ESTs

20 5.0e-104:516:96

Hs.35461:AA777644

R-NT2RP3002015

25 R-NT2RP3002160

ESTs

1.4e-34:178:99

Hs.130783:AI263114

30 R-NT2RP3002281

Homo sapiens mRNA for KIAA0765 protein, partial cds

3.5e-83:446:93

Hs.62318:AB018308

35 R-NT2RP3002286

ESTs

2.1e-103:513:97

Hs.58570:AA521423

40 R-NT2RP3002311

ESTs

1.4e-108:538:96

Hs.3741:AI057614

45 R-NT2RP3002324

ESTs

3.7e-102:483:99

Hs.99668:AA829521

50 R-NT2RP3002342

ESTs, Weakly similar to transporter protein [H.sapiens]

2.0e-60:339:95

Hs.18272:N78499

55 R-NT2RP3002353

ESTs

6.8e-98:484:97

Hs.9732:AA527784

NNNNNNNNNNNNNNNN

Homo sapiens mRNA for KIAA0788 protein, partial cds

2.7e-29:214:85

Hs.2397:Z70200

5

NNNNNNNNNNNNNNNN

ESTs

3.0e-72:389:94

Hs.32246:AA464020

10

R-NT2RP3002448

ESTs, Weakly similar to Y48E1B.t [C.elegans]

1.0e-19:131:75

Hs.8715:H58021

15

R-NT2RP3002571

ESTs

1.1e-78:407:95

Hs.27356:AA740928

20

R-NT2RP3002664

ESTs

1.2e-56:341:90

Hs.23308:AA115020

25

R-NT2RP3002721

EST

2.8e-41:302:82

Hs.124936:AA825548

30

R-NT2RP3002737

EST

1.7e-51:267:97

Hs.161348:AI422470

35

R-NT2RP3002738

ESTs, Weakly similar to enhancer of filamentation 1 [H.sapiens]

1.7e-106:530:96

Hs.4894:AI191323

40

R-NT2RP3002790

R-NT2RP3002836

ESTs

4.6e-49:282:92

Hs.107979:AA146994

45

R-NT2RP3002887

ESTs

6.3e-98:516:94

Hs.11900:AA535065

50

R-NT2RP3002900

ESTs

2.0e-29:155:99

Hs.153329:AA112325

55

R-NT2RP3002958

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Homo sapiens clone 23851 mRNA sequence

6.6e-119:575:98

Hs.10065:AF035313

5 R-NT2RP3002983  
ESTs  
1.1e-61:374:90  
Hs.17834:AA128246

10 R-NT2RP3003000  
Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds  
4.1e-65:358:94  
Hs.122359:AF051946

15 R-NT2RP3003076  
ESTs  
2.6e-95:507:93  
Hs.21910:AA020743

20 R-NT2RP3003354  
ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]  
2.1e-78:385:96  
Hs.92177:AI207792

25 R-NT2RP3003448  
ESTs  
6.7e-105:521:96  
Hs.106833:AA470128

30 R-NT2RP3003469  
ESTs  
1.1e-91:461:96  
Hs.75425:AA149434

35 R-NT2RP3003473

R-NT2RP3003527  
Homo sapiens mRNA for protein kinase Dyrk1B

1.6e-92:445:97

40 Hs.130988:Y17999

R-NT2RP3003532  
ESTs

0.022:193:63

45 Hs.122593:Z99400

R-nnnnnnnnnnnnnnn  
EST

0.036:279:59

50 Hs.158745:AI375513

R-NT2RP3003559  
ESTs

9.8e-106:513:97

55 Hs.44970:AI061464

R-NT2RP3003614  
Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510

0.00016:113:69  
Hs.92660:AB007979

5 R-NT2RP3003729  
ESTs  
1.2e-43:289:86  
Hs.106401:R50967

10 R-NT2RP3003849  
ESTs  
5.4e-91:435:98  
Hs.144840:AI221746

15 R-NT2RP3003874  
ESTs  
0.21:323:59  
Hs.42919:AA805764

20 R-NT2RP3003963  
ESTs  
1.7e-90:438:97  
Hs.105894:AA564110

25 R-NT2RP3004000  
ESTs  
2.9e-101:559:91  
Hs.21910:AA020743

30 R-NT2RP3004025  
ESTs  
2.3e-108:517:98  
Hs.15356:AA911109

35 R-NT2RP3004075  
ESTs  
7.4e-84:453:93  
Hs.22412:AA523036

40 R-NT2RP3004083  
ESTs, Weakly similar to R06B9.b [C.elegans]  
4.2e-84:474:91  
Hs.30432:W28988

45 R-NT2RP3004090  
ESTs  
1.0:207:61  
Hs.92832:AA631027

50 R-NT2RP3004119  
EST  
1.8e-50:248:99  
Hs.162023:AA506128

55 R-NT2RP3004130  
ESTs  
1.1e-103:520:96  
Hs.10491:W28968

5 R-NT2RP3004133  
ESTs  
4.7e-104:545:93  
Hs.15727:H98190

10 R-NT2RP3004202  
ESTs  
1.1e-98:471:98  
Hs.61884:AI335985

15 R-NT2RP3004294  
ESTs, Weakly similar to R06B9.b [C.elegans]  
2.4e-96:500:94  
Hs.30432:W28988

20 R-NT2RP3004309  
ESTs, Weakly similar to T13F2.1 [C.elegans]  
3.5e-48:308:90  
Hs.6281:AA523081

25 R-NT2RP3004321  
ESTs  
2.6e-99:494:97  
Hs.19306:N53491

30 R-NT2RP3004345  
ESTs  
5.4e-95:444:99  
Hs.107149:AI379497

35 R-NT2RP3004355  
ESTs  
3.9e-99:490:97  
Hs.43410:N23651

40 R-NT2RP3004374  
ESTs  
1.2e-90:462:95  
Hs.75425:AA149434

45 R-NT2RP3004406  
ESTs  
1.9e-100:502:96  
Hs.24936:AA479402

50 R-NT2RP3004481  
ESTs  
1.6e-53:370:87  
Hs.11953:AA194120

55 R-NT2RP3004552  
ESTs, Weakly similar to gene SEZ-6 [M.musculus]  
7.8e-92:488:93  
Hs.6314:AA522619

R-NT2RP3004625  
Homo sapiens I-1 receptor candidate protein mRNA, complete cds  
2.6e-50:352:84

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Hs.26285:AF082516

R-NT2RP3004640

ESTs

5 1.1e-105:551:94

Hs.83348:AA527170

R-NT2RP3004647

Homo sapiens mRNA for KIAA0446 protein, complete cds

10 4.9e-111:555:96

Hs.158286:AB007915

R-NT2RP4000108

ESTs

15 2.9e-94:479:96

Hs.6625:AA115182

R-NT2RP4000634

ESTs

20 3.0e-120:572:98

Hs.28827:AI125541

R-NT2RP4000962

ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [*Saccharomyces cerevisiae*]

25 6.0e-17:98:98

Hs.4789:AI418298

R-NT2RP4001001

ESTs

30 3.1e-117:567:97

Hs.4931:AA523860

R-NT2RP4001009

Homo sapiens mRNA for Hs Ste24p, complete cds

35 1.6e-83:404:98

Hs.25846:AB016068

R-NT2RP4001467

5' nucleotidase (CD73)

40 5.9e-113:545:97

Hs.153952:X55740

R-NT2RP4001877

ESTs, Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [*Rattus norvegicus*]

45 2.2e-67:375:93

Hs.16389:AA206356

R-NT2RP4001879

50 R-NT2RP4002187

EST

0.010:117:70

Hs.160416:AI394161

55 R-NT2RP4002451

EST

1.3e-62:386:87

Hs.57082:H25761

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R-NT2RP4002715  
ESTs  
6.9e-111:552:96  
Hs.12305:AA166889

5

R-NT2RP4002750  
ESTs, Moderately similar to HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 [H.sapiens]  
7.0e-109:532:97  
Hs.86362:AA205485

10

R-OVARC1000003  
ESTs  
1.3e-74:391:95  
Hs.105039:AA477819

15

R-OVARC1000090  
Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds  
9.9e-44:471:75  
Hs.129735:AF010144

20

R-OVARC1000105  
60S RIBOSOMAL PROTEIN L38  
8.8e-14:83:100  
Hs.2017:Z26876

25

R-OVARC1000137  
ESTs  
3.0e-84:387:95  
Hs.22028:AA167715

30

R-OVARC1000208  
Human mRNA for KIAA0392 gene, partial cds  
2.8e-51:313:89  
Hs.40100:AB002390

35

R-OVARC1000255  
Spleen tyrosine kinase  
2.8e-106:510:98  
Hs.74101:L28824

40

R-OVARC1000275  
ESTs, Highly similar to PROBABLE PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE FAB [Saccharomyces cerevisiae]  
6.9e-105:556:94  
Hs.5748:AA608559

45

R-OVARC1000298  
ESTs, Weakly similar to T03G11.6 gene product [C.elegans]  
2.4e-56:338:90  
Hs.108354:W19984

50

R-OVARC1000307  
ESTs  
2.4e-101:563:93  
Hs.24479:N25972

55

R-OVARC1000313  
Homo sapiens mRNA for KIAA0573 protein, partial cds

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5.0e-98:534:93  
Hs.154023:AB011145

5 R-OVARC1000331  
Homo sapiens chromosome 9, P1 clone 11659  
1.0e-55:281:97  
Hs.3439:AC004472

10 R-OVARC1000410  
Homo sapiens clone 23767 and 23782 mRNA sequences  
3.3e-90:462:94  
Hs.8025:AF007150

15 R-OVARC1000439  
ESTs, Highly similar to HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III  
[Caenorhabditis elegans]  
1.6e-99:510:95  
Hs.7471:AI143226

20 R-OVARC1000467

R-OVARC1000529  
ESTs  
5.7e-93:461:96  
25 Hs.21396:AA114834

R-OVARC1000553  
ESTs  
4.3e-51:351:87  
30 Hs.42979:W31096

R-OVARC1000775

35 R-OVARC1000811  
ESTs  
1.3e-82:441:95  
Hs.73452:AA581386

40 R-OVARC1000853  
ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]  
3.1e-95:492:95  
Hs.6853:AA401703

45 R-OVARC1000873  
ESTs  
2.4e-46:281:91  
Hs.43857:R91358

50 R-OVARC1000916  
H.sapiens PISSLRE mRNA  
1.9e-112:588:94  
Hs.77313:X78342

55 R-OVARC1000956  
Homo sapiens mRNA for MDC3, complete cds  
0.18:259:62  
Hs.7164:AB009672



R-OVARC1000995  
EST  
6.6e-43:343:81  
Hs.149580:AI281881

5

R-OVARC1001030  
ESTs, Weakly similar to neuroendocrine-specific protein C [H.sapiens]  
1.5e-21:116:100  
Hs.65450:AA055913

10

R-OVARC1001049  
ESTs  
1.2e-70:369:95  
Hs.42949:N21131

15

R-OVARC1001086  
Homo sapiens cyclin T2a mRNA, complete cds  
1.3e-106:569:94  
Hs.155478:AF048731

20

R-OVARC1001132  
INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR  
0.16:170:64  
Hs.149894:L34600

25

R-OVARC1001163  
ESTs  
1.9e-39:219:94  
Hs.126067:AI344351

30

R-OVARC1001222  
ESTs  
0.62:177:63  
Hs.141162:H66213

35

R-OVARC1001260  
ESTs  
2.1e-79:425:94  
Hs.105039:AA477819

40

R-OVARC1001336  
ESTs  
9.2e-75:439:91  
Hs.105039:AA477819

45

R-OVARC1001338  
ESTs  
2.3e-19:139:92  
Hs.7978:W05059

50

R-OVARC1001569  
ESTs  
2.4e-83:412:97  
Hs.21396:AA114834

55

R-OVARC1001570  
ESTs  
2.6e-49:280:94

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Hs.3854:R12478

5 R-OVARC1001596  
EST  
8.2e-15:93:97  
Hs.136918:AA811543

10 R-OVARC1001607  
ESTs  
0.019:413:56  
Hs.24684:AA587245

15 R-OVARC1001725  
ESTs  
1.4e-96:504:95  
Hs.23754:N29716

20 R-OVARC1001727

20 R-OVARC1001807  
Hormone receptor (growth factor-inducible nuclear protein N10)  
8.5e-78:425:94  
Hs.1119:D49728

25 R-OVARC1001833  
ESTs  
1.0e-63:325:96  
Hs.126912:AA469087

30 R-OVARC1001991  
ESTs  
1.3e-92:467:95  
Hs.26506:AI348000

35 R-OVARC1002058  
ESTs  
2.5e-89:512:91  
Hs.58093:W63576

40 R-OVARC1002178  
ESTs  
3.3e-99:487:96  
Hs.136527:AI419398

45 R-PLACE1000033  
ESTs  
0.012:202:59  
Hs.157400:AI370528

50 R-PLACE1000231  
ESTs  
2.9e-56:285:96  
Hs.36688:AA603479

55 R-PLACE1000258  
EST  
3.4e-50:353:83  
Hs.146794:AI149478

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R-PLACE1000442

ESTs, Moderately similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]

5.5e-91:437:98

Hs.14831:AI261191

5

R-PLACE1000560

ESTs

3.7e-60:317:94

Hs.65713:AI269328

10

R-PLACE1000740

ESTs

4.2e-67:362:94

Hs.163434:T79849

15

R-PLACE1000912

ESTs

3.4e-57:329:92

Hs.121907:R66773

20

R-PLACE1000914

ESTs

2.6e-71:419:89

Hs.90809:AA010979

25

R-PLACE1000927

ESTs, Weakly similar to N-methyl-D-aspartate receptor-associated protein [D.melanogaster]

7.8e-111:545:97

Hs.8661:AI189791

30

R-PLACE1000986

ESTs

1.5e-91:431:99

Hs.42458:AA452296

35

R-PLACE1001016

ESTs

3.4e-45:231:97

Hs.121013:AA324765

40

R-PLACE1001100

Homo sapiens nephrin (NPHS1) mRNA, complete cds

3.5e-43:321:83

Hs.128834:AF035835

45

R-PLACE1001114

Human clone 23732 mRNA, partial cds

1.6e-42:305:83

Hs.81281:U79258

50

R-PLACE1001123

ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD [Saccharomyces cerevisiae]

1.2e-51:310:90

Hs.7773:AA127629

55

R-PLACE1001183

Human mRNA for KIAA0308 gene, partial cds

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0.88:182:65  
Hs.10351:AB002306

5 R-PLACE1001229  
ESTs  
5.2e-90:471:95  
Hs.18271:N92774

10 R-PLACE1001231

R-PLACE1001340  
Homo sapiens mRNA for KIAA0719 protein, complete cds  
6.6e-53:265:98  
Hs.21198:AB018262

15 R-PLACE1001401  
ESTs  
1.9e-72:362:96  
Hs.20161:AA056410

20 R-PLACE1001407  
ESTs  
2.1e-36:249:85  
Hs.23579:W38893

25 R-PLACE1001464  
5' nucleotidase (CD73)  
1.0e-91:457:96  
Hs.153952:X55740

30 R-PLACE1001500  
ESTs, Weakly similar to DNA helicase Q1 [H.sapiens]  
2.0e-19:150:87  
Hs.154199:AA155882

35 R-PLACE1001516  
EST  
1.9e-11:109:82  
Hs.137486:AA425225

40 R-PLACE1001536  
Human BRCA2 region, mRNA sequence CG016  
0.28:146:63  
Hs.112434:U50529

45 R-PLACE1001564  
ESTs  
6.3e-14:109:88  
Hs.26519:AA442703

50 R-PLACE1001655  
Homo sapiens Shab-related delayed-rectifier K<sup>+</sup> channel alpha subunit (KCNS3) mRNA, complete cds  
1.2e-118:578:97  
Hs.47584:AF043472

55 R-PLACE1001788  
ESTs  
8.4e-38:205:95

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Hs.23800:AA524095

R-PLACE1001795

ESTs, Weakly similar to HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-MRPL8 INTERGENIC REGION PRE-CURSOR [S.cerevisiae]

2.5e-77:392:96

Hs.7745:H92988

R-PLACE1001836

ESTs

1.5e-49:296:90

Hs.17691:H60366

R-PLACE1001918

ESTs, Weakly similar to multispanning membrane protein [H.sapiens]

2.0e-42:304:85

Hs.110439:N93209

R-PLACE1001949

R-PLACE1002080

Small inducible cytokine A5 (RANTES)

8.5e-41:296:82

Hs. 155464:AF088219

R-PLACE1002095

ESTs

8.5e-25:227:81

Hs.110488:AA034235

R-PLACE1002153

Homo sapiens TACC2 protein (TACC2) mRNA, partial cds

1.5e-101:514:95

Hs.90415:AF095791

R-PLACE1002329

ESTs

8.7e-48:257:94

Hs.126062:AA411593

R-PLACE1002355

ESTs

7.7e-71:362:95

Hs.120866:AI076780

R-PLACE1002374

Cathepsin L

8.4e-103:501:97

Hs.78056:X12451

R-PLACE1002518

ESTs

6.9e-97:471:97

Hs.104893:AA576941

R-PLACE1002547

Homo sapiens mRNA for KIAA0719 protein, complete cds

6.5e-55:276:97

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Hs.21198:AB018262

R-PLACE1002726

Human DNA-binding protein ABP/ZF mRNA, complete cds

3.8e-39:212:94

Hs.86185:U82613

R-PLACE1002905

Homo sapiens mRNA for KIAA0563 protein, complete cds

2.9e-41:330:81

Hs.15731:AB011135

R-PLACE1002911

R-PLACE1002967

ESTs

1.0e-43:384:77

Hs.132722:AA618531

R-PLACE1003135

ESTs

8.2e-94:462:97

Hs.23643:AI299952

R-PLACE1003163

Homo sapiens DBI-related protein mRNA, complete cds

3.5e-110:541:96

Hs.15250:AF069301

R-PLACE1003407

Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds

5.5e-49:287:91

Hs.30213:AF068227

R-PLACE1003428

ESTs, Moderately similar to BIOTINIDASE PRECURSOR [Homo sapiens]

6.8e-83:406:97

Hs.17586:AA461448

R-PLACE1003438

ESTs

2.9e-83:463:92

Hs.11067:H30385

R-PLACE1003460

ESTs

7.0e-27:187:87

Hs.18763:H56292

R-nnnnnnnnnnnnnnn

ESTs

1.7e-52:265:97

Hs.114049:AI091839

R-PLACE1003573

Human mRNA for KIAA0160 gene, partial cds

0.13:102:69

Hs.79880:D63881

5  
R-PLACE1003598  
ESTs  
8.0e-39:210:95  
Hs.26286:AA040823

10  
R-PLACE1003644  
EST  
0.47:84:73  
Hs.105856:AA551478

15  
R-PLACE1003737  
ESTs  
1.1e-77:366:100  
Hs.62699:AA707766

20  
R-PLACE1003772  
Human mRNA for KIAA0355 gene, complete cds  
6.1e-27:551:65  
Hs.153014:AB002353

25  
R-PLACE1003839  
ESTs  
0.019:244:59  
Hs.137825:AA778400

30  
R-PLACE1003845  
EST  
5.3e-79:416:93  
Hs.150153:AI300555

35  
R-PLACE1003852  
Homo sapiens mRNA for KIAA0758 protein, partial cds  
2.2e-87:439:96  
Hs.22039:AB018301

40  
R-PLACE1004028  
Sialyltransferase 4A (beta-galactosidase alpha-2,3-sialyltransferase)  
0.73:128:71  
Hs.60617:L13972

45  
R-PLACE1004078  
ESTs  
1.7e-69:353:96  
Hs.142075:AA654529

50  
R-PLACE1004166  
ESTs  
1.7e-64:362:92  
Hs.10177:AA191619

55  
R-PLACE1004199  
ESTs  
1.3e-55:279:97

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Hs.147585:AI217699

R-PLACE1004279

ESTs

5 3.7e-68:373:93

Hs.145531:H87181

R-PLACE1004282

10 R-PLACE1004305

Homo sapiens mRNA for KIAA0740 protein, complete cds

6.4e-79:377:99

Hs.15099:AB018283

15 R-PLACE1004441

ESTs

1.8e-46:244:95

Hs.107082:R63714

20 R-PLACE1004450

R-PLACE1004482

ESTs

1.2e-92:491:93

25 Hs.17840:AI269915

R-PLACE1004492

ESTs

6.1e-54:278:95

30 Hs.55862:A1341676

R-PLACE1004519

ESTs

3.1e-25:133:100

35 Hs.47378:AI193598

R-PLACE1004520

Pregnancy-specific beta-1 glycoprotein 4

2.8e-66:390:89

40 Hs.108936:X17097

R-PLACE1004630

ESTs

7.3e-58:338:92

45 Hs.155506:AI281549

R-PLACE1004637

ESTs

1.1e-37:309:82

50 Hs.20102:AA150165

R-PLACE1004648

ESTs

2.3e-67:340:96

55 Hs.69321:AA633240

R-PLACE1004816

Homo sapiens mRNA for Hakata antigen, complete cds



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1.8e-104:586:90  
Hs.9225:D88587

5 R-PLACE1004887  
ESTs, Weakly similar to GOLIATH PROTEIN [D.melanogaster]  
2.6e-30:222:86  
Hs.18557:AA203416

10 R-PLACE1005003  
ESTs  
0.99:123:68  
Hs.146244:AI276718

15 R-PLACE1005005  
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds  
6.8e-58:299:95  
Hs.151614:AF032456

20 R-PLACE1005031  
ESTs  
4.7e-57:325:92  
Hs.31196:H13265

25 R-PLACE1005239  
Homo sapiens mRNA for HIRIP3 protein, clone pH4-17  
1.4e-86:450:93  
Hs.26484:AJ223351

30 R-PLACE1005250  
ESTs, Moderately similar to maternal transcript Maid [M.musculus]  
1.7e-106:521:97  
Hs.36794:AI038407

35 R-PLACE1005383  
Homo sapiens UP50 mRNA, complete cds  
6.3e-79:471:88  
Hs.11494:AF093118

40 R-PLACE1005410  
EST  
2.3e-49:296:90  
Hs.7260:T23737

45 R-PLACE1005426  
Pregnancy-specific beta-1 glycoprotein 4  
8.0e-109:576:93  
Hs.108936:X17097

50 R-PLACE1005519  
ESTs  
5.4e-108:569:93  
Hs.23643:AI299952

55 R-PLACE1005539  
ESTs, Weakly similar to p20 protein [R.norvegicus]  
4.5e-05:107:77  
Hs.56874:W61026

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R-PLACE1005544  
 ESTs  
 4.2e-57:280:98  
 Hs.155391:AA451633  
 5

R-PLACE1005569  
 ESTs  
 2.7e-90:470:94  
 Hs.8904:AI129815  
 10

R-PLACE1005601  
 R-PLACE1005660  
 ESTs, Highly similar to HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III  
 [Caenorhabditis elegans]  
 1.4e-91:483:93  
 Hs.7471:AI143226  
 15

R-PLACE1005669  
 ESTs  
 1.7e-84:438:95  
 Hs.18271:N92774  
 20

R-PLACE1005682  
 ESTs  
 6.3e-80:482:88  
 Hs.128679:AI160081  
 25

R-PLACE1005725  
 ESTs  
 1.5e-98:519:93  
 Hs.11360:AI147467  
 30

R-PLACE1005736  
 ESTs  
 3.1e-110:561:95  
 Hs.24111:AI346026  
 35

R-PLACE1005745  
 ESTs  
 2.4e-96:473:97  
 Hs.126935:AA603217  
 40

R-PLACE1005768  
 Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2  
 4.0e-46:387:77  
 Hs.1361:M55053  
 45

R-PLACE1005815  
 Homo sapiens PYRIN (MEFV) mRNA, complete cds  
 7.1e-56:324:79  
 Hs.113283:AF018080  
 50

R-PLACE1005878  
 ESTs  
 3.1e-75:388:94  
 Hs.153483:AA569128  
 55

5 R-PLACE1005927  
ESTs  
4.3e-64:403:87  
Hs.126899:N50907

10 R-PLACE1006071  
ESTs  
5.3e-96:510:93  
Hs.24398:AI262946

15 R-PLACE1006073  
Homo sapiens mRNA for glucuronyltransferase I, complete cds  
3.0e-97:504:93  
Hs.26492:AB009598

20 R-PLACE1006079  
ESTs  
3.1e-79:453:90  
Hs.134194:AI142137

25 R-PLACE1006093  
ESTs  
1.3e-78:378:98  
Hs.129327:AI201040

R-nnnnnnnnnnnnnnn

30 R-PLACE1006219  
EST  
1.6e-75:412:92  
Hs.150153:AI300555

35 R-PLACE1006277  
ESTs  
2.8e-92:493:93  
Hs.8904:AI129815

40 R-PLACE1006290  
ESTs  
2.8e-92:433:99  
Hs.23445:AA489015

45 R-PLACE1006443  
ESTs  
2.5e-73:419:91  
Hs.90809:AA010979

50 R-PLACE1006515  
Homo sapiens mRNA for KIAA0576 protein, partial cds  
6.9e-78:413:94  
Hs.14687:AB011148

55 R-PLACE1006716  
ESTs  
4.8e-44:262:88  
Hs.8503:AI393886

R-PLACE1006786

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- ESTs  
6.3e-89:431:98  
Hs.42458:AA452296
- 5 R-PLACE1006809  
ESTs  
1.6e-68:377:92  
Hs.8956:AI146421
- 10 R-PLACE1006959  
EST  
0.00065:211:63  
Hs.136605:AA665784
- 15 R-PLACE1007028  
ESTs  
7.4e-92:475:94  
Hs.110222:AA532444
- 20 R-PLACE1007040  
ESTs  
5.1e-103:509:97  
Hs.71190:AA524036
- 25 R-PLACE1007077  
ESTs  
1.0e-98:529:93  
Hs.24398:AI262946
- 30 R-PLACE1007081  
Human growth factor independence-1 (Gfi-1) mRNA, complete cds  
0.57:238:61  
Hs.73172:U67369
- 35 R-PLACE1007096  
ESTs  
1.2e-88:466:94  
Hs.8268:N70144
- 40 R-PLACE1007296  
EST  
4.3e-53:338:86  
Hs.147274:AI206582
- 45 R-PLACE1007591  
EST  
4.6e-76:384:97  
Hs.94445:N90719
- 50 R-PLACE1007626  
Homo sapiens unknown mRNA, complete cds  
5.0e-30:179:91  
Hs.11441:AF047439
- 55 R-PLACE1007702  
ESTs  
1.0e-52:341:87  
Hs.103382:AA026923

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5 R-PLACE1007845  
 ESTs  
 2.2e-102:541:93  
 Hs.15727:H98190

10 R-PLACE1007881  
 ESTs  
 4.1e-75:398:93  
 Hs.55560:AI142804

15 R-PLACE1007971  
 ESTs  
 2.8e-43:304:85  
 Hs.82933:AA058963

20 R-PLACE1008282  
 ESTs, Highly similar to HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE [Oryc-  
 tolagus cuniculus]  
 2.2e-74:393:94  
 Hs.77613:AI367385

25 R-PLACE1008297  
 ESTs  
 6.5e-101:506:96  
 Hs.44274:AA523749

30 R-PLACE1008359  
 ESTs  
 1.8e-94:469:96  
 Hs.160551:AI281417

35 R-PLACE1008469  
 ESTs  
 7.0e-74:421:90  
 Hs.90809:AA010979

40 R-PLACE1008549  
 ESTs  
 2.0e-81:474:90  
 Hs.11713:T65960

45 R-PLACE1008657  
 ESTs  
 9.5e-89:512:89  
 Hs.142075:AA654529

50 R-PLACE1008716  
 Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds  
 5.6e-100:504:95  
 Hs.154844:U15128

55 R-PLACE1008744  
 ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]  
 2.3e-107:528:96  
 Hs.8963:AI379350

R-PLACE1008984  
 ESTs

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2.0e-76:464:89  
Hs.40094:D12041

5 R-PLACE1008985  
EST, Highly similar to SYNAPTOTAGMIN B [Discopyge ommata]  
2.2e-59:343:90  
Hs.161031:H72014

10 R-PLACE1009067  
ESTs  
7.7e-90:503:92  
Hs.55067:AA037664

15 R-PLACE1009196  
EST  
0.011:243:60  
Hs.149839:AI287601

20 R-PLACE1009279  
Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds  
5.4e-27:553:62  
Hs.75111:D87258

25 R-PLACE1009527  
Human DNA-binding protein ABP/ZF mRNA, complete cds  
2.7e-92:497:91  
Hs.86185:U82613

30 R-PLACE1009546  
ESTs  
5.9e-80:461:90  
Hs.134292:AA603031

35 R-PLACE1009600  
ESTs  
5.5e-98:509:93  
Hs.21015:AA428288

40 R-PLACE1009735  
ESTs  
1.1e-85:462:93  
Hs.48563:AA526595

45 R-nnnnnnnnnnnnn  
ESTs  
6.8e-82:499:87  
Hs.43498:AA570507

50 R-PLACE1010011  
ESTs, Moderately similar to synaptonemal complex protein [M.musculus]  
2.7e-15:171:78  
Hs.31655:AI075991

55 R-PLACE1010078  
ESTs  
1.2e-48:267:92  
Hs.12101:AA677423

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5 R-PLACE1010081  
 Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds  
 3.0e-106:560:93  
 Hs.103755:AF027706

10 R-PLACE1010251  
 ESTs  
 0.00049:248:60  
 Hs.154164:AI246893

15 R-PLACE1010445  
 ESTs  
 1.5e-90:496:92  
 Hs.163999:AA778110

20 R-PLACE1010713  
 Interleukin 1 receptor antagonist  
 4.1e-07:307:59  
 Hs.81134:U65590

25 R-PLACE1010784  
 ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]  
 1.5e-21:206:78  
 Hs.29202:R71586

30 R-PLACE1010827  
 R-PLACE 1010968  
 ESTs  
 2.6e-75:385:95  
 Hs.109884:AA766018

35 R-PLACE1011045  
 Homo sapiens E1-like protein mRNA, complete cds  
 5.3e-92:453:96  
 Hs.28190:AF094516

40 R-PLACE1011116  
 Homo sapiens embryonic lung protein (HUEL) mRNA, complete cds  
 1.5e-73:385:94  
 Hs.44053:AF006621

45 R-PLACE1011236  
 R-PLACE1011364  
 ESTs  
 2.3e-47:289:89  
 Hs.6163:W26652

50 R-PLACE1011407  
 ESTs  
 1.1e-09:191:64  
 Hs.118620:T60326

55 R-PLACE1011516  
 ESTs, Weakly similar to HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION [S.cerevisiae]  
 6.3e-75:441:88

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Hs.110978:AA843431

R-PLACE1011708

Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds

7.7e-93:521:91

Hs.148318:AF034611

R-PLACE1011824

ESTs

0.013:199:62

Hs.44343:AA532514

R-PLACE1011978

EST

4.0e-97:462:98

Hs.116391:AA644085

R-PLACE2000118

ESTs

1.2e-83:468:92

Hs.110578:AA115763

R-PLACE2000219

Homo sapiens KIAA0414 mRNA, partial cds

2.0e-44:344:81

Hs.127649:AB007874

R-PLACE3000181

Human protocadherin 42 mRNA, 3' end of cds for alternative splicing PC42-8

1.3e-82:441:94

Hs.115642:L11369

R-PLACE3000213

ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]

2.3e-114:557:97

Hs.8963:AI379350

R-PLACE4000354

ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]

3.4e-105:518:97

Hs.8963:AI379350

R-PLACE4000455

ESTs

9.0e-57:289:96

Hs.42458:AA452296

R-THYRO1000036

Collagen, type IX, alpha 3

1.3e-100:527:93

Hs.53563:L41162

R-THYRO1000061

ESTs

1.8e-87:460:94

Hs.124869:H98977

R-THYRO1000099



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## ESTs

1.2e-34:193:94  
Hs.149488:AI243816

- 5 R-THYRO1000196  
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds  
3.7e-106:530:96  
Hs.115418:AF016272
- 10 R-THYRO1000400  
Human HU-K4 mRNA, complete cds  
0.99:227:60  
Hs.74573:U60644
- 15 R-THYRO1000580  
Homo sapiens mRNA for KIAA0628 protein, complete cds  
0.21:126:67  
Hs.43133:AB014528
- 20 R-THYRO1000584  
ESTs, Weakly similar to golgi alpha-mannosidasell [H.sapiens]  
3.0e-106:529:96  
Hs.12183:AA888145
- 25 R-THYRO1000678  
EST  
2.9e-62:304:99  
Hs.48956:N64339
- 30 R-THYRO1000776  
ESTs  
1.3e-102:533:94  
Hs.4866:AA582196
- 35 R-THYRO1000795  
ESTs  
3.3e-98:529:92  
Hs.55263:AI344338
- 40 R-THYRO1000846  
ESTs  
1.6e-105:522:96  
Hs.135106:AI335251
- 45 R-THYRO1000866  
Homo sapiens SKB1Hs mRNA, complete cds  
1.3e-43:251:92  
Hs.12912:AF015913
- 50 R-THYRO1000956  
ESTs, Highly similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [Homo sapiens]  
5.2e-106:548:94  
Hs.9305:W84893
- 55 R-THYRO1000964  
  
R-THYRO1000999  
ESTs

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1.9e-18:150:84  
Hs.111583:AA463590

5 R-THYRO1001063  
ESTs  
1.5e-95:464:97  
Hs.142684:AA902402

10 R-THYRO1001071  
ESTs  
2.5e-104:496:98  
Hs.6071:AA868544

15 R-THYRO1001102  
  
R-THYRO1001113  
ESTs, Weakly similar to FER-1 [C.elegans]  
7.1e-90:446:97  
Hs.8076:AA115644

20 R-THYRO1001128  
ESTs  
1.9e-16:270:68  
Hs.140194:N35720

25 R-THYRO1001205  
Small inducible cytokine A5 (RANTES)  
1.9e-58:400:84  
Hs.155464:AF088219

30 R-THYRO1001237  
ESTs  
1.5e-104:532:96  
Hs.6603:AA772122

35 R-THYRO1001242  
EST  
1.7e-50:281:93  
Hs.101727:H16171

40 R-THYRO1001266  
Homo sapiens mRNA for KIAA0650 protein, partial cds  
0.00037:403:60  
Hs.8118:AB014550

45 R-THYRO1001327  
ESTs  
1.2e-96:530:93  
Hs.28786:AA034412

50 R-THYRO1001456  
ESTs, Weakly similar to Similar to phytoene desaturase [C.elegans]  
3.3e-43:257:92  
Hs.97031:AA773647

55 R-THYRO1001457  
ESTs, Highly similar to MYOSIN LIGHT CHAIN KINASE [Dictyostelium discoideum]  
4.8e-59:284:99

Hs.9915:AI300083

R-THYRO1001471

ESTs

5 1.1e-67:378:93  
Hs.52113:R40587

R-THYRO1001478

10 R-THYRO1001495

H.sapiens mRNA for Zinc-finger protein (ZNFpT17)

1.6e-63:434:84

Hs.32954:X65233

15 R-THYRO1001523

ESTs

5.8e-75:388:96

Hs.6527:R21517

20 R-THYRO1001529

ESTs

1.1e-25:184:87

Hs.18441:AA005104

25 R-THYRO1001593

ESTs

4.7e-34:182:98

Hs.8312:AA813022

30 R-THYRO1001608

ESTs

2.8e-107:547:95

Hs.23765:AA524283

35 R-THYRO1001641

Homo sapiens clone 24448 unknown mRNA, partial cds

1.1e-111:562:96

Hs.4973:AF070638

40 R-THYRO1001700

ESTs

1.3e-78:407:95

Hs.86987:N99896

45 R-THYRO1001702

ESTs

4.3e-98:566:92

Hs.119447:AA524436

50 R-THYRO1001725

ESTs

1.3e-84:424:96

Hs.38039:AI360128

55 R-THYRO1001770

ESTs

1.0e-62:325:97

Hs.20137:R08273

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5 R-THYRO1001803  
 ESTs  
 6.8e-90:456:96  
 Hs.134438:R42585

10 R-Y79AA1000030  
 ESTs, Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]  
 2.4e-98:515:94  
 Hs.32822:AI194045

15 R-Y79AA1000127  
 ESTs, Weakly similar to ! ! ! ALU SUBFAMILY J WARNING ENTRY ! ! ! [H.sapiens]  
 1.1e-57:307:95  
 Hs.83513:W05849

20 R-Y79AA1000207  
 EST  
 1.0e-97:411:96  
 Hs.141431:N21286

25 R-Y79AA1000226  
 ESTs, Highly similar to HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV [Caenorhabditis  
 elegans]  
 7.2e-102:545:94  
 Hs.11221:AI192291

30 R-Y79AA1000270  
 Human mRNA for ORF, Xq terminal portion  
 3.3e-107:564:93  
 Hs.6551:D16469

35 R-Y79AA1000426  
 H.sapiens mRNA for activin beta-C chain  
 2.5e-10:217:66  
 Hs.83267:X82540

40 R-Y79AA1000521  
 Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds  
 0.73:257:59  
 Hs.113286:U77783

45 R-Y79AA1000750  
 ESTs  
 4.3e-75:391:95  
 Hs.157192:W84862

50 R-Y79AA1000776  
 ESTs  
 3.5e-56:303:95  
 Hs.118559:AA887084

55 R-Y79AA1000777  
 ESTs, Weakly similar to LIS-1 protein [H.sapiens]  
 9.5e-98:515:95  
 Hs.59461:W93217

R-Y79AA1000876  
 EST

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2.7e-23:173:84  
Hs.135872:AI037885

5 R-Y79AA1000959  
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds  
3.4e-80:453:92  
Hs.53066:AF093420

10 R-Y79AA1000967  
ESTs  
7.3e-86:461:93  
Hs.6262:T89093

15 R-Y79AA1001013  
ESTs  
1.4e-115:566:97  
Hs.108408:N31922

20 R-Y79AA1001056  
ESTs, Moderately similar to maternal transcript Maid [M.musculus]  
8.7e-111:557:95  
Hs.36794:AI038407

25 R-Y79AA1001062  
ESTs  
0.0021:365:59  
Hs.106129:AA292171

30 R-Y79AA1001090  
ESTs  
5.0e-52:255:99  
Hs.106214:AI123831

35 R-Y79AA1001212  
Homo sapiens SL15 protein mRNA, complete cds  
1.8e-83:407:97  
Hs.6710:AF038961

40 R-Y79AA1001264  
ESTs, Highly similar to DNAJ PROTEIN HOMOLOG 2 [Homo sapiens]  
2.8e-111:552:96  
Hs.62489:AI057091

45 R-Y79AA1001272  
Zinc finger protein, X-linked  
0.019:317:59  
Hs.2074:X59739

50 R-Y79AA1001328  
ESTs  
3.6e-67:385:92  
Hs.127792:AI421472

55 R-Y79AA1001426  
ESTs  
2.0e-13:92:93  
Hs.105607:AA478379

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R-Y79AA1001430  
 Homo sapiens mRNA for KIAA0469 protein, complete cds  
 2.0e-112:555:96  
 Hs.7764:AB007938  
 5

R-Y79AA1001523  
 EST  
 1.7e-07:120:73  
 Hs.130984:AI015430  
 10

R-Y79AA1001530  
 Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds  
 0.030:169:63  
 Hs.155489:AF037448  
 15

R-Y79AA1001592  
 ESTs  
 5.0e-60:340:91  
 Hs.87019:AA760977  
 20

R-Y79AA1001727  
 ESTs  
 6.1e-101:547:93  
 Hs.7404:W29012  
 25

R-Y79AA1001787  
 ESTs  
 8.8e-84:449:95  
 Hs.128866:AA977749  
 30

R-Y79AA1001795  
 Homo sapiens mRNA for GalT4 protein  
 9.9e-110:541:97  
 Hs.21495:AL031228  
 35

R-Y79AA1001799  
 ESTs, Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN MSR4 [Saccharomyces cerevisiae]  
 1.6e-94:567:90  
 Hs.34401:AA447775  
 40

R-Y79AA1001803  
 ESTs, Highly similar to SECRETOTRANIN III PRECURSOR [Mus musculus]  
 1.2e-86:509:90  
 Hs.22215:AI371482  
 45

R-Y79AA1001863  
 ESTs  
 1.4e-23:268:73  
 Hs.131613:AI190576  
 50

R-Y79AA1002022  
 ESTs  
 8.9e-97:462:98  
 Hs.6140:D52151  
 55

R-nnnnnnnnnnnnn  
 R-nnnnnnnnnnnnn

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Homo sapiens DNA recombination and repair protein (MRE11B) mRNA, complete cds  
0.00075:456:59  
Hs.153855:AF022778

- 5 R-Y79AA1002213  
Human mRNA for KIAA0392 gene, partial cds  
6.2e-45:304:85  
Hs.40100:AB002390
- 10 R-Y79AA1002334  
ESTs  
7.7e-91:495:92  
Hs.90804:W28091
- 15 R-Y79AA1002373  
Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end  
5.2e-98:545:91  
Hs.103948:K00627
- 20 R-Y79AA1002376  
ESTs  
2.0e-91:455:97  
Hs.153375:AI287812
- 25 R-Y79AA1002378  
ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-35 [Mus musculus]  
9.4e-15:131:83  
Hs.20082:W89121
- 30 R-Y79AA1002381  
ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1/thailand)]  
1.5e-104:531:95  
Hs.26322:AA156858
- 35

Homology search result 10

[0305] Data obtained by the homology search for full length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in matching data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of matching data. These items are shown in this order, separated by a double-slash mark, //.

- 45 C-HEMBA1000006//Homo sapiens mRNA; cDNA DKFZp564G1762 (from clone DKFZp564G1762)//0//1230bp//92%//AB026894  
C-oooooooooooo//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//2.30E-71//344aa//50%//P50636  
C-HEMBA1000121//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//4.80E-05//83aa//27%//P34679  
C-HEMBA1000128//PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).//3.20E-07//89aa//34%//P33154
- 50 C-HEMBA1000275  
C-HEMBA1000300  
C-HEMBA1000349//ATP-BINDING CASSETTE TRANSPORTER 1.//5.30E-65//352aa//39%//P41233  
C-HEMBA1000443//Homo sapiens CGI-96 protein mRNA, complete cds.//4.70E-129//686bp//91%//AF151854
- 55 C-HEMBA1000590//Homo sapiens mRNA for matrilin-4, partial.//2.00E-273//1254bp//99%//AJ007581  
C-HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.//0//994bp//99%//AF116272  
C-HEMBA1000713//Homo sapiens 10kD protein (BC10) mRNA, complete cds.//0//1254bp//99%//AF053470

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C-HEMBA1000745//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//2.00E-07//445aa//27%//P02454  
 C-HEMBA1000907  
 C-HEMBA1000940//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//2.90E-39//362aa//31%//  
 P41987  
 5 C-HEMBA1000962  
 C-HEMBA1001221//AGRIN PRECURSOR.//2.50E-25//294aa//29%//P31696  
 C-HEMBA1001228//Human germline oligomeric matrix protein (COMP) mRNA, complete cds.//7.80E-286//  
 1105bp//94%//L32137  
 C-HEMBA1001297  
 10 C-HEMBA1001390//Mus musculus polymerase I-transcript release factor mRNA, complete cds.//2.50E-57//  
 464bp//82%//AF036249  
 C-HEMBA1001563  
 C-HEMBA1001621//PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.//3.50E-123//259aa//89%//P35414  
 C-nnnnnnnnnnnn//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.40E-85//293aa//50%//  
 15 P51523  
 C-HEMBA1001878//Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.//0//1488bp//99%//  
 AF090988  
 C-HEMBA1002131//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1//4.10E-10//140aa//  
 30%//P24802  
 20 C-HEMBA1002163//HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION.//9.40E-28//  
 309aa//30%//Q04651  
 C-HEMBA1002164  
 C-HEMBA1002167//Rattus norvegicus neuroligin I mRNA, complete cds.//1.30E-305//1643bp//91%//U22952  
 C-HEMBA1002178//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC  
 25 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1).//3.70E-10//140aa//30%//P24802  
 C-nnnnnnnnnnnn//Human glycyl-tRNA synthetase mRNA, complete cds.//0//2380bp//99%//U09587  
 C-HEMBA1002195//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.80E-23//221aa//31%//Q00808  
 C-HEMBA1002227//Homo sapiens mRNA for 80K-L protein, complete cds.//0//1324bp//98%//D10522  
 C-HEMBA1002239  
 30 C-HEMBA1002316  
 C-HEMBA1002420  
 C-HEMBA1002421//Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.//0//2097bp//99%//J04621  
 C-HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds.//0//1763bp//95%//  
 U63336  
 35 C-HEMBA1002551//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//9.80E-08//110aa//  
 37%//P49695  
 C-HEMBA1002767//Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.//  
 0//1497bp//99%//AF038660  
 C-HEMBA1002992//UBIQUITIN-LIKE PROTEIN DSK2.//2.00E-21//216aa//35%//P48510  
 40 C-HEMBA1003047//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1768bp//  
 99%//AF034611  
 C-HEMBA1003072//Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.//3.30E-93//927bp//  
 73%//U68380  
 C-HEMBA1003101//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1854bp//99%//  
 45 AF049891  
 C-HEMBA1003230//Homo sapiens fibulin-5.//5.60E-308//1398bp//99%//AJ133490  
 C-HEMBA1003294  
 C-HEMBA1003315//Mus musculus mRNA for DNA helicase, complete cds.//6.30E-250//1426bp//88%//AB013912  
 C-HEMBA1003392//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//1721bp//  
 50 100%//AF074264  
 C-HEMBA1003399//MVP1 PROTEIN.//2.30E-15//279aa//23%//P40959  
 C-HEMBA1003487  
 C-HEMBA1003530//S.scrofa mRNA for BM88 antigen.//1.20E-60//900bp//66%//X82027  
 C-HEMBA1003602//Homo sapiens CGI-67 protein mRNA, complete cds.//3.50E-70//732bp//66%//AF151825  
 55 C-HEMBA1003732//SFT2 PROTEIN.//1.50E-06//162aa//30%//P38166  
 C-HEMBA1003945//Homo sapiens hypothetical 43.2 Kd protein mRNA, complete cds.//8.90E-287//757bp//97%//  
 AF077030  
 C-HEMBA1004110//Homo sapiens intersectin short form mRNA, complete cds.//0//2033bp//99%//AF064243



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C-HEMBA1004250//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//6.40E-51//  
277aa//35%/P33450  
C-HEMBA1004391//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.//5.60E-20//194aa//26%/P70211  
C-HEMBA1004444//GLYCOPROTEIN 25L PRECURSOR (GP25L).//4.60E-41//148aa//52%/P27869  
5 C-HEMBA1004454  
C-HEMBA1004505//MANNOsyl-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC  
3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE).//2.70E-45//239aa//43%/P53624  
C-HEMBA1004797  
10 C-HEMBA1004982//TETRACYCLINE RESISTANCE PROTEIN, CLASS E (TETA(E)).//6.30E-10//149aa//26%/  
Q07282  
C-HEMBA1005070//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.10E-05//187aa//  
29%/P17437  
C-HEMBA1005084//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-  
TEIN KINASE 1).//1.20E-07//102aa//37%/P18160  
15 C-HEMBA1005145  
C-HEMBA1005430  
C-HEMBA1005449//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-  
DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//5.40E-10//224aa//24%/P13983  
C-HEMBA1005489  
20 C-HEMBA1005522//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//7.70E-15//78aa//51%/P98139  
C-HEMBA1005545//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0//2121aa//100%/U29589  
C-HEMBA1005698//Homo sapiens vesicle trafficking protein (SEC22C) mRNA, complete cds.//6.60E-163//  
753bp//99%/AF039568  
C-HEMBA1005913  
25 C-HEMBA1005929//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.50E-92//1092bp//69%/X97630  
C-HEMBA1005945//Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete Gds.//  
1.90E-44//666bp//65%/AF004161  
C-HEMBA1006016  
C-HEMBA1006171  
30 C-HEMBA1006299  
C-HEMBA1006311  
C-HEMBA1006335  
C-HEMBA1006430//Human putative transmembrane protein precursor (B5) mRNA, complete cds.//2.40E-70//  
1108bp//65%/L38961  
35 C-HEMBA1006482//Homo sapiens h-scol (SCOI) mRNA, nuclear gene encoding mitochondrial protein, complete  
cds.//0//1101bp//98%/AF026852  
C-HEMBA1006572//ODD-SKIPPED PROTEIN.//2.60E-39//85aa//83%/P23803  
C-HEMBA1006707//Homo sapiens mRNA for matrilin-4, partial.//0//2003bp//99%/AJ007581  
C-HEMBA1006724  
40 C-HEMBA1006902//Homo sapiens mRNA for matrilin-4, partial.//4.80E-275//1799bp//85%/AJ007581  
C-HEMBA1006916//Homo sapiens Grb14 mRNA, complete cds.//3.00E-277//1010bp//95%/L76687  
C-HEMBA1006960  
C-HEMBA1007013  
C-HEMBA1007057  
45 C-HEMBA1007241  
C-HEMBA1007291  
C-HEMBA1007332  
C-HEMBB1000276  
C-HEMBB1000447//Homo sapiens JWA protein mRNA, complete cds.//0//2059bp//99%/AF070523  
50 C-HEMBB1000642  
C-HEMBB1000668//Homo sapiens mRNA for KIAA0893 protein, complete cds.//0//2375bp//99%/AB020700  
C-HEMBB1000679//C.familiaris mRNA for TRAM-protein.//4.10E-210//1149bp//80%/X63678  
C-HEMBB1000881//Danio rerio mRNA for MINDIN2, complete cds.//1.70E-67//948bp//66%/AB006085  
C-HEMBB1000905//TRANSCRIPTIONAL REPRESSOR RCO-1.//1.00E-11//311aa//27%/P78706  
55 C-HEMBB1001026//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-  
ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-  
NENT).//5.30E-11//142aa//30%/P32802  
C-HEMBB1001048//Human Hpast (HPAST) mRNA, complete cds.//6.50E-39//448bp//75%/AC000159

C-HEMBB1001200  
 C-HEMBB1001407  
 C-HEMBB1001530//SLS1 PROTEIN PRECURSOR.//9.80E-10//273aa//27%//Q99158  
 C-HEMBB1001573  
 5 C-nnnnnnnnnnnn//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds.//1.50E-251//  
 1146bp//99%//AF118670  
 C-HEMBB1001847//NEUROGENIC PROTEIN BIG BRAIN.//4.70E-06//258aa//24%//P23645  
 C-HEMBB1001978  
 C-HEMBB1002162//Homo sapiens genethonin 1 mRNA, complete cds.//8.30E-67//328bp//99%//AP062354  
 10 C-HEMBB1002228  
 C-HEMBB1002245//PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR  
 (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN).//0//879aa//89%//Q62786  
 C-HEMBB 1002427//FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYL GALACTOSAMINYLTRANSFERASE (EC  
 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-AL-  
 15 PHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANS-  
 FERASE) (NAGAT).//1.80E-70//221aa//50%//P16442  
 C-HEMBB1002465//ACYL-COA DEHYDROGENASE (EC 1.3.99.-).//2.30E-53//249aa//48%//P45857  
 C-HEMBB1002663  
 C-HEMBB1002693  
 20 C-MAMMA1000046  
 C-MAMMA1000118  
 C-nnnnnnnnnnnn//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.50E-312//1594bp//93%//  
 AF067420  
 C-MAMMA1000449  
 25 C-MAMMA1000457//Human NADH-cytochrome b5 reductase mRNA, 3' end.//9.50E-79//829bp//71%//M16462  
 C-MAMMA1000591//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-  
 UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOS-  
 AMINYLTRANSFERASE) (GALNAC-T1).//1.20E-115//515aa//49%//Q07537  
 C-MAMMA1000681//PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.//9.40E-82//311aa//52%//O08530  
 30 C-MAMMA1001043//MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN)(BLAST-1)  
 (CD48).//2.90E-12//239aa//28%//P10252  
 C-MAMMA1001893  
 C-NT2RM2000241  
 C-NT2RM2000306//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//4.50E-130//362aa//68%//P91917  
 35 C-NT2RM2000410  
 C-NT2RM2000423//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.80E-38//308aa//35%//  
 P48982  
 C-NT2RM2000497//CHL1 PROTEIN.//9.90E-24//296aa//29%//P22516  
 C-NT2RM2000514//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0//2381bp//99%//AB020682  
 40 C-NT2RM2000622  
 C-NT2RM2001126//Homo sapiens mRNA for multi PDZ domain protein.//0//1600bp//99%//AJ0001319  
 C-NT2RM2001902//Homo sapiens mRNA for PAK4 protein.//5.40E-216//988bp//99%//AJ011855  
 C-NT2RM2001939//Human G protein-coupled receptor GPR-NGA gene, complete cds.//0//1559bp//98%//U55312  
 C-NT2RM2001941//MUSCARINIC ACETYLCHOLINE RECEPTOR M1.//7.40E-38//193aa//34%//P08482  
 45 C-NT2RM4000198  
 C-NT2RM4000284//Human IgG Fc receptor hFcRn mRNA, complete cds.//1.30E-257//603bp//96%//U12255  
 C-NT2RM4000295  
 C-NT2RM4000326//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//9.00E-100//434aa//43%//  
 P51523  
 50 C-NT2RM4000444//ANTIGEN PEPTIDE TRANSPORTER 1 (APT1).//1.70E-112//493aa//44%//P36370  
 C-NT2RM4000587  
 C-NT2RM4000648//K-GLYPICAN PRECURSOR.//4.00E-193//531aa//66%//P51655  
 C-NT2RM4000997//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//1.80E-10//  
 189aa//30%//P25234  
 55 C-NT2RM4001321  
 C-NT2RM4001325//CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST).//2.90E-48//343aa//34%//  
 Q92179  
 C-NT2RM4001735

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C-NT2RM4002352//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.//0//2184bp//99%//AB009462  
C-NT2RP1000002  
C-NT2RP1000050  
5 C-NT2RP1000181//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//3.30E-121//1394bp//69%//AF126799  
C-NT2RP1000261//ORM1 PROTEIN.//2.40E-17//137aa//35%//P53224  
C-NT2RP1000300//Human transporter protein (g17) mRNA, complete cds.//3.80E-26//758bp//62%//U49082  
C-NT2RP1000325//H.sapiens gene for phosphate carner.//0//439bp//98%//X77337  
10 C-NT2RP1000448  
C-NT2RP1000551//Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds.//0//1761bp//99%//U09585  
C-NT2RP1000579//Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds.//0//1951bp//94%//L21936  
15 C-NT2RP1000613//CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).//3.40E-52//304aa//40%//P08060  
C-NT2RP1000903  
C-NT2RP1000981//CELL SURFACE A33 ANTIGEN PRECURSOR.//3.60E-14//286aa//27%//Q99795  
C-NT2RP1001004//F-SPONDIN PRECURSOR.//9.20E-43//322aa//35%//P35446  
20 C-NT2RP1001020//SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTIVATED KINASE 3) (CDC42/RAC EFFECTOR KINASE PAK-B).//9.70E-22//227aa//31%//Q61036  
C-NT2RP1001563//TESTIS-SPECIFIC PROTEIN TPX-1 PRECURSOR (AUTOANTIGEN 1) (25 KD ACROSOM-AL AUTOANTIGEN) (AA1).//9.70E-19//201aa//31%//Q60477  
C-NT2RP2000394//Gallus gallus p52 pro-apototic protein mRNA, complete cds.//1.60E-90//956bp//70%//AF029071  
25 C-NT2RP2000479  
C-NT2RP2000514//Homo sapiens roundabout 2 (robo2) mRNA, partial cds.//3.00E-185//855bp//99%//AF040991  
C-NT2RP2000533//Homo sapiens cornichon protein mRNA, complete cds.//1.30E-290//1324bp//99%//AF070654  
C-NT2RP2000649//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2847bp//99%//AB016068  
30 C-NT2RP2000663  
C-NT2RP2000694//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2278bp//99%//AJ012159  
C-NT2RP2000903//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2276bp//100%//AJ012159  
C-NT2RP2001480//Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.//0//2547bp//99%//L38969  
C-NT2RP2001495//Human transporter protein (g17) mRNA, complete cds.//2.20E-65//641bp//65%//U49082  
35 C-NT2RP2001514//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//1.20E-133//429aa//41%//P39986  
C-NT2RP2001529//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2079bp//99%//AB007144  
C-NT2RP2001769//SERINE/THREONINE-PROTEIN KINASE ORB6 (EC 2.7.1.-).//9.10E-47//185aa//44%//O13310  
40 C-NT2RP2001878  
C-NT2RP2001903//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//3.80E-58//475aa//34%//P00789  
C-NT2RP2001915  
C-NT2RP2001956//ORM1 PROTEIN.//3.90E-19//137aa//37%//P53224  
45 C-NT2RP2002063//GNS1 PROTEIN.//3.60E-18//231aa//33%//P25358  
C-NT2RP2002188//Rattus norvegicus neuroligin 3 mRNA, complete cds.//2.50E-226//1284bp//89%//U41663  
C-NT2RP2002232//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//1.90E-93//420aa//43%//Q09782  
C-NT2RP2002304//Human mRNA for KIAA0383 gene, partial cds.//0//1640bp//99%//AB002381  
50 C-NT2RP2002409  
C-NT2RP2002510  
C-NT2RP2002527//CYTOCHROME B5.//1.30E-11//92aa//38%//P40312  
C-NT2RP2002533//Homo sapiens alpha 2 delta calcium channel subunit isoform I mRNA, complete cds.//0//2365bp//99%//AF042792  
55 C-NT2RP2002564//Human zinc-finger protein C2H2-150 mRNA, complete cds.//0//2237bp//99%//U38864  
C-NT2RP2002674//SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CYTOSOLIC EPOXIDE HYDROLASE) (CEH).//5.50E-38//201aa//39%//P34913  
C-NT2RP2002721//REGULATORY PROTEIN UHPC.//1.60E-23//153aa//30%//P27669

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C-NT2RP2002824//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-  
ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-  
NENT) //3.50E-63//404aa//33%///P32802

C-NT2RP2002942//Homo sapiens mRNA for KIAA0806 protein, complete cds.//0//2090bp//99%//AB018349

C-NT2RP2002974//HOMEOBOX PROTEIN SIX5 (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HOMOLOG) (FRAGMENT)//8.20E-241//555aa//84%//P70178

C-NT2BP2002976

G-NT2RP2003042//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)  
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE)  
(FRAGMENT).//2.10E-109//385aa//52%/P53760

C-NT2RP2003179//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-)//2.60E-67//256aa//49%//Q05512

C-NT2RP2003210//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//9.80E-272//1265bp//98%//AF055899

C-NT2RP2003369//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//5.90E-20//204aa//34%//Q15404

C-NT2RP2003383//Homo sapiens mRNA for KIAA0458 protein, complete cds.//0//2565bp//99%//AB007927

C-NT2RP2003469//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).//1.10E-45//324aa//29%//P37021

C-NT2RP2003545//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//5.40E-48//578bp//71%//AF024636

C-NT2RP2003593

C-NT2RP2003599

C-NT2RP2003655//HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC//4.80E-15//93aa//47%//P38869

C-NT2RP2003931

C-NT2BP2004141

C-NT2RP2004179

C-NT2RP2004205//BUTYROPHILIN PRECURSOR (BT)//1.60E-21//276aa//32%/Q62556

C-NT2RP2004447

C-NT2RP2004495//Human transporter protein (g17) mRNA, complete cds.//9.80E-64//642bp//64%//U49082

C-NT2RP2004524

C-NT2RP2004556

C-NT2RP2004606//Human fibroblast collagenase inhibitor mRNA, complete cds.//2.10E-166//768bp//99%//M12670

C-NT2RP2004648//Mouse beta-galactosidase (BGAL) gene, complete cds.//1.20E-33//1136bp//59%//M57734

C-NT2RP2004670//Rattus norvegicus vesicle-associate calmodulin-binding protein mRNA, complete cds./0//1250bp//86%/L22557

C-NT2RP2004794//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.//2.70E-09//203aa//26%/P40857

C-NT2RP2004837

C-NT2RP2004847//ZINC FINGER PROTEIN 135.//8.00E-35//193aa//40%//P52742

-nnnnnnnnnnnn//Homo sapiens SCG10-like-protein (SCLIP) mRNA, complete cds.//2.90E-170//813bp//98%//AF069709

C-NT2RP2005027

C-NT2RP2005163

C-NT2RP2005181//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//5.30E-315//  
126bp//81%//U70859

C-NT2RP2005247//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN)//5.00E-53//296aa//37%//Q62158

-N12RP2005425//Homo sapiens mRNA for AKAP450 protein.//0//4341bp//99%//AJ131693

C-NT2RP2005463//PROTEIN PTM1 PRECURSOR.//7.40E-15//284aa//28%//P32857

C-NT2RP2005514

-NT2RP2005541//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//4.70E-24//78aa//51%/P15586

C-NT2RP2005632

-NT2RP2005878//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-)//3.60E-55//238aa//50%/57314

DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-

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HYDROXYLASE) (DBH).//6.70E-72//512aa//34%//P15101

C-NT2RP2005887

C-NT2RP2005941//Human paired box gene (PAX6) homologue, complete cds.//1.40E-308//1396bp//99%//  
M93650

5 C-NT2RP2005994//HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.//3.50E-35//144aa//47%//P49191

C-NT2RP2006042//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) //9.40E-15//501aa//25%//P08640

10 C-NT2RP2006269//DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 2 (E,C  
2.4.1.109)//2.30E-78//679aa//32%//P31382

C-NT2RP2006512//GNS 1 PROTEIN.//2.00E-21//290aa//29%//P25358

C-NT2RP3000059//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//  
3.70E-12//133aa//32%/Q01485

15 C-NT2RP3000063//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//  
5.00E-29//596aa//30%//P19246

C-NT2RP3000125//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2)//6.30E-08//70aa//41%//P29375

C-NT2BP3000169//Homo sapiens MRS1 mRNA, complete cds.//0//1519bp//97%//AF093239

C-NT2RP3000172//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) //1 30E-80//359aa//44%//Q14012

20 C-NT2RP3000201//Homo sapiens mRNA for KIAA0687 protein, partial cds.//2.00E-305//1224bp//99%//AB014587  
G-NT2RP3000436//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1)//6.20E-27//

C-NT2BP3000460//Canis familiaris sec61 homologue mRNA, complete cds//1.80E-198//643bp//89%//M96629

25 C-NT2RP3000616//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//5.20E-26//  
227aa//36%//Q06828

C-NT2RP3000721//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.//1.10E-22//171aa//36%//P38800

C-NT2RP3000820//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//1.90E-30//269aa//33%//P49695

30 C-NT2RP3000871  
C-NT2RP3000907//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38)//2.20E-134//296aa//

C:NT2BP3001012//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//2906bp//98%//AB020636

C-NT2RP3001061//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0/3591bp/99%/AB020660

C-NT2RP355163//Homo sapiens mRNA; cDNA DKFZp586K2120 (from clone DKFZp586K2120).//0//2421bp//99%//AL080163

C-NT2RP3001195//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER)//4.70E-48//339aa//29%//P37021

40 C-NT2RP3001240//Canis familiaris sec61 homologue mRNA, complete cds./1.20E-301//1141bp//89%/M96629  
C-NT2RP3001322//PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETIC-

CLUM CA2+-ATPASE)/1.1.70E-21//220aa//30%/P39524  
 C-NT2BP3001388//SYNAPTOTAGMIN IV//2.00E-118//430aa//54%/P50232

C-ooooooooooooo//Human mRNA for KIAA0315 gene, partial cds //0//2971bp//99%//AB002313

C-ntntnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0017 protein, complete cds. //0//3243bp//99%//D87686

C-NT2BP3001522//N2 N2-DIMETHYL GUANOSINE TRNA METHYL TRANSFERASE PRECURSOR (EC

C. NT2B23001738//CYTOCHROME P450 11 305.11//133aa//33%/P00169

C-NT2RP3001754

C-NT2RP3002160//Canis familiaris forssman synthetase mRNA, complete cds.//5.00E-152/789bp//84%/U66140

55 43%//P48982  
C-NT2RP3002312//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) [LACTASE].//9.80E-103//347 aa

C-NT2RP3002342//Human transporter protein (glt1) mRNA, complete cds.//1,702-637/641bp//83%//C49662

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C-NT2RP3002738//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds.//2.20E-47//763bp//65%//L43821  
 C-NT2RP3002790  
 C-NT2RP3002836//Homo sapiens mRNA for KIAA0463 protein, partial cds.//0//1617bp//99%//AB007932  
 5 C-NT2RP3002958//TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.//8.00E-08//197aa//26%//P19814  
 C-NT2RP3003000//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds.//0//3160bp//96%//AF051946  
 C-NT2RP3003076  
 10 C-NT2RP3003354//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.//5.10E-55//208aa//51%//O35609  
 C-NT2RP3003469  
 C-NT2RP3003527//Homo sapiens mRNA for protein kinase Dyrk1B.//0//2483bp//99%//Y17999  
 C-NT2RP3003535//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE  
 15 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//8.80E-18//368aa//25%//P56558  
 C-NT2RP3003559  
 C-NT2RP3003614  
 C-NT2RP3003729  
 C-NT2RP3003849//PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)). PKC1.//1.20E-13//126aa//34%//P05130  
 20 C-NT2RP3003874//Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c.//0//2160bp//98%//AJ001381  
 C-NT2RP3003963  
 C-NT2RP3004000  
 25 C-NT2RP3004075  
 C-NT2RP3004083  
 C-NT2RP3004090//GOLIATH PROTEIN (G1 PROTEIN).//9.00E-33//179aa//47%//Q06003  
 C-NT2RP3004130//CELL SURFACE ANTIGEN 114/A10 PRECURSOR.//8.10E-06//71aa//42%//P19467  
 C-NT2RP3004133//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.50E-48//198aa//37%//P43636  
 30 C-NT2RP3004202  
 C-NT2RP3004309//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2584bp//99%//AL050118  
 C-NT2RP3004321  
 C-NT2RP3004355  
 35 C-NT2RP3004374  
 C-NT2RP3004406//HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.//3.20E-15//165aa//33%//P40544  
 C-NT2RP3004552//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTI-GEN).//8.50E-24//263aa//33%//P17927  
 40 C-NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds.//0//2181bp//96%//U11292  
 C-NT2RP3004625//Homo sapiens mRNA for KIAA0975 protein, partial cds.//0//1339bp//99%//AB023192  
 C-NT2RP3004640//Bos taurus tuftelin mRNA, complete cds.//0//1204bp//88%//AF105228  
 C-NT2RP3004647//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.00E-15//220aa//27%//Q03829  
 C-NT2RP4000108//Human gene for neurofilament subunit NF-L.//0//1998bp//99%//AF176680  
 45 C-NT2RP4000962//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//2.60E-18//225aa//32%//P08458  
 C-NT2RP4001009//Homo sapiens mRNA for farnesylated-proteins converting enzyme 1.//0//2965bp//99%//Y13834  
 C-NT2RP4001467//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2140bp//99%//X55740  
 C-OVARC1000090  
 50 C-OVARC1000105//UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//4.20E-47//171aa//56%//P33296  
 C-OVARC1000137  
 C-OVARC1000208  
 C-OVARC1000255//H.sapiens syk mRNA for protein-tyrosine kinase.//0//1525bp//97%//Z29630  
 55 C-OVARC1000275//DESMOPLAKIN I AND II (DPI AND DPII) (FRAGMENT).//9.90E-16//352aa//23%//P15924  
 C-OVARC1000298  
 C-OVARC1000410//Homo sapiens angiopoietin Y1 mRNA, complete cds.//2.10E-63//744bp//69%//AF107253  
 C-OVARC1000439//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.40E-

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33//143aa//53%/P34280  
C-OVARC1000467  
C-OVARC1000529//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-)//1.40E-23//  
165aa//39%/P34244  
5 C-OVARC1000775  
C-nnnnnnnnnnnn//ZINC FINGER PROTEIN 157//1.00E-35//130aa//46%/P51786  
C-OVARC1000811//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT)//6.40E-13//115aa//34%/Q01177  
C-OVARC1000853  
C-OVARC1000916//H.sapiens PISSLRE mRNA//7.30E-280//1117bp//95%/X78342  
10 C-OVARC1000956//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//2.20E-09//250aa//  
28%/P17437  
C-OVARC1001030//Homo Sapiens mRNA for KIAA0886 protein, complete cds//0//907bp//99%/AB020693  
C-OVARC1001049//TRANSCRIPTION FACTOR HES- (C-HAIRY1)//7.50E-14//96aa//36%/O57337  
C-OVARC1001086//Homo Sapiens cyclin T2a mRNA, complete cds//0//1593bp//98%/AF048731  
15 C-OVARC10011321//GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9)  
(TCF-9)//2.30E-44//268aa//36%/P16383  
C-OVARC1001163//HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I//2.30E-20//152aa//  
30%/Q09906  
C-OVARC1001222  
20 C-OVARC1001338//AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 (EC 2.7.1.-)//8.80E-30//  
125aa//40%/P53104  
C-OVARC1001569//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-)//1.50E-22//  
164aa//39%/P34244  
C-OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds//0//1766bp//99%/AF126062  
25 C-OVARC1001725  
C-OVARC1001727  
C-OVARC1001807//Human TR3 orphan receptor mRNA, complete cds//1.10E-243//1145bp//98%/L13740  
C-OVARC1001991//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)//8.30E-06//114aa//  
30 35%/Q01956  
C-OVARC1002058//Human 18S rRNA gene, complete//1.50E-164//921bp//91%/M10098  
C-OVARC1002178  
C-PLACE100033//VON WILLEBRAND FACTOR PRECURSOR//3.80E-17//190aa//28%/Q28295  
C-PLACE1000231//Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds//  
35 2.70E-101//947bp//74%/AF037272  
C-PLACE1000258//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//1.70E-55//431aa//  
35%/Q05481  
C-PLACE1000442//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//1.00E-88//213aa//67%/P16415  
C-PLACE1000560  
40 C-PLACE1000740//Mus musculus (Notch2) mRNA, complete cds//5.60E-122//893bp//81%/M93661  
C-PLACE1000912  
C-PLACE1000914//Homo sapiens PB39 mRNA, complete cds//7.50E-88//500bp//69%/AF045584  
C-PLACE1000927//HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X//6.30E-21//123aa//  
37%/Q11079  
45 C-PLACE1001016//SODIUM CHANNEL PROTEIN PARA (PARALYTIC  
PROTEIN)//6.80E-12//133aa//28%/P35500  
C-nnnnnnnnnnnn//Homo sapiens T245 protein (T245) mRNA, complete cds//0//1801bp//99%/AF043906  
C-PLACE1001100  
C-PLACE1001114//HYPOTHETICAL BHLF1 PROTEIN//9.20E-06//389aa//31%/P03181  
50 C-PLACE1001123  
C-PLACE1001183  
C-PLACE1001229  
C-PLACE1001231//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete  
cds//2.20E-137//918bp//80%/AF026554  
55 C-nnnnnnnnnnnn//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds//  
7.60E-293//1631bp//90%/U18469  
C-PLACE1001340//Homo sapiens mRNA for KIAA0719 protein, complete cds//0//2868bp//99%/AB018262  
C-PLACE1001401//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE

FC RECEPTOR, BETA-SUBUNIT).//3.70E-18//148aa//39%/P13386

C-PLACE1001407

C-PLACE1001464//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2756bp//99%/X55740

C-PLACE1001500//Homo sapiens RecQ5 mRNA for DNA helicase, complete cds.//2.30E-271//1230bp//99%/AB006533

C-PLACE1001516//240 KD PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL [CONTAINS: GLUTAMIC ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)].//2.30E-08//274aa//28%/Q28181

C-PLACE1001536

C-PLACE1001564//H.sapiens mRNA for HE6 Tm7 receptor.//5.10E-36//499bp//70%/X81892

C-PLACE1001655//Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds.//0//1708bp//99%/AF043472

C-nnnnnnnnnnnn//Homo sapiens calumein (Calu) mRNA, complete cds.//0//1776bp//99%/AF013759

C-PLACE1001788

C-PLACE1001795//HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECURSOR.//3.40E-20//159aa//40%/P47032

C-PLACE1001836//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P2OE].//5.00E-27//134aa//47%/P10269

C-PLACE1001918//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//2.30E-53//339aa//33%/P32802

C-PLACE1001949//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//3.00E-75//315aa//44%/Q12697

C-PLACE1002080//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//0//1588bp//99%/AF039691

C-PLACE1002095

C-PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.//0//1202bp//99%/AF095791

C-PLACE1002329//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//6.50E-105//213aa//45%/Q08509

C-PLACE1002355//COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN].//4.20E-12//131aa//40%/P01029

C-PLACE1002374//Human mRNA for pro-cathepsin L (major excreted protein MEP).//1.30E-313//1363bp//97%/X12451

C-PLACE1002518

C-PLACE1002547//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2985bp//99%/AB018262

C-PLACE1002726//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//2.80E-202//926bp//82%/AJ133128

C-PLACE1002905//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//2.40E-37//188aa//40%/P07106

C-PLACE1002911//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//4.50E-39//345aa//32%/P32507

C-PLACE1002967//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT).//4.60E-08//156aa//30%/Q01362

C-PLACE1003135//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-47//210aa//49%/P08458

C-PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.//1.00E-294//1344bp//99%/AF069301

C-PLACE1003428//Homo sapiens mRNA for VNN1 protein.//1.80E-142//676bp//72%/AJ132099

C-PLACE1003438

C-PLACE1003460

C-PLACE1003529//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//1.30E-09//281aa//22%/P11414

C-PLACE1003573//T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).//3.70E-16//226aa//26%/P20937

C-PLACE1003598//TRP-ASP REPEATS CONTAINING PROTEIN RBA-1.//1.80E-07//161aa//27%/P90917

C-PLACE1003644

C-PLACE1003737//TOLL PROTEIN PRECURSOR.//5.40E-07//203aa//27%/P08953

C-PLACE1003772//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//2.40E-12//124aa//38%/P 13983

C-PLACE1003839//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//8.10E-18//



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771bp//58%//AF095448  
 C-PLACE1003845//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-  
 GALACTOSE 4-EPIMERASE).//3.40E-37//302aa//30%//Q57664  
 C-PLACE1003852//Homo sapiens mRNA for KIAA0758 protein, partial cds.//0//1667bp//99%//AB018301  
 5 C-PLACE1004028  
 C-PLACE1004166//CREB-BINDING PROTEIN.//1.80E-12//147aa//35%//P45481  
 C-PLACE1004168//Homo sapiens mRNA for KIAA1007 protein, partial cds.//0//2637bp//99%//AB023224  
 C-PLACE1004199  
 C-PLACE1004279//HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.//1.40E-08//166aa//  
 10 30%//P30638  
 C-PLACE1004282//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//2.10E-11//  
 189aa//30%//P25234  
 C-PLACE1004305//RAS-RELATED PROTEIN RAC1.//9.60E-29//197aa//41%//P40792  
 C-PLACE1004441//Human G protein-coupled receptor (GPR1) gene, complete cds.//0//1880bp//98%//AC007383  
 15 C-PLACE1004450//AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (LEUKEMIA AN-  
 TIGEN CD13).//1.30E-91//562aa//35%//P15541  
 C-PLACE 1004482//Rattus norvegicus hematopoietic lineage switch 2 related protein (Hls2-rp) mRNA, complete  
 cds.//1.90E-246//1643bp//83%//AF097723  
 C-PLACE1004519  
 20 C-PLACE1004520//Human pregnancy-specific beta-glycoprotein d mRNA, complete cds.//9.10E-279//882bp//  
 88%//M20881  
 C-PLACE1004630  
 C-PLACE1004637  
 C-PLACE1004648//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-  
 25 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.40E-18//395aa//25%//P08640  
 C-nnnnnnnnnnnn//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1825bp//99%//  
 AF049891  
 C-PLACE1004816//Homo sapiens mRNA for Hakata antigen, complete cds.//1.00E-166//856bp//94%//D88587  
 C-PLACE1004887//GOLIATH PROTEIN (G1 PROTEIN).//4.80E-33//179aa//47%//Q06003  
 30 C-PLACE1005003//PROSTASIN PRECURSOR (EC 3.4.21.-).//2.20E-52//269aa//41%//Q16651  
 C-PLACE1005005//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.//4.10E-261//  
 1209bp//98%//AF032456  
 C-PLACE1005031//CHLORINE CHANNEL PROTEIN P64.//8.00E-92//205aa//87%//P35526  
 C-PLACE1005239//Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, pH4-17).//1.80E-235//1010bp//84%//  
 35 AJ223351  
 C-PLACE1005250//Homo sapiens D-type cyclin-interacting protein 1 (DIP1) mRNA, complete cds.//0//1046bp//  
 96%//AF082569  
 C-PLACE1005383//Homo sapiens UP50 mRNA, complete cds.//0//2019bp//99%//AF093118  
 C-PLACE1005410//Canis familiaris sec61 homologue mRNA, complete cds.//2.40E-204//673bp//89%//M96629  
 40 C-PLACE1005426//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds.//  
 0//1629bp//95%//U18469  
 C-PLACE1005519//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//4.60E-108//1070bp//73%//  
 AF024636  
 C-PLACE1005544//Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.//2.00E-159//  
 45 1237bp//76%//U89915  
 C-PLACE1005660//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.90E-  
 33//143aa//53%//P34280  
 C-PLACE1005669  
 C-PLACE1005682//B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).//4.90E-09//183aa//33%//  
 50 P20749  
 C-PLACE1005725//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//7.60E-17//295aa//  
 27%//Q11073  
 C-PLACE1005736//Human mRNA for BAS-GRIP protein.//0//2378bp//99%//E16311  
 C-PLACE1005768  
 55 C-PLACE1005878//Bovine chlorine channel protein (p64) mRNA, complete cds.//5.90E-137//889bp//85%//L16547  
 C-PLACE1006093  
 C-PLACE1006208//Homo sapiens nGAP mRNA, complete cds.//3.30E-151//694bp//100%//AP047711  
 C-PLACE1006219//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-

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GALACTOSE 4-EPIMERASE).//3.50E-37//302aa//30%/Q57664  
 C-PLACE1006277//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%/AJ132502  
 C-PLACE1006290//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-)//8.50E-75//301aa//39%/P43636  
 C-PLACE1006443//Homo sapiens PB39 mRNA, complete cds.//4.30E-98//553bp//70%/AF045584  
 5 C-PLACE1006515//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2846bp//99%/AB011148  
 C-PLACE1006716//30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADI-  
 POCYTE SPECIFIC PROTEIN ADIPOQ).//4.60E-25//181aa//35%/Q60994  
 C-PLACE1006809//SLS1 PROTEIN PRECURSOR.//9.10E-10//273aa//27%/P08124  
 C-PLACE1006959  
 10 C-PLACE1007028  
 C-PLACE1007040  
 C-PLACE1007096//PUTATIVE SUGAR TRANSPORT PROTEIN GETA.//2.70E-17//174aa//27%/O34368  
 C-nnnnnnnnnnnnn//Homo sapiens mRNA for putative glucosyltransferase, partial cds.//0//1373bp//99%/AJ224875  
 C-PLACE1007296//Human mRNA for a presumptive KDEL receptor.//1.10E-185//1038bp//91%/X55885  
 15 C-PLACE1007591  
 C-PLACE1007626//Homo sapiens unknown mRNA, complete cds.//3.00E-246//1122bp//99%/AF047439  
 C-PLACE1007702//Mus musculus TRA1 mRNA, complete cds.//7.50E-41//662bp//64%/D78335  
 C-PLACE1007845//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-)//4.80E-14//158aa//40%/P43636  
 C-PLACE1007881//HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.//3.10E-99//504aa//  
 20 42%/Q19425  
 C-PLACE1008297//MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).//1.30E-14//187aa//33%/P90648  
 C-nnnnnnnnnnnnn//Homo sapiens mRNA for putative glucosyltransferase, partial cds.//0//1616bp//99%/AJ224875  
 C-PLACE1008469  
 25 C-PLACE1008549//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//0//2274bp//99%/AF115403  
 C-PLACE1008657//Bovine mRNA for adseverin, complete cds.//7.80E-227//1246bp//90%/D26549  
 C-PLACE1008716//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//  
 1888bp//99%/U15128  
 30 C-PLACE1008984  
 C-PLACE1008985//Mus musculus synaptotagmin VIII mRNA, partial cds.//3.80E-140//650bp//81%/U20107  
 C-PLACE1009067  
 C-PLACE1009196  
 C-PLACE1009279//cDNA encoding novel physiologically active protein which have serine protease activity.//  
 35 6.60E-86//1414bp//64%/E12965  
 C-PLACE1009527//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//1.20E-87//585bp//83%/AJ133128  
 C-PLACE1009546  
 C-PLACE1009600//Mouse mRNA for tetracycline transporter-like protein, complete cds.//1.10E-264//924bp//  
 40 88%/D88315  
 C-PLACE1009735  
 C-PLACE1009982//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//5.20E-08//166aa//28%/P02840  
 C-PLACE1010078//ORM1 PROTEIN.//3.70E-19//137aa//37%/P53224  
 C-PLACE1010081//Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.//0//2033bp//99%/AF027706  
 45 C-PLACE1010251//FIBRILLIN 2 PRECURSOR.//1.70E-31//201aa//35%/Q61555  
 C-PLACE1010784//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds.//2.30E-252//  
 1146bp//99%/AF008670  
 C-PLACE1010827//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.90E-  
 50 19//163aa//34%/P49020  
 C-PLACE1010968//PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN- TY-  
 ROSINE-PHOSPHATE PHOSPHOHYDROLASE).//3.40E-30//690aa//26%/P16621  
 C-PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds.//0//2376bp//99%/AF094516  
 C-PLACE1011116//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE)  
 55 (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.30E-09//234aa//27%/P08640  
 C-PLACE1011236//Mus musculus mRNA for RST, complete cds.//1.70E-90//1398bp//65%/AB005451  
 C-PLACE1011407//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.80E-133//342aa//59%/Q99676  
 C-PLACE1011516//HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//1.30E-13//

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139aa//34%//P53073  
 C-PLACE1011708//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1840bp//98%//AF034611  
 C-PLACE1011824//Human Ste20-like kinase (MST2) mRNA, complete cds.//6.40E-202//561bp//92%//U26424  
 5 C-PLACE1011978//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-194//547aa//57%//Q05481  
 C-PLACE2000118//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//3.20E-27//205aa//43%//P70315  
 C-PLACE2000219  
 10 C-SKNMC1000004  
 C-THYRO1000036//Homo sapiens collagen alpha 3 type IX (COL9A3) mRNA, complete cds.//1.20E-258//1376bp//93%//L41162  
 C-THYRO1000061  
 C-THYRO1000099  
 15 C-THYRO1000196//Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.//0//1632bp//91%//AF016272  
 C-THYRO1000400//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 25795.//0//1893bp//99%//AL109665  
 C-THYRO1000580//ZINC FINGER PROTEIN 184 (FRAGMENT).//9.90E-114//279aa//59%//Q99676  
 C-THYRO1000584//Homo sapiens mRNA for KIAA0935 protein, partial cds.//0//1338bp//99%//AB023152  
 20 C-THYRO1000678//Homo sapiens Cx30 gene.//0//1741bp//97%//AJ005585  
 C-THYRO1000795//C.elegans mRNA for Oxoglutarate/malate carrier protein.//8.80E-42//821bp//63%//X76114  
 C-THYRO1000846  
 C-THYRO1000866//SHK1 KINASE-BINDING PROTEIN 1.//4.40E-91//449aa//44%//P78963  
 C-THYRO1000956//Human G protein-coupled receptor APJ gene, complete cds.//0//1583bp//99%//U03642  
 25 C-THYRO1000999  
 C-THYRO1001063  
 C-THYRO1001071//GAMMA-ADAPTIN (GOLGI ADAPTOR HA1/AP1 ADAPTIN GAMMA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 GAMMA LARGE CHAIN).//8.20E-14//157aa//33%//P22892  
 C-THYRO1001102  
 30 C-THYRO1001113//Homo sapiens mRNA; cDNA DKFZp564E1616 (from clone DKFZp564E1616).//0//1361bp//99%//AL096713  
 C-THYRO1001128  
 C-THYRO1001205  
 C-THYRO1001237//PHYTOENE DEHYDROGENASE (EC 1.3.-.-) (PHYTOENE DESATURASE) (ALBINO-1 PROTEIN).//3.10E-13//346aa//22%//P21334  
 35 C-THYRO1001266//Human sodium iodide symporter mRNA, complete cds.//7.20E-81//1466bp//62%//U66088  
 C-THYRO1001327  
 C-THYRO1001456//HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.//9.40E-32//355aa//31%//Q10555  
 C-THYRO1001457//H.sapiens mRNA for protein kinase C mu.//2.30E-218//1183bp//73%//X75756  
 40 C-THYRO1001471  
 C-THYRO1001478//CYTOCHROME B-245 HEAVY CHAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEUTROPHIL CYTOCHROME B, 91 KD POLYPEPTIDE) (CGD91-PHOX) (GP91-PHOX) (CYTOCHROME B(558) BETA CHAIN) (SUPEROXIDE-GENERATING NADPH OXIDASE HEAVY CHAIN SUBUNIT).//8.90E-50//296aa//35%//P04839  
 45 C-THYRO1001495  
 C-THYRO1001523//Homo sapiens mRNA for TM7XN1 protein.//0//3663bp//99%//AJ011001  
 C-THYRO1001529//SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2).//5.50E-25//115aa//53%//Q09925  
 C-THYRO1001700//SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RECEPTOR INTERACTING PROTEIN).//9.70E-33//268aa//37%//Q60855  
 50 C-THYRO1001702//Mus musculus mRNA for myeloid associated differentiation protein.//1.50E-128//1204bp//73%//AJ001616  
 C-THYRO1001725  
 C-THYRO1001803  
 55 C-Y79AA1000127  
 C-Y79AA1000207  
 C-Y79AA1000226  
 C-Y79AA1000270//Bos taurus vacuolar H+ ATPase subunit Ac45 mRNA, complete cds.//1.00E-271//1490bp//

83%/U10039  
 C-Y79AA1000426//Mus musculus activin beta E subunit mRNA, complete cds.//7.70E-200//1533bp//78%/U96386  
 C-Y79AA1000521  
 C-Y79AA1000776  
 5 C-Y79AA1000777//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.10E-48//283aa//38%/Q00808  
 C-nnnnnnnnnnnn//Homo sapiens intersectin long form mRNA, complete cds.//0//1519bp//99%/AF064244  
 C-Y79AA1000876//PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72).//1.60E-44//210aa//38%/P13667  
 10 C-Y79AA1000959//Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.//4.80E-283//1405bp//95%/AF093420  
 C-Y79AA1000967//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).//1.00E-77//359aa//44%/Q14012  
 C-Y79AA1001013  
 C-Y79AA1001056  
 15 C-Y79AA1001062//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//8.90E-12//132aa//38%/Q13829  
 C-Y79AA1001090//NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP-1) (NF-KAPPA-B1 P84/NF-KAPPA-B1 P98)[CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] (FRAGMENT).//4.50E-09//144aa//31 %/Q63369  
 20 C-Y79AA1001264//HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.//5.10E-106//351aa//58%/Q10005  
 C-Y79AA1001272  
 C-Y79AA1001328//Mus musculus mRNA for DII3 protein, complete cds.//1.90E-263//1988bp//79%/ABO13440  
 C-Y79AA1001430//Homo sapiens mRNA for KIAA0469 protein, complete cds.//0//2943bp//99%/AB007938  
 25 C-Y79AA1002022//POLIOVIRUS RECEPTOR HOMOLOG PECURSOR.//2.20E-06//140aa//26%/P32507  
 C-BNGH41000020//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//9.80E-159//347aa//90%/P03891  
 C-BNGH41000091//POTASSIUM CHANNEL PROTEIN EAG.//1.20E-249//625aa//65%/Q02280  
 C-HEMBA1000462//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//935bp//99%/U71267  
 30 C-HEMBA1000477//HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//1.40E-38//344aa//34%/P40085  
 C-HEMBA1000671//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.90E-104//388aa//46%/Q99676  
 C-HEMBA1000732//Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.//0//2153bp//94%/Y13622  
 35 C-HEMBA1000835  
 C-HEMBA1000875  
 C-HEMBA1001184//SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP).//2.50E-32//100aa//60%/P55822  
 40 C-HEMBA1001272//Homo sapiens mRNA for KIAA1171 protein, partial cds.//0//1490bp//99%/AB032997  
 C-HEMBA1001296  
 C-HEMBA1002048//ODD-SKIPPED PROTEIN.//1.60E-55//122aa//75%/P23803  
 C-HEMBA1002985  
 C-HEMBA1003120//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.00E-193//547aa//54%/Q99676  
 45 C-HEMBA1003497//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//4.00E-28//358aa//29%/Q60821  
 C-HEMBA1004007  
 C-HEMBA1004085  
 C-HEMBA1004785//MODIFIER 3 PROTEIN (M33).//1.40E-27//221aa//33%/P30658  
 50 C-HEMBA1004952  
 C-HEMBA1004971  
 C-HEMBA1005230//ZINC FINGER PROTEIN 140.//2.00E-17//83aa//66%/P52738  
 C-HEMBA1005246  
 C-HEMBA1005267//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//8.40E-14//187aa//33%/Q01484  
 55 C-HEMBA1006276//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//1.70E-06//56aa//57%/Q61967  
 C-HEMBA1006357//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.//3.70E-39//136aa//52%/

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O15127  
 C-HEMBA1006517  
 C-HEMBA1006544  
 C-HEMBA1006749//Homo sapiens mRNA for matrilin-4, partial.//1.40E-275//1942bp//83%//AJ007581  
 5 C-HEMBA1006770//FLOWERING TIME CONTROL PROTEIN FCA//1.20E-33//352aa//34%//O04425  
 C-HEMBA1006912  
 C-HEMBA1007063  
 C-HEMBA1000106//CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP)//1.60E-10//139aa//30%//P53996  
 C-HEMBA1000407  
 10 C-HEMBA1000542//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.60E-232//1452bp//85%//AF084259  
 C-HEMBA1001547//Homo sapiens CGI-02 protein mRNA, complete cds.//0//2311bp//99%//AF132937  
 C-HEMBA1001959//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B)//7.30E-14//97aa//38%//P25210  
 15 C-HEMBA1002039  
 C-HEMBA1002041//Homo sapiens transmembrane protein TENB2 (TENB2) mRNA, complete cds.//0//1746bp//99%//AF179274  
 C-HEMBA1002051//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//1.30E-95//454bp//99%//AF115403  
 20 C-HEMBA1002120//UDP-N-ACETYLGLUCOSAMINE-PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT)//4.90E-22//337aa//27%//P56558  
 C-HEMBA1002302  
 C-HEMBA1002661//Homo sapiens cardiovascular helix-loop-helix factor 2 (CHF2) mRNA, complete cds.//0//2174bp//99%//AF179274  
 25 C-HEMBA1000106  
 C-HEMBA1000141  
 C-HEMBA1000204//Homo sapiens dysferlin mRNA, complete cds.//0//2028bp//99%//AF075575  
 C-HEMBA1000226  
 C-HEMBA1000403//Homo sapiens CDK4-binding protein p34SEI1 (SEI1) mRNA, complete cds.//1.20E-255//1165bp//99%//AF117959  
 30 C-HEMBA1000473//HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.//5.10E-45//299aa//34%//P47088  
 C-HEMBA1000496//MIC1 PROTEIN.//3.00E-25//202aa//33%//P53258  
 C-HEMBA1000528  
 35 C-HEMBA1000614//Homo sapiens pseudouridine synthase 1 (PUS1) mRNA, partial cds.//2.10E-302//1370bp//99%//AF116238  
 C-HEMBA1000652  
 C-HEMBA1000706  
 C-HEMBA1000788//Bos taurus P14 (p14) mRNA, complete cds.//3.90E-85//502bp//89%//AF037349  
 40 C-HEMBA1000810  
 C-HEMBA1000814  
 C-HEMBA1000881//Homo sapiens protein kinase (SGK3) mRNA, complete cds.//0//1292bp//100%//AF169035  
 C-HEMBA1000986  
 45 C-HEMBA1000994//Homo sapiens ISLR(immunoglobulin superfamily containing leucine-rich repeat) mRNA, complete cds, alternatively spliced transcript ISLR-2.//0//2211bp//99%//AB024536  
 C-HEMBA1001141  
 C-HEMBA1001150//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//7.50E-304//587aa//68%//Q15139  
 C-HEMBA1001237//MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).//7.70E-64//196aa//41%//P53988  
 C-HEMBA1001284  
 50 C-HEMBA1001310//HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-REC114 INTERGENIC REGION.//1.50E-67//441aa//37%//Q04225  
 C-HEMBA1001344  
 C-HEMBA1001418//HYPOTHETICAL PROTEIN HI0519.//6.90E-27//181aa//38%//P44742  
 C-HEMBA1001532//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.60E-126//319aa//56%//P51523  
 55 C-HEMBA1001615//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.80E-11//90aa//42%//Q13562  
 C-HEMBA1001623//Homo sapiens mRNA; cDNA DKFZp434J1027 (from clone DKFZp434J1027); partial cds.//1.30E-269//1222bp//99%//AL133084

C-MAMMA1001634  
 C-MAMMA1001957  
 C-MAMMA1001978//Cimex lectularius apyrase (APY) mRNA, complete cds.//6.70E-19//988bp//56%//AF085499  
 C-MAMMA1002070//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).//1.10E-07//103aa//33%//Q01177  
 5 C-MAMMA1002080//RAS-RELATED PROTEIN RAB-13.//1.80E-29//208aa//37%//P51153  
 C-MAMMA1002087  
 C-MAMMA1002095//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE).//3.70E-22//867aa//52%//O43108  
 C-MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR.//2.50E-97//464aa//45%//Q92338  
 10 C-MAMMA1002142//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//9.80E-17//146aa//35%//P18160  
 C-MAMMA1002165//Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.//4.80E-60//382bp//89%//AF100780  
 C-MAMMA1002205//Homo sapiens mRNA; cDNA DKFZp586C091 (from clone DKFZp586C091).//2.00E-81//308bp//81%//AL050119  
 15 C-MAMMA1002234//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//0//627aa//96%//Q00004  
 C-MAMMA1002586//Homo sapiens alpha 1,2-mannosidase mRNA, complete cds.//0//2228bp//99%//AF148509  
 C-MAMMA1002633  
 C-MAMMA1003126//Human Hpast (HPAST) mRNA, complete cds.//3.70E-162//1355bp//75%//AF001434  
 20 C-NT2RM1000580//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636  
 C-NT2RM1000858//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//2.10E-98//1035bp//70%//S70011  
 C-NT2RM2000565//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//9.40E-94//394aa//43%//Q09782  
 C-NT2RM2000582//Homo sapiens mRNA for KIAA1053 protein, partial cds.//0//2666bp//99%//AB028976  
 25 C-NT2RM2000589//Bos taurus myosin X, complete cds.//0//4376bp//84%//U55042  
 C-NT2RM2000632//EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).//6.40E-62//183aa//47%//Q03468  
 C-NT2RM2000773//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//3.00E-289//1092bp//99%//AB017335  
 30 C-NT2RM2001558//Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds.//0//2398bp//99%//AF093408  
 C-NT2RM2001626//FLIGHTLESS-1 PROTEIN HOMOLOG.//4.30E-19//362aa//26%//P34268  
 C-NT2RM2001643  
 C-NT2RM2001738//SOF1 PROTEIN.//3.00E-110//325aa//47%//P33750  
 35 C-NT2RM2001792//Homo sapiens angiopoietin-related protein-2 mRNA, complete cds.//7.10E-149//995bp//86%//AF125175  
 C-NT2RM2001818//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//4.30E-11//488aa//26%//P23253  
 C-NT2RM4000100//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2678bp//99%//AB023206  
 40 C-NT2RM4000115//HYPOTHETICAL 68.8 KD PROTEIN B0464.6 IN CHROMOSOME III.//1.20E-16//204aa//30%//Q03564  
 C-NT2RM4000417//SYNAPTOTAGMIN II.//2.70E-23//293aa//30%//P46097  
 C-NT2RM4000593//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//3.90E-27//576aa//24%//Q10297  
 45 C-NT2RM4000761//H.sapiens mitochondrial genome (consensus sequence).//0//1931bp//99%//X62996  
 C-NT2RM4000965//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//9.00E-44//520aa//29%//O60100  
 C-NT2RM4001377//Homo sapiens mRNA for KIAA0638 protein, partial cds.//0//1346bp//99%//AB014538  
 C-NT2RM4001768//Homo sapiens CGI-82 protein mRNA, complete cds.//0//1925bp//99%//AF151840  
 50 C-NT2RM4001843//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//6.20E-33//263aa//38%//P48982  
 C-NT2RP1000239  
 C-NT2RP1000465//UBIQUITIN-LIKE PROTEIN SMT3.//5.10E-07//81aa//33%//P55857  
 C-NT2RP1000468//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.00E-13//97aa//38%//P25210  
 55 C-NT2RP1000679  
 C-NT2RP1000740//Homo sapiens mRNA; cDNA DKFZp586F1918 (from clone DKFZp586F1918).//4.60E-97//456bp//99%//AL050091

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C-NT2RP1001031//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//3.40E-42//285aa//35%//Q00808  
C-NT2RP2000178//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//2.40E-192//  
778aa//48%//P93647  
C-NT2RP2000240  
5 C-NT2RP2000447//GOLGIN-95.//2.80E-33//99aa//66%//Q08379  
C-NT2RP2000610//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN  
B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//1.50E-13//97aa//38%//P25210  
C-NT2RP2000616//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//  
4.10E-12//323aa//30%//P13983  
10 C-NT2RP2000712//ZINC FINGER PROTEIN 135.//3.70E-87//296aa//53%//P52742  
C-NT2RP2000739//ZINC FINGER PROTEIN 83 (ZNNC FNNGER PROTENN HPF1).//7.50E-73//387aa//37%//  
P51522  
C-NT2RP2000818//Homo sapiens xenotropic and polytropic murine leukemia virus receptor (X3) mRNA, complete  
cds.//0//2724bp//99%//AF089744  
15 C-NT2RP2001200//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1539bp//100%//AB014576  
C-NT2RP2001223//MYOTUBULARIN-RELATED PROTEIN 3 (FRAGMENT).//3.30E-05//76aa//39%//Q13615  
C-NT2RP2001276//NPDC-1 PROTEIN PRECURSOR.//3.00E-133//331aa//77%//Q64322  
C-NT2RP2001388//TRNA-SPUCING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-  
NUCLEASE).//5.90E-13//157aa//33%//P16658  
20 C-NT2RP2001469//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%//Q00808  
C-NT2RP2001562//Homo Sapiens GLE1 (GLE1) mRNA, complete cds.//0//1899bp//98%//AF058922  
C-NT2RP2001662//HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN).//1.80E-49//  
94aa//81%//Q90655  
C-NT2RP2001755//Rattus norvegicus f-spondin mRNA, complete cds.//0//2974bp//86%//M88469  
25 C-NT2RP2001817//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds.//0//3092bp//99%//AF083106  
C-NT2RP2001948//HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2).//1.40E-08//191aa//27%//P53686  
C-NT2RP2002015  
C-NT2RP2003390//Homo sapiens mRNA for SEC63 protein.//0//2629bp//99%//AJ011779  
C-NT2RP2003664//Homo sapiens mRNA for leptin receptor gene-related protein.//1.90E-237//1081bp//99%//  
Y12670  
30 C-NT2RP2003940//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//7.00E-111//401aa//43%//P28160  
C-NT2RP2004069//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.//3.00E-45//188aa//  
52%//Q09297  
C-NT2RP2004108//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.30E-171//474aa//62%//P16415  
35 C-nnnnnnnnnnnnn/Homo sapiens calumein (Calu) mRNA, complete cds.//0//2415bp//99%//AF013759  
C-NT2RP2005069//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//1792bp//87%//  
U35245  
C-NT2RP2005378//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).//6.30E-  
28//183aa//47%//P10496  
40 C-NT2RP2005391//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor  
Sp1.//0//1544bp//99%//AJ242978  
C-NT2RP2005597//Homo sapiens protein O-mannosyl-transferase 1 (POMT1) mRNA, complete cds.//0//1821bp//  
97%//AF095136  
C-NT2RP2005666  
45 C-NT2RP2006004//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//3.00E-26//  
227aa//36%//Q06828  
C-NT2RP2006092//Homo sapiens mRNA for Fe65L2, complete cds.//0//1156bp//99%//AB018247  
C-NT2RP2006134  
C-NT2RP3000011//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.00E-14//320aa//24%//Q00808  
50 C-NT2RP3000022//Homo sapiens mRNA for KIAA0936 protein, complete cds.//0//2881bp//99%//AB023153  
C-NT2RP3000171//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene).//4.40E-99//571bp//89%//  
Z97207  
C-NT2RP3000304//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//2895bp//99%//  
AF074264  
55 C-NT2RP3000378//PAIRED AMPHIPATHIC HELIX PROTEIN.//4.20E-39//186aa//36%//P22579  
C-NT2RP3000444  
C-NT2RP3000645  
C-NT2RP3000676//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.10E-15//220aa//27%//Q03829

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C-NT2RP3000677//DNA BINDING PROTEIN RFX2.//3.60E-56//233aa//41%/P48378  
C-NT2RP3000789//Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA, complete cds.//0//1458bp//100%/AF117106  
C-NT2RP3000818  
5 C-NT2RP3000838//TRICHOHYALIN//9.80E-11//491aa//26%/Q07283  
C-NT2RP3000921//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).//4.00E-21//316aa//29%/P43146  
C-NT2RP3001159//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2558bp//99%/AL050118  
10 C-NT2RP3001271//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//2.60E-09//334aa//22%/P52178  
C-NT2RP3001542//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//4.70E-11//132aa//37%/Q13829  
C-NT2RP3001685//PRPE PROTEIN.//1.00E-68//382aa//41%/P77495  
15 C-NT2RP3001976//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.90E-143//379aa//55%/P51523  
C-NT2RP3002015//Homo sapiens CGI-71 protein mRNA, complete cds.//0//1991bp//99%/AF151829  
C-NT2RP3002281//Homo sapiens mRNA for KIAA0765 protein, partial cds.//0//2286bp//99%/AB018308  
C-NT2RP3002286//Homo sapiens candidate tumor suppressor protein DICE 1 mRNA, complete cds.//0//2719bp//99%/AF097645  
20 C-NT2RP3002324  
C-NT2RP3002353  
C-NT2RP3002571//Homo sapiens mRNA for KIAA1108 protein, partial cds.//4.40E-273//1311bp//97%/AB029031  
C-NT2RP3002664  
25 C-NT2RP3002737//Homo sapiens voltage-gated potassium channel KCNQ4 (KCNQ4) mRNA, complete cds.//0//1552bp//99%/AF105202  
C-NT2RP3002887  
C-NT2RP3002900//Homo sapiens CGI-109 protein mRNA, complete cds.//8.70E-298//1321bp//92%/AF151867  
C-NT2RP3002983  
30 C-NT2RP3003473//Homo sapiens CGI-55 protein mRNA, complete cds.//5.50E-275//1309bp//98%/AF151813  
C-NT2RP3003532//OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).//4.40E-139//263aa//99%/P41217  
C-NT2RP3004025  
C-NT2RP3004067//Homo sapiens mRNA for NESCA, complete cds.//0//1962bp//99%/AB026894  
35 C-NT2RP3004119//PEREGRIN (BE140 PROTEIN).//7.30E-39//227aa//43%/P55201  
C-NT2RP3004294//Xenopus laevis ER1 mRNA, complete cds.//1.20E-71//335bp//79%/AF015454  
C-NT2RP3004345//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32).//3.90E-18//279aa//27%/P15565  
C-NT2RP4000634//Homo sapiens mitogen-activated protein kinase kinase MEKK2 mRNA, complete cds.//0//1501bp//98%/AF111105  
40 C-NT2RP4001001//Homo sapiens clone 24856 mRNA sequence, complete cds.//3.90E-301//1374bp//99%/AF131856  
C-NT2RP4001877//Homo sapiens ribonucleoprotein RBM8 (RBM8) mRNA, complete cds.//0//2770bp//99%/AF127761  
45 C-NT2RP4001879  
C-NT2RP4002187//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2373bp//99%/AF078850  
C-NT2RP4002451  
C-NT2RP4002750//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//1.00E-310//2084bp//81%/U70859  
50 C-OVARC1000003//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete cds.//4.30E-220//1158bp//94%/AF111856  
C-OVARC1000313//Homo sapiens mRNA for KIAA0573 protein, partial cds.//0//1833bp//99%/AB011145  
C-OVARC1000331//GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE).//9.40E-44//106aa//59%/P36959  
55 C-OVARC1000553//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM).//1.30E-23//169aa//40%/P28843  
C-OVARC1000873//Homo sapiens mRNA for KIAA1247 protein, partial cds.//0//2178bp//99%/AB033073



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C-OVARC1000995  
 C-OVARC1001260  
 C-OVARC1001336//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete  
 cds.//0//1435bp//99%//AF111856  
 5 C-OVARC1001570//Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete cds.//0//1792bp//  
 100%//AF190725  
 C-OVARC1001607//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//  
 1836bp//96%//U15128  
 C-OVARC1001833//CIS-GOLGI MATRIX PROTEIN GM130.//6.60E-136//363aa//76%//Q62839  
 10 C-OVARC1001952//TRICHOHYALIN.//3.30E-16//487aa//27%//Q07283  
 C-PLACE1000986//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//2055bp//  
 99%//AL117450  
 C-PLACE1003407//Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.//0//1965bp//  
 99%//AF068227  
 15 C-PLACE1004078//Bovine mRNA for adseverin, complete cds.//0//2218bp//89%//D26549  
 C-PLACE1004492//VERPROLIN.//3.30E-07//149aa//29%//P37370  
 C-PLACE1005539//ACTIN POLYMERIZATION INHIBITOR (HEAT SHOCK 25 KD PROTEIN) (25-KD IAP).//  
 3.10E-08//84aa//34%//Q00649  
 C-PLACE1005569//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502  
 20 C-PLACE1005601  
 C-PLACE1005745//ORM1 PROTEIN.//2.40E-17//137aa//35%//P53224  
 C-PLACE1005815//COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).//1.50E-26//274aa//26%//  
 P23508  
 C-PLACE1005927//HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.//1.60E-38//333aa//  
 25 33%//Q09875  
 C-PLACE1006071//LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).//6.00E-08//215aa//26%//  
 P02469  
 C-PLACE1006073//Homo sapiens mRNA for glucuronyltransferase I, complete cds.//4.10E-316//1020bp//96%//  
 AB009598  
 30 C-PLACE1006079//Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.//0//1379bp//97%//  
 AF028233  
 C-PLACE1006786  
 C-PLACE1007077//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//2578bp//99%//AB023194  
 C-PLACE1007971  
 35 C-PLACE1008282//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-)  
 (HRI).//7.10E-274//627aa//82%//P33279  
 C-PLACE1008359//BEM46 PROTEIN (FRAGMENT).//1.70E-50//289aa//42%//P54069  
 C-PLACE1008744//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 248114.//0//1757bp//99%//  
 AL079279  
 40 C-PLACE1010445  
 C-PLACE1010713//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//  
 AF078850  
 C-nnnnnnnnnnnnn//Homo sapiens angiopoietin-2 mRNA, complete cds.//0//2227bp//99%//AF004327  
 C-PLACE1011181//MSP1 PROTEIN HOMOLOG.//9.40E-82//353aa//47%//P54815  
 45 C-PLACE1011364//MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DYSTROPHY PROTEIN KINASE)  
 (MDPK) (DM-KINASE) (DMK) (DMPK) (MT-PK).//2.20E-09//153aa//32%//Q09013  
 C-PLACE3000181//Human protocadherin 42 mRNA, complete cds for abbreviated PC42.//0//2719bp//95%//  
 L11370  
 C-SKNMC1000014  
 50 C-SKNMC1000082//BRITTLE-1 PROTEIN PRECURSOR.//3.70E-31//307aa//30%//P29518  
 C-THYRO1000964  
 C-THYRO1001242//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//  
 0//2468bp//99%//AF037339  
 C-THYRO1001608  
 55 C-THYRO1001641//Homo sapiens CGI-57 protein mRNA, complete cds.//0//1668bp//99%//AF151815  
 C-THYRO1001770//PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).//6.30E-  
 20//1169aa//35%//P53974  
 C-Y79AA1000030//Homo sapiens mRNA for Fe65L2, complete cds.//0//1828bp//100%//AB018247

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C-Y79AA1001212//Homo sapiens SL15 protein mRNA, complete cds.//6.30E-306//1388bp//99%//AF038961  
C-Y79AA1001426//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//  
6.20E-66//609aa//31%//P48751  
5 C-Y79AA1001427//Homo sapiens cytochrome b5 reductase 1 (B5R.1) mRNA, complete cds.//0//1588bp//99%//  
AF169481  
C-Y79AA1001523//Homo sapiens transcriptional intermediary factor 1 alpha mRNA, complete cds.//0//2263bp//  
99%//AF119042  
C-Y79AA1001530//Human beta-tubulin gene (5-beta) with ten Alu family members.//0//1920bp//98%//X00734  
C-Y79AA1001592  
10 C-Y79AA1001727//CELL SURFACE A33 ANTIGEN PRECURSOR.//1.10E-13//286aa//27%//Q99795  
C-Y79AA1001787//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//1.70E-133//544aa//37%//  
Q12697  
C-Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.//3.70E-126//532bp//78%//D87325  
C-Y79AA1001795//Homo sapiens mRNA for GaIT4 protein.//2.30E-250//1137bp//99%//Y15061  
15 C-Y79AA1001799//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//3.40E-54//182aa//39%//P23500  
C-Y79AA1001803//Homo sapiens secretogranin III mRNA, complete cds.//0//1871bp//99%//AF078851  
C-Y79AA1001863  
C-Y79AA1002058//Mus musculus Gng31g mRNA, complete cds.//4.10E-167//1145bp//83%//AF069954  
C-Y79AA1002121//HISTONE H1.//4.90E-12//114aa//35%//P35060  
20 C-Y79AA1002213//HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.//1.20E-98//262aa//  
41%//Q03567  
C-Y79AA1002373//Mus musculus mRNA for GSG1, complete cds.//7.20E-147//680bp//79%//D87325  
C-Y79AA1002376//Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.//1.50E-  
304//1667bp//90%//U39045  
25 C-Y79AA1002378//Homo sapiens zinc finger protein NY-REN-21 antigen mRNA, partial cds.//0//963bp//99%//  
AF155100  
C-Y79AA1002381//Homo sapiens cell cycle related kinase mRNA, complete cds.//0//1791bp//98%//AF035013  
C-BNGH41000087//Homo sapiens mRNA for KIAA1247 protein, partial cds.//0//2294bp//99%//AB033073  
C-HEMBA1001886  
30 C-HEMBA1004067//Homo sapiens mRNA for KIAA0859 protein, complete cds.//8.30E-309//623bp//99%//  
AB020666  
C-HEMBA1007226//Homo sapiens RPA-binding trans-activator (RBT1) mRNA, complete cds.//7.30E-273//  
1242bp//99%//AF192529  
C-HEMBA1000309  
35 C-HEMBA1000567  
C-MAMMA1000102//APOLIPOPROTEIN L PRECURSOR (APO-L).//1.40E-21//221aa//35%//O14791  
C-MAMMA1001066  
C-MAMMA1001094//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//  
1394bp//93%//U71267  
40 C-MAMMA1001609  
C-MAMMA1001901  
C-MAMMA1002091//Homo sapiens CD39L2 (CD39L2) mRNA, complete cds.//0//2564bp//99%//AF039916  
C-NT2RM1000462  
45 C-NT2RM1000542//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.40E-103//566aa//  
43%//P48982  
C-NT2RM1000789//Homo sapiens mRNA for hTCF-4.//2.80E-221//757bp//99%//Y11306  
C-NT2RM1000855//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%//AF084458  
C-NT2RM1000899//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//1.10E-54//182aa//39%//P23500  
C-NT2RP2000092//ZINC FINGER PROTEIN 136.//1.90E-117//419aa//54%//P52737  
50 C-NT2RP2001538//Homo sapiens mRNA; cDNA DKFZp434K2235 (from clone DKFZp434K2235).//0//2139bp//  
99%//AL117513  
C-NT2RP2001921  
C-NT2RP2003138//5'-TG-3'INTERACTING FACTOR (HOMEODOMAIN PROTEIN TGIF).//2.10E-08//104aa//46%//  
P70284  
55 C-NT2RP2003302//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete  
cds.//0//2891bp//99%//AB021644  
C-NT2RP2003950//Homo sapiens clone 24778 unknown mRNA.//0//1545bp//99%//AF070572  
C-NT2RP2005535//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.90E-172//489aa//

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62%//Q03923  
 C-NT2RP2005774//Homo sapiens GLOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.//6.90E-224//1461bp//72%//AB021644  
 C-NT2RP3000148//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.10E-106//350aa//47%//P51523  
 5 C-NT2RP3000232//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.40E-130//693aa//41%//Q99676  
 C-NT2RP3000427  
 C-NT2RP3000652//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.90E-153//441aa//62%//P28160  
 C-NT2RP3001650//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//2.20E-22//107aa//42%//P98063  
 10 C-NT2RP3002409//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2404bp//99%//AB018262  
 C-NT2RP3002411//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//AF078850  
 C-NT2RP3003448  
 15 C-NT2RP4002715  
 C-OVARC1000307//HYPOTHETICAL 29.7 KD PROTEIN CY339.02.//3.00E-19//194aa//35%//Q50658  
 C-PLACE1000907//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.30E-204//396aa//85%//P51522  
 C-PLACE1007081  
 20 C-PLACE1010011//Homo sapiens AAPT1-like protein mRNA, partial cds.//1.70E-237//1092bp//99%//AF047431  
 C-PLACE3000213//COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR).//4.60E-68//317aa//34%//P19070  
 C-PLACE4000354//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).//1.00E-129//482aa//29%//P17927  
 25 C-PLACE4000455  
 C-THYRO1000776//PROBABLE SULFATE PERMEASE SPBC3H7.02.//1.30E-68//442aa//36%//O74377  
 C-THYRO1001593//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//3.10E-203//550aa//62%//P27448  
 C-Y79AA1000750  
 30 C-Y79AA1000888//TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE).//1.50E-21//267aa//32%//P70973  
 C-Y79AA1002129  
 C-Y79AA1002334//GLUCOSE REPRESSION MEDIATOR PROTEIN.//1.70E-10//333aa//23%//P14922  
 C-BNGH41000020//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//9.80E-159//347aa//90%//P03891  
 35 C-BNGH41000087//N-ACETYLGALUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//1.20E-17//83aa//40%//P50426  
 C-BNGH41000091//POTASSIUM CHANNEL PROTEIN EAG.//1.20E-249//625aa//65%//Q02280  
 C-HEMBA1000006//Homo sapiens mRNA for NESCA, complete cds.//0//1230bp//92%//AB026894  
 40 C-HEMBA1000121//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//4.80E-05//83aa//27%//P34679  
 C-HEMBA1000128//PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).//3.20E-07//89aa//34%//P33154  
 C-HEMBA1000275  
 45 C-HEMBA1000300  
 C-HEMBA1000349//ATP-BINDING CASSETTE TRANSPORTER 1.//5.30E-65//352aa//39%//P41233  
 C-HEMBA1000443//Homo sapiens CGI-96 protein mRNA, complete cds.//4.70E-129//686bp//91%//AF151854  
 C-HEMBA1000462//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//935bp//99%//U71267  
 50 C-HEMBA1000477//HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//1.40E-38//344aa//34%//P40085  
 C-HEMBA1000590//Homo sapiens mRNA for matrilin-4, partial.//2.00E-273//1254bp//99%//AJ007581  
 C-HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.//0//994bp//99%//AF116272  
 55 C-HEMBA1000671//ZINC FINGER. PROTEIN 184 (FRAGMENT).//3.90E-104//388aa//46%//Q99676  
 C-HEMBA1000713//Homo sapiens 10kD protein (BC10) mRNA, complete cds.//0//1254bp//99%//AF053470  
 C-HEMBA1000732//Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.//0//2153bp//94%//Y13622

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C-HEMBA1000745//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//2.00E-07//445aa//27%/P02454  
 C-HEMBA1000835//FIBRILLIN 2 PRECURSOR.//1.30E-42//214aa//45%/P35556  
 C-HEMBA1000875  
 C-HEMBA1000907  
 5 C-HEMBA1000940//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//2.90E-39//362aa//31%/P41987  
 C-HEMBA1000962  
 C-HEMBA1001184//SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP).//2.50E-32//100aa//60%/P55822  
 10 C-HEMBA1001221//AGRIN PRECURSOR.//2.50E-25//294aa//29%/P31696  
 C-HEMBA1001228//Human germline oligomeric matrix protein (COMP) mRNA, complete cds.//7.80E-286//1105bp//94%/L32137  
 C-HEMBA1001272//Homo sapiens mRNA for KIAA1171 protein, partial cds.//0//1490bp//99%/AB032997  
 C-HEMBA1001296  
 15 C-HEMBA1001297//Homo sapiens putative transcription factor CA150 mRNA, complete cds.//4.60E-276//1081bp//99%/AF017789  
 C-HEMBA1001390//Mus musculus polymerase I-transcript release factor mRNA, complete cds.//2.50E-57//464bp//82%/AF036249  
 C-HEMBA1001563  
 20 C-HEMBA1001621//PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.//3.50E-123//259aa//89%/P35414  
 C-HEMBA1001878//Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.//0//1488bp//99%/AF090988  
 C-HEMBA1001886//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.40E-148//421aa//60%/Q03923  
 25 C-HEMBA1002048//ODD-SKIPPED PROTEIN.//1.60E-55//122aa//75%/P23803  
 C-HEMBA1002131//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1//4.10E-10//140aa//30%/P24802  
 C-HEMBA1002163//HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION.//9.40E-28//309aa//30%/Q04651  
 30 C-HEMBA1002164  
 C-HEMBA1002167//Rattus norvegicus neuroligin I mRNA, complete cds.//1.30E-305//1643bp//91%/U22952  
 C-HEMBA1002178//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1).//3.70E-10//140aa//30%/P24802  
 C-HEMBA1002195//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.80E-23//221aa//31%/Q00808  
 35 C-HEMBA1002227//Homo sapiens mRNA for 80K-L protein, complete cds.//0//1324bp//98%/D10522  
 C-HEMBA1002239  
 C-HEMBA1002316//GTP-BINDING PROTEIN HFLX.//5.80E-12//196aa//29%/P25519  
 C-HEMBA1002420  
 C-HEMBA1002421//Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.//0//2097bp//99%/J04621  
 40 C-HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds.//0//1763bp//95%/U63336  
 C-HEMBA1002551//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//9.80E-08//110aa//37%/P49695  
 C-HEMBA1002767//Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.//0//1497bp//99%/AF038660  
 45 C-HEMBA1002985  
 C-HEMBA1002992//UBIQUITIN-LIKE PROTEIN DSK2.//2.00E-21//216aa//35%/P48510  
 C-HEMBA1003047//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1768bp//99%/AF034611  
 50 C-HEMBA1003072//Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.//3.30E-93//927bp//73%/U68380  
 C-HEMBA1003101//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1854bp//99%/AF049891  
 C-HEMBA1003120//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.00E-193//547aa//54%/Q99676  
 55 C-HEMBA1003230//Homo sapiens fibulin-5.//5.60E-308//1398bp//99%/AJ133490  
 C-HEMBA1003294  
 C-HEMBA1003315//Mus musculus mRNA for DNA helicase, complete cds.//6.30E-250//1426bp//88%/AB013912  
 C-HEMBA1003392//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//1721bp//

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100%//AF074264  
 C-HEMBA1003399//MVP1 PROTEIN.//2.30E-15//279aa//23%//P40959  
 C-HEMBA1003487  
 C-HEMBA1003497//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING  
 5 PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//4.00E-28//358aa//29%//Q60821  
 C-HEMBA1003530//S.scrofa mRNA for BM88 antigen.//1.20E-60//900bp//66%//X82027  
 C-HEMBA1003602//HYPOTHETICAL 29.7 KD PROTEIN CY339.02.//2.80E-21//200aa//33%//Q50658  
 C-HEMBA1003732//SFT2 PROTEIN.//1.50E-06//162aa//30%//P38166  
 C-HEMBA1003945//Homo sapiens hypothetical 43.2 Kd protein mRNA, complete cds.//8.90E-287//757bp//97%//  
 10 AF077030  
 C-HEMBA1004007  
 C-HEMBA1004067//Homo sapiens mRNA for KIAA0859 protein, complete cds.//0.00E+00//623bp//99%//  
 AB020666  
 C-HEMBA1004085  
 15 C-HEMBA1004110//Homo sapiens intersectin short form mRNA, complete cds.//0//2033bp//99%//AF064243  
 C-HEMBA1004250//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//6.40E-51//  
 277aa//35%//P33450  
 C-HEMBA1004391//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.//5.60E-20//194aa//26%//F70211  
 C-HEMBA1004444//GLYCOPROTEIN 25L PRECURSOR (GP25L).//4.60E-41//148aa//52%//P27869  
 20 C-HEMBA1004454  
 C-HEMBA1004505//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC  
 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE).//2.70E-45//239aa//43%//P53624  
 C-HEMBA1004785//MODIFIER 3 PROTEIN (M33).//1.40E-27//221aa//33%//P30658  
 C-HEMBA1004797  
 25 C-HEMBA1004952  
 C-HEMBA1004971  
 C-HEMBA1004982//TETRACYCLINE RESISTANCE PROTEIN, CLASS E (TETA(E)).//6.30E-10//149aa//26%//  
 Q07282  
 C-HEMBA1005070//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.10E-05//187aa//  
 30 29%//P17437  
 C-HEMBA1005084//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-  
 TEIN KINASE 1).//1.20E-07//102aa//37%//P18160  
 C-HEMBA1005145  
 C-HEMBA1005230//ZINC FINGER PROTEIN 140.//2.00E-17//83aa//66%//P52738  
 35 C-HEMBA1005246//HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 4 (HFH-4).//2.10E-15//  
 230aa//28%//Q92949  
 C-HEMBA1005267//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//8.40E-14//  
 187aa//33%//Q01484  
 C-HEMBA1005430  
 40 C-HEMBA1005449//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//  
 5.40E-10//224aa//24%//P13983  
 C-HEMBA1005489//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA,  
 complete cds.//8.40E-255//924bp//80%//AF127084  
 C-HEMBA1005522//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//7.70E-15//78aa//51%//P98139  
 45 C-HEMBA1005545//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0//590aa//100%//P20309  
 C-HEMBA1005698//Homo sapiens vesicle trafficking protein (SEC22C) mRNA, complete cds.//6.60E-163//  
 753bp//99%//AF039568  
 C-HEMBA1005913  
 C-HEMBA1005929//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.50E-92//1092bp//69%//X97630  
 50 C-HEMBA1005945//BRITTLE-1 PROTEIN PRECURSOR.//1.70E-29//220aa//35%//P29518  
 C-HEMBA1006016  
 C-HEMBA1006171  
 C-HEMBA1006276//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//1.70E-06//56aa//  
 57%//Q61967  
 55 C-HEMBA1006299  
 C-HEMBA1006311  
 C-HEMBA1006335  
 C-HEMBA1006357//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.//3.70E-39//136aa//52%//

O15127

C-HEMBA1006430//Human putative transmembrane protein precursor (B5) mRNA, complete cds.//2.40E-70//1108bp//65%//L38961

C-HEMBA1006482//Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//1101bp//98%//AF026852

C-HEMBA1006517

C-HEMBA1006544

C-HEMBA1006572//ODD-SKIPPED PROTEIN.//2.60E-39//85aa//83%//P23803

C-HEMBA1006658//Homo sapiens mRNA for NIK, partial cds.//0//1500bp//98%//AB013385

C-HEMBA1006707//Homo sapiens mRNA for matrilin-4, partial.//0//2003bp//99%//AJ007581

C-HEMBA1006724

C-HEMBA1006749//Homo sapiens mRNA for matrilin-4, partial.//1.40E-275//1942bp//83%//AJ007581

C-HEMBA1006770//FLOWERING TIME CONTROL PROTEIN FCA.//1.20E-33//352aa//34%//O04425

C-HEMBA1006902//Homo sapiens mRNA for matrilin-4, partial.//4.80E-275//1799bp//85%//AJ007581

C-HEMBA1006912

C-HEMBA1006916//Homo sapiens Grb14 mRNA, complete cds.//3.00E-277//1010bp//95%//L76687

C-HEMBA1006960

C-HEMBA1007013//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds.//1.10E-14//412bp//63%//AF068749

C-HEMBA1007057

C-HEMBA1007063

C-HEMBA1007226//Homo sapiens RPA-binding trans-activator (RBT1) mRNA, complete cds.//7.30E-273//1242bp//99%//AF192529

C-HEMBA1007241//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.//2.70E-14//106aa//42%//P40857

C-HEMBA1007291

C-HEMBA1007332//Homo sapiens mRNA for unr-interacting protein.//6.40E-83//266bp//98%//AJ010025

C-HEMBA1000106//CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).//1.60E-10//139aa//30%//P53996

C-HEMBA1000276

C-HEMBA1000309

C-HEMBA1000407

C-HEMBA1000447//Homo sapiens JWA protein mRNA, complete cds.//0//2059bp//99%//AF070523

C-HEMBA1000542//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.60E-232//1452bp//85%//AF084259

C-HEMBA1000567

C-HEMBA1000642

C-HEMBA1000668//Homo sapiens mRNA for KIAA0893 protein, complete cds.//0//2375bp//99%//AB020700

C-HEMBA1000679//C.familiaris mRNA for TRAM-protein.//4.10E-210//1149bp//80%//X63678

C-HEMBA1000881//Danio rerio mRNA for MINDIN2, complete cds.//1.70E-67//948bp//66%//AB006085

C-HEMBA1000905//TRANSCRIPTIONAL REPRESSOR RCO-1.//1.00E-11//311aa//27%//P78706

C-HEMBA1001026//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//5.30E-11//142aa//30%//P32802

C-HEMBA1001048//SARCALUMENIN PRECURSOR.//6.50E-18//154aa//33%//P13666

C-HEMBA1001200

C-HEMBA1001407

C-HEMBA1001530//SLS1 PROTEIN PRECURSOR.//9.80E-10//273aa//27%//Q99158

C-HEMBA1001547//Homo sapiens CGI-02 protein mRNA, complete cds.//0//2311bp//99%//AF132937

C-HEMBA1001573

C-HEMBA1001847//NEUROGENIC PROTEIN BIG BRAIN.//4.70E-06//258aa//24%//P23645

C-HEMBA1001959//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//7.30E-14//97aa//38%//P25210

C-HEMBA1001978

C-HEMBA1002039

C-HEMBA1002041//Homo sapiens transmembrane protein TENB2 (TENB2) mRNA, complete cds.//0//1746bp//99%//AF179274

C-HEMBA1002051//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//1.30E-95//454bp//99%//AF115403

C-HEMBB1002120//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE  
 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//4.90E-22//337aa//27%//P56558  
 C-HEMBB1002162//Homo sapiens genethonin 1 mRNA, complete cds.//8.30E-67//328bp//99%//AF062534  
 C-HEMBB1002228  
 5 C-HEMBB 1002245//PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR  
 (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN).//0//879aa//89%//Q62786  
 C-HEMBB1002302  
 C-HEMBB1002427//FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYL GALACTOSAMINYLTRANSFERASE (EC  
 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-AL-  
 10 PHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANS-  
 FERASE) (NAGAT).//1.80E-70//221aa//50%//P16442  
 C-HEMBB1002465//ACYL-COA DEHYDROGENASE (EC 1.3.99.-).//2.30E-53//249aa//48%//P45857  
 C-HEMBB1002661//Homo sapiens cardiovascular helix-loop-helix factor 2 (CHF2) mRNA, complete cds.//0//  
 2174bp//99%//AF176422  
 15 C-HEMBB1002663  
 C-HEMBB1002693  
 C-MAMMA1000046  
 C-MAMMA1000102//APOLIPOPROTEIN L PRECURSOR (APO-L).//1.40E-21//221aa//35%//O14791  
 C-MAMMA1000106  
 20 C-MAMMA1000118  
 C-MAMMA1000141  
 C-MAMMA1000204//Homo sapiens dysferlin mRNA, complete cds.//0//2028bp//99%//AF075575  
 C-MAMMA1000226  
 C-MAMMA1000403//Homo sapiens CDK4-binding protein p34SEI1 (SEI1) mRNA, complete cds.//1.20E-255//  
 25 1165bp//99%//AF117959  
 C-MAMMA1000449  
 C-MAMMA1000457//Human NADH-cytochrome b5 reductase mRNA, 3' end.//9.50E-79//829bp//71%//M16462  
 C-MAMMA1000473//HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.//5.10E-45//  
 299aa//34%//P47088  
 30 C-MAMMA1000496//MIC1 PROTEIN.//3.00E-25//202aa//33%//P53258  
 C-MAMMA1000528  
 C-MAMMA1000591//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-  
 UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOS-  
 AMINYLTRANSFERASE) (GALNAC-T1).//1.20E-115//515aa//49%//Q07537  
 35 C-MAMMA10006141//Homo sapiens pseudouridine synthase I (PUS1) mRNA, partial cds.//2.10E-302//1370bp//  
 99%//AF116238  
 C-MAMMA1000652  
 C-MAMMA1000681//PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.//9.40E-82//311aa//52%//O08530  
 C-MAMMA1000706  
 40 C-MAMMA1000788//Bos taurus P14 (p14) mRNA, complete cds.//3.90E-85//502bp//89%//AF037349  
 C-MAMMA1000810  
 C-MAMMA1000814  
 C-MAMMA1000881//Homo sapiens protein kinase (SGK3) mRNA, complete cds.//0//1292bp//100%//AF169035  
 C-MAMMA1000986  
 45 C-MAMMA1000994//Homo sapiens ISLR(immunoglobulin superfamily containing leucine-rich repeat) mRNA,  
 complete cds, alternatively spliced transcript ISLR-2.//0//2211bp//99%//AB024536  
 C-MAMMA1001043//MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1)  
 (CD48).//2.90E-12//239aa//28%//P10252  
 C-MAMMA1001066  
 50 C-MAMMA1001094//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//  
 1394bp//93%//U71267  
 C-MAMMA1001141  
 C-MAMMA1001150//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//7.50E-304//587aa//68%//Q15139  
 C-MAMMA1001237//MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).//7.70E-64//196aa//41%//P53988  
 55 C-MAMMA1001284  
 C-MAMMA1001310//HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-  
 REC114 INTERGENIC REGION.//1.50E-67//441aa//37%//Q04225  
 C-MAMMA1001344

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C-MAMMA1001418//HYPOTHETICAL PROTEIN HI0519.//6.90E-27//181aa//38%/P44742  
 C-MAMMA1001532//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.60E-126//319aa//56%/P51523  
 C-MAMMA1001609//MYOSIN II HEAVY CHAIN, NON MUSCLE.//1.50E-26//204aa//38%/P05659  
 5 C-MAMMA1001615//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.80E-11//90aa//42%/Q13562  
 C-MAMMA1001623  
 C-MAMMA1001634  
 C-MAMMA1001893  
 C-MAMMA1001901  
 10 C-MAMMA1001957  
 C-MAMMA1001978//Cimex lectularius apyrase (APY) mRNA, complete cds.//6.70E-19//988bp//56%/AF085499  
 C-MAMMA1002070//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).//1.10E-07//103aa//33%/Q01177  
 C-MAMMA1002080//RAS-RELATED PROTEIN RAB-13.//1.80E-29//208aa//37%/P51153  
 C-MAMMA1002087  
 15 C-MAMMA1002091//Homo sapiens CD39L2 (CD39L2) mRNA, complete cds.//0//2564bp//99%/AF039916  
 C-MAMMA1002095//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE).//3.70E-222//867aa//52%/O43108  
 C-MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR.//2.50E-97//464aa//45%/Q92338  
 C-MAMMA1002142//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-  
 20 TEIN KINASE 1).//9.80E-17//146aa//35%/P18160  
 C-MAMMA1002165//Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.//4.80E-60//382bp//89%/AF100780  
 C-MAMMA1002205//Homo sapiens mRNA; cDNA DKFZp586C091 (from clone DKFZp586C091).//2.00E-81//308bp//81%/AL050119  
 25 C-MAMMA1002224  
 C-MAMMA1002234//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//0//627aa//96%/Q00004  
 C-MAMMA1002586//Homo sapiens alpha 1,2-mannosidase mRNA, complete cds.//0//2228bp//99%/AF148509  
 C-MAMMA1002633  
 C-MAMMA1003126//SARCALUMENIN PRECURSOR.//1.10E-51//388aa//32%/P13666  
 30 C-NT2RM1000462//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//8.60E-14//104aa//40%/P15287  
 C-NT2RM1000542//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.40E-103//566aa//43%/P48982  
 C-NT2RM1000580//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%/P43636  
 35 C-NT2RM1000789//Homo sapiens mRNA for hTCF-4.//2.80E-221//757bp//99%/Y11306  
 C-NT2RM1000855//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%/AF084458  
 C-NT2RM1000858//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//2.10E-98//1035bp//70%/S70011  
 C-NT2RM1000899//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//1.10E-54//182aa//39%/P23500  
 C-NT2RM2000241  
 40 C-NT2RM2000306//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//4.50E-130//362aa//68%/P91917  
 C-NT2RM2000410  
 C-NT2RM2000423//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.80E-38//308aa//35%/P48982  
 C-NT2RM2000497//CHL1 PROTEIN.//9.90E-24//296aa//29%/P22516  
 45 C-NT2RM2000514//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//4.40E-304//1374bp//99%/AF174601  
 C-NT2RM2000565//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//4.40E-304//394aa//43%/Q09782  
 C-NT2RM2000582//Homo sapiens mRNA for KIAA1053 protein, partial cds.//0//2666bp//99%/AB028976  
 50 C-NT2RM2000589//Bos taurus myosin X, complete cds.//0//4376bp//84%/U55042  
 C-NT2RM2000622//Mus musculus F-box protein FBL10 mRNA, partial cds.//3.00E-203//915bp//91%/AF176524  
 C-NT2RM2000632//EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).//6.40E-62//183aa//47%/Q03468  
 C-NT2RM2000773//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//3.00E-289//1092bp//99%/AB017335  
 55 C-NT2RM2001126//Homo sapiens mRNA for multi PDZ domain protein.//0//1600bp//99%/AJ001319  
 C-NT2RM2001558//Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds.//0//2398bp//99%/AF093408



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C-NT2RM2001626//FLIGHTLESS-I PROTEIN HOMOLOG.//4.30E-19//362aa//26%//P34268  
 C-NT2RM2001643  
 C-NT2RM2001738//SOF1 PROTEIN.//3.00E-110//325aa//47%//P33750  
 C-NT2RM2001792//Homo sapiens angiopoietin-related protein-2 mRNA, complete cds.//7.10E-149//995bp//86%//  
 5 AF125175  
 C-NT2RM2001818//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//4.30E-  
 11//488aa//26%//P23253  
 C-NT2RM2001902//Homo sapiens mRNA for PAK4 protein.//5.40E-216//988bp//99%//AJ011855  
 C-NT2RM2001939//Human G protein-coupled receptor GPR-NGA gene, complete cds.//0//1559bp//98%//U55312  
 10 C-NT2RM2001941//MUSCARINIC ACETYLCHOLINE RECEPTOR M1.//7.40E-38//193aa//34%//P08482  
 C-NT2RM4000100//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//0//2678bp//99%//  
 AF175966  
 C-NT2RM4000115  
 C-NT2RM4000198//BUTYROPHILIN PRECURSOR (BT).//5.10E-12//162aa//33%//Q13410  
 15 C-NT2RM4000284//Human IgG Fc receptor hFcRn mRNA, complete cds.//1.30E-257//603bp//96%//U12255  
 C-NT2RM4000295  
 C-NT2RM4000326//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//9.00E-100//434aa//43%//  
 P51523  
 C-NT2RM4000417//SYNAPTOTAGMIN II.//2.70E-23//293aa//30%//P46097  
 20 C-NT2RM4000444//ANTIGEN PEPTIDE TRANSPORTER 1 (APT1).//1.70E-112//493aa//44%//P36370  
 C-NT2RM4000587  
 C-NT2RM4000593//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//3.90E-27//576aa//  
 24%//Q10297  
 C-NT2RM4000648//K-GLYPICAN PRECURSOR.//4.00E-193//531aa//66%//P51655  
 25 C-NT2RM4000761//CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).//2.50E-245//306aa//91%//  
 P00395  
 C-NT2RM4000965//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//9.00E-44//  
 520aa//29%//O60100  
 C-NT2RM4000997//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//1.80E-10//  
 30 189aa//30%//P25234  
 C-NT2RM4001321  
 C-NT2RM4001325//CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST).//2.90E-48//343aa//34%//  
 Q92179  
 C-NT2RM4001377//R.norvegicus LL5 mRNA.//8.50E-236//990bp//87%//X74226  
 35 C-NT2RM4001735  
 C-NT2RM4001768//Homo sapiens CGI-82 protein mRNA, complete cds.//0//1925bp//99%//AF151840  
 C-NT2RM4001843//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//6.20E-33//263aa//38%//  
 P48982  
 C-NT2RM4002352//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.//0//  
 40 2184bp//99%//AB009462  
 C-NT2RP1000002  
 C-NT2RP1000050  
 C-NT2RP1000181//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//3.30E-121//1394bp//69%//  
 AF126799  
 45 C-NT2RP1000239  
 C-NT2RP1000261//ORM1 PROTEIN.//2.40E-17//137aa//35%//P53224  
 C-NT2RP1000271//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//4.70E-199//547aa//  
 66%//Q03923  
 C-NT2RP1000300//Human transporter protein (g17) mRNA, complete cds.//3.80E-26//758bp//62%//U49082  
 50 C-NT2RP1000325//H.sapiens gene for phosphate carrier.//0//439bp//98%//X77337  
 C-NT2RP1000448  
 C-NT2RP1000465//UBIQUITIN-LIKE PROTEIN SMT3.//5.10E-07//81aa//33%//P55857  
 C-NT2RP1000468//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN  
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.00E-13//97aa//38%//P25210  
 55 C-NT2RP1000551//Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds.//0//1761bp//  
 99%//U09585  
 C-NT2RP1000579//Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds.//0//  
 1951bp//94%//L21936

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C-NT2RP1000613//CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).//  
 3.40E-52//304aa//40%//P08060  
 C-NT2RP1000679  
 C-NT2RP1000740  
 5 C-NT2RP1000903  
 C-NT2RP1000981//CELL SURFACE A33 ANTIGEN PRECURSOR.//3.60E-14//286aa//27%//Q99795  
 C-NT2RP1001004//F-SPONDIN PRECURSOR.//9.20E-43//322aa//35%//P35446  
 C-NT2RP1001020//SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTI-  
 VATED KINASE 3) (CDC42/RAC EFFECTOR KINASE PAK-B).//9.70E-22//227aa//31%//Q61036  
 10 C-NT2RP1001031//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//3.40E-42//285aa//35%//Q00808  
 C-NT2RP1001563//TESTIS-SPECIFIC PROTEIN TPX-1 PRECURSOR (AUTOANTIGEN 1) (25 KD ACROSOM-  
 AL AUTOANTIGEN) (AA1).//9.70E-19//201aa//31%//Q60477  
 C-NT2RP2000092//ZINC FINGER PROTEIN 136.//1.90E-117//419aa//54%//P52737  
 C-NT2RP2000178//MITOCHONDRIAL ION PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//2.40E-192//  
 15 778aa//48%//P93647  
 C-NT2RP2000240  
 C-NT2RP2000394//Gallus gallus p52 pro-apototic protein mRNA, complete cds.//1.60E-90//956bp//70%//  
 AF029071  
 C-NT2RP2000447//GOLGIN-95.//2.80E-33//99aa//66%//Q08379  
 20 C-NT2RP2000479  
 C-NT2RP2000514//Homo sapiens roundabout 2 (robo2) mRNA, partial cds.//3.00E-185//855bp//99%//AF040991  
 C-NT2RP2000533//Homo sapiens cornichon protein mRNA, complete cds.//1.30E-290//1324bp//99%//AF070654  
 C-NT2RP2000610//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN  
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//1.50E-13//97aa//38%//P25210  
 25 C-NT2RP2000616//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//  
 4.10E-12//323aa//30%//P13983  
 C-NT2RP2000649//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2847bp//99%//AB016068  
 C-NT2RP2000663  
 C-NT2RP2000694//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2278bp//99%//AJ012159  
 30 C-NT2RP2000712//ZINC FINGER PROTEIN 135.//3.70E-87//296aa//53%//P52742  
 C-NT2RP2000739//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.50E-73//387aa//37%//  
 P51522  
 C-NT2RP2000818//Homo sapiens xenotropic and polytropic murine leukemia virus receptor (X3) mRNA, complete  
 cds.//0//2724bp//99%//AF089744  
 35 C-NT2RP2000903//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2276bp//100%//AJ012159  
 C-NT2RP2001200//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1539bp//100%//AB014576  
 C-NT2RP2001223//MYOTUBULARIN-RELATED PROTEIN 3 (FRAGMENT).//3.30E-05//76aa//39%//Q13615  
 C-NT2RP2001276//NPDC-1 PROTEIN PRECURSOR.//3.00E-133//331aa//77%//Q64322  
 C-NT2RP2001388//TRNA-SPLICING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-  
 40 NUCLEASE).//5.90E-13//157aa//33%//P16658  
 C-NT2RP2001469//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%//Q00808  
 C-NT2RP2001480//Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.//0//2547bp//99%//L38969  
 C-NT2RP2001495//Human transporter protein (g17) mRNA, complete cds.//2.20E-65//641bp//65%//U49082  
 C-NT2RP2001514//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//1.20E-133//429aa//  
 45 41%//P39986  
 C-NT2RP2001529//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2079bp//99%//AB007144  
 C-NT2RP2001538//Mus musculus mSin3A (sin3A) mRNA, complete cds.//7.60E-272//1480bp//84%//U22394  
 C-NT2RP2001562//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//0//1899bp//98%//AF058922  
 C-NT2RP2001662//HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN).//1.80E-49//  
 50 94aa//81%//Q90655  
 C-NT2RP2001755//Rattus norvegicus f-spondin mRNA, complete cds.//0//2974bp//86%//M88469  
 C-NT2RP2001769//SERINE/THREONINE-PROTEIN KINASE ORB6 (EC 2.7.1.-).//9.10E-47//185aa//44%//  
 O13310  
 C-NT2RP2001817//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds.//0//3092bp//99%//AF083106  
 55 C-NT2RP2001878  
 C-NT2RP2001903//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEU-  
 TRAL PROTEINASE) (CANP) (MU/M-TYPE).//3.80E-58//475aa//34%//P00789  
 C-NT2RP2001915

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C-NT2RP2001921  
 C-NT2RP2001948//HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2)//1.40E-08//191aa//27%//P53686  
 C-NT2RP2001956//ORM1 PROTEIN//3.90E-19//137aa//37%//P53224  
 C-NT2RP2002015  
 5 C-NT2RP2002063//GNS1 PROTEIN//3.60E-18//231aa//33%//P25358  
 C-NT2RP2002188//Rattus norvegicus neuroligin 3 mRNA, complete cds.//2.50E-226//1284bp//89%//U41663  
 C-NT2RP2002232//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I//1.90E-93//420aa//43%//Q09782  
 10 C-NT2RP2002304//Homo sapiens histone acetyltransferase MORF mRNA, complete cds.//0//2737bp//99%//AF113514  
 C-NT2RP2002409  
 C-NT2RP2002510  
 C-NT2RP2002527//CYTOCHROME B5//1.30E-11//92aa//38%//P40312  
 15 C-NT2RP2002533//Homo sapiens alpha 2 delta calcium channel subunit isoform I mRNA, complete cds.//0//2365bp//99%//AF042792  
 C-NT2RP2002564//Human zinc-finger protein C2H2-150 mRNA, complete cds.//0//2237bp//99%//U38864  
 C-NT2RP2002674//SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CYTOSOLIC EPOXIDE HYDROLASE) (CEH)//5.50E-38//201aa//39%//P34913  
 C-NT2RP2002721//REGULATORY PROTEIN UHPC//1.60E-23//153aa//30%//P27669  
 20 C-NT2RP2002824//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT)//3.50E-63//404aa//33%//P32802  
 C-NT2RP2002942//Homo sapiens mRNA for KIAA0806 protein, complete cds.//0//2090bp//99%//AB018349  
 25 C-NT2RP2002974//HOMEBOX PROTEIN SIXS (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HOMOLOG) (FRAGMENT)//8.20E-241//555aa//84%//P70178  
 C-NT2RP2002976//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION//1.30E-20//99aa//47%//P38800  
 C-NT2RP2003042//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT)//2.10E-109//385aa//52%//P53760  
 30 C-NT2RP2003138//5'-TG-3' INTERACTING FACTOR (HOMEBOX PROTEIN TGIF)//2.10E-08//104aa//46%//P70284  
 C-NT2RP2003179//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-)//2.60E-67//256aa//49%//Q05512  
 35 C-NT2RP2003210//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//9.80E-272//1265bp//98%//AF055899  
 C-NT2RP2003302//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.//0//2891bp//99%//AB021644  
 C-NT2RP2003369//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)//5.90E-20//204aa//34%//Q15404  
 40 C-NT2RP2003383//Homo sapiens mRNA for KIAA0458 protein, complete cds.//0//2565bp//99%//AB007927  
 C-NT2RP2003390//Homo sapiens mRNA for SEC63 protein.//0//2629bp//99%//AJ011779  
 C-NT2RP2003469//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER)//1.10E-45//324aa//29%//P37021  
 45 C-NT2RP2003545//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//5.40E-48//578bp//71%//AF024636  
 C-NT2RP2003593  
 C-NT2RP2003599  
 C-NT2RP2003655//HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC//4.80E-15//93aa//47%//P38869  
 50 C-NT2RP2003664//Homo sapiens mRNA for leptin receptor gene-related protein.//1.90E-237//1081bp//99%//Y12670  
 C-NT2RP2003931  
 C-NT2RP2003940//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//7.00E-111//401aa//43%//P28160  
 55 C-NT2RP2003950//Homo sapiens clone 24778 unknown mRNA.//0//1545bp//99%//AF070572  
 C-NT2RP2004069  
 C-NT2RP2004108//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//3.30E-171//474aa//62%//P16415  
 C-NT2RP2004141

- C-NT2RP2004179  
 C-NT2RP2004205//BUTYROPHILIN PRECURSOR (BT)//1.60E-21//276aa//32%//Q62556  
 C-NT2RP2004447  
 5 C-NT2RP2004495//Human transporter protein (g17) mRNA, complete cds.//9.80E-64//642bp//64%//L149082  
 C-NT2RP2004524  
 C-NT2RP2004556  
 C-NT2RP2004606//Human fibroblast collagenase inhibitor mRNA, complete cds.//2.10E-166//768bp//99%//M12670  
 10 C-NT2RP2004648//Mouse beta-galactosidase (BGAL) gene, complete cds.//1.20E-33//1136bp//59%//M57734  
 C-NT2RP2004670//Rattus norvegicus vesicle-associated calmodulin-binding protein mRNA, complete cds.//0//1250bp//86%//L22557  
 C-NT2RP2004794//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.//2.70E-09//203aa//26%//P40857  
 C-NT2RP2004837  
 15 C-NT2RP2004847//ZINC FINGER PROTEIN 135.//8.00E-35//193aa//40%//P52742  
 C-NT2RP2005027//GLUCOSE TRANSPORTER TYPE 3, BRAIN.//6.20E-67//130aa//100%//P11169  
 C-NT2RP2005069//Rat vacuolar protein sorting homolog vps33b mRNA, complete cds.//0//1792bp//87%//U35245  
 C-NT2RP2005163  
 20 C-NT2RP2005181//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//5.30E-315//2126bp//81%//U70859  
 C-NT2RP2005247//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//5.00E-53//296aa//37%//Q62158  
 C-NT2RP2005378//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).//6.30E-28//183aa//47%//P10496  
 25 C-NT2RP2005391//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%//AJ242978  
 C-NT2RP2005425//Homo sapiens mRNA for AKAP450 protein.//0//4341bp//99%//AJ131693  
 C-NT2RP2005463//PROTEIN PTM1 PRECURSOR.//7.40E-15//284aa//28%//P32857  
 C-NT2RP2005514  
 30 C-NT2RP2005535//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.90E-172//489aa//62%//Q03923  
 C-NT2RP2005541//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//4.70E-24//78aa//51%//P15586  
 C-NT2RP2005597//Homo sapiens protein O-mannosyl-transferase 1 (POMT1) mRNA, complete cds.//0//1821bp//97%//AF095136  
 35 C-NT2RP2005632  
 C-NT2RP2005666  
 C-NT2RP2005774//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.//6.90E-224//1461bp//72%//AB021644  
 40 C-NT2RP2005878//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//3.60E-55//238aa//50%//O57314  
 C-NT2RP2005883//DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-HYDROXYLASE) (DBH).//6.70E-72//512aa//34%//P15101  
 C-NT2RP2005887  
 45 C-NT2RP2005941//Human paired box gene (PAX6) homologue, complete cds.//1.40E-308//1396bp//99%//M93650  
 C-NT2RP2005994//HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.//3.50E-35//144aa//47%//P49191  
 C-NT2RP2006004//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//3.00E-26//227aa//36%//Q06828  
 50 C-NT2RP2006042//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.40E-15//501aa//25%//P08640  
 C-NT2RP2006092//Homo sapiens mRNA for Fe65L2, complete cds.//0//1156bp//99%//AB018247  
 C-NT2RP2006099  
 55 C-NT2RP2006134  
 C-NT2RP2006269//DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 2 (EC 2.4.1.109).//2.30E-78//679aa//32%//P31382  
 C-NT2RP2006512//GNS1 PROTEIN.//2.00E-21//290aa//29%//P25358

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C-NT2RP2006580//Homo sapiens transitional epithelia response protein (TERE1) mRNA, complete cds.//0//1483bp//99%//AF117064

C-NT2RP3000011//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.00E-14//320aa//24%//Q00808

5 C-NT2RP3000022//Rat heart mRNA serine/threonine protein kinase, complete cds.//4.80E-203//1496bp//78%//D26178

C-NT2RP3000059//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//3.70E-12//133aa//32%//Q01485

C-NT2RP3000063//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//5.00E-29//596aa//30%//P19246

10 C-NT2RP3000125//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//6.30E-08//70aa//41%//P29375

C-NT2RP3000148//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.10E-106//350aa//47%//P51523

C-NT2RP3000169//Homo sapiens MRS1 mRNA, complete cds.//0//1519bp//97%//AF093239

15 C-NT2RP3000171//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene).//4.40E-99//571bp//89%//Z97207

C-NT2RP3000172//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).//1.30E-80//359aa//44%//Q14012

C-NT2RP3000201//Homo sapiens HPK/GCK-like kinase HGK mRNA, complete cds.//1.30E-270//1231bp//99%//AF096300

20 C-NT2RP3000232//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.40E-130//693aa//41%//Q99676

C-NT2RP3000304//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//2895bp//99%//AF074264

C-NT2RP3000378//PAIRED AMPHIPATHIC HELIX PROTEIN.//4.20E-39//186aa//36%//P22579

C-NT2RP3000427

25 C-NT2RP3000436//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.20E-27//90aa//42%//P38660

C-NT2RP3000444

C-NT2RP3000460//Canis familiaris sec61 homologue mRNA, complete cds.//1.80E-198//643bp//89%//M96629

C-NT2RP3000481//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//0//2623bp//100%//AF098799

30 C-NT2RP3000616//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//5.20E-26//227aa//36%//Q06828

C-NT2RP3000645

C-NT2RP3000652//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.90E-153//441aa//62%//P28160

C-NT2RP3000676//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.10E-15//220aa//27%//Q03829

35 C-NT2RP3000677//DNA BINDING PROTEIN RFX2.//3.60E-56//233aa//41%//P48378

C-NT2RP3000721//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.//1.10E-22//171aa//36%//P38800

C-NT2RP3000789//Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA, complete cds.//0//1458bp//100%//AF117106

40 C-NT2RP3000818

C-NT2RP3000820//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//1.90E-30//269aa//33%//P49695

C-NT2RP3000838//TRICHOHYALIN.//9.80E-11//491aa//26%//Q07283

C-NT2RP3000871

45 C-NT2RP3000907//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//2.20E-134//296aa//42%//P39986

C-NT2RP3000921//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).//4.00E-21//316aa//29%//P43146

C-NT2RP3001012//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//2906bp//98%//AB020636

50 C-NT2RP3001044

C-NT2RP3001061//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//3591bp//99%//AB020660

C-NT2RP3001159//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2558bp//99%//AL050118

55 C-NT2RP3001170//Mus musculus activity-dependent neuroprotective protein (Adnp) mRNA, complete cds.//4.80E-240//850bp//88%//AF068198

C-NT2RP3001195//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).//4.70E-48//339aa//29%//P37021

C-NT2RP3001240//Canis familiaris sec61 homologue mRNA, complete cds.//1.20E-301//1141bp//89%//M96629

C-NT2RP3001271//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//  
 2.60E-09//34aa//22%//P52178  
 C-NT2RP3001322//PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETIC-  
 ULUM CA2+-ATPASE).//1.70E-21//220aa//30%//P39524  
 5 C-NT2RP3001388//SYNAPTOTAGMIN IV.//2.00E-118//430aa//54%//P50232  
 C-NT2RP3001542//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-  
 TEIN).//4.70E-11//132aa//37%//Q13829  
 C-NT2RP3001560//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//  
 0//2468bp//99%//AF037339  
 10 C-NT2RP3001592//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC  
 2.1.1.32).//1.30E-18//279aa//27%//P15565  
 C-NT2RP3001650//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1)//2.20E-22//  
 107aa//42%//P98063  
 C-NT2RP3001685//PRPE PROTEIN.//1.00E-68//382aa//41%//P77495  
 15 C-NT2RP3001738//CYTOCHROME B5.//1.30E-11//133aa//33%//P00169  
 C-NT2RP3001754  
 C-NT2RP3001858  
 C-NT2RP3001976//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.90E-143//379aa//55%//  
 P51523  
 20 C-NT2RP3002015//Homo sapiens CGI-71 protein mRNA, complete cds.//0//1991bp//99%//AF151829  
 C-NT2RP3002160//HISTO-BLOOD GROUP ABO SYSTEM TRANSFERASE (NAGAT) [INCLUDES: GLYCO-  
 PROTEIN-FUCOSYLGALACTOSIDE ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.40)  
 (FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE) (HISTO-BLOOD GROUP  
 A TRANSFERASE) (A TRANSFERASE); GLYCOPROTEIN-FUCOSYLGALACTOSIDE ALPHA- GALACTOSYL-  
 25 TRANSFERASE (EC 2.4.1.37) (FUCOSYLGLYCOPROTEIN 3-ALPHA- GALACTOSYLTRANSFERASE) (HISTO-  
 BLOOD GROUP B TRANSFERASE) (B TRANSFERASE)].//3.50E-72//231aa//49%//P16442  
 C-NT2RP3002281//Homo sapiens mRNA for KIAA0765 protein, partial cds.//0//2286bp//99%//AB018308  
 C-NT2RP3002286//Homo sapiens candidate tumor suppressor protein DICE1 mRNA, complete cds.//0//2719bp//  
 99%//AF097645  
 30 C-NT2RP3002311//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//9.80E-103//547aa//  
 43%//P48982  
 C-NT2RP3002324  
 C-NT2RP3002342//Human transporter protein (g17) mRNA, complete cds.//1.70E-65//641bp//65%//U49082  
 C-NT2RP3002353  
 35 C-NT2RP3002409//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2404bp//99%//AB018262  
 C-NT2RP3002411//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//  
 AF078850  
 C-NT2RP3002448  
 C-NT2RP3002571//Bos taurus mRNA for lyncein.//7.30E-169//1115bp//84%//Y17923  
 40 C-NT2RP3002664  
 C-NT2RP3002721//CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).//5.80E-249//466aa//  
 98%//O75390  
 C-NT2RP3002737//Homo sapiens voltage-gated potassium channel KCNQ4 (KCNQ4) mRNA, complete cds.//0//  
 1552bp//99%//AF105202  
 45 C-NT2RP3002738//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds.//2.20E-47//763bp//  
 65%//L43821  
 C-NT2RP3002790  
 C-NT2RP3002836//Homo sapiens mRNA for KIAA0463 protein, partial cds.//0//1617bp//99%//AB007932  
 C-NT2RP3002887  
 50 C-NT2RP3002900//Homo sapiens CGI-109 protein mRNA, complete cds.//8.70E-298//1321bp//92%//AF151867  
 C-NT2RP3002958//TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.//  
 8.00E-08//197aa//26%//P19814  
 C-NT2RP3002983  
 C-NT2RP3003000//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds.//0//3160bp//  
 96%//AF051946  
 55 C-NT2RP3003076  
 C-NT2RP3003354//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.//5.10E-55//208aa//51%//  
 O35609

C-NT2RP3003448  
 C-NT2RP3003469  
 C-NT2RP3003473//Homo sapiens CGI-55 protein mRNA, complete cds.//5.50E-275//1309bp//98%//AF151813  
 C-NT2RP3003527//Homo sapiens mRNA for protein kinase Dyrk1B.//0//2483bp//99%//Y17999  
 5 C-NT2RP3003532//OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).//4.40E-139//263aa//99%//P41217  
 C-NT2RP3003535//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//8.80E-18//368aa//25%//P56558  
 C-NT2RP3003559  
 10 C-NT2RP3003614  
 C-NT2RP3003729//HYPOTHETICAL 42.1 KD PROTEIN IN SNZ1-YPK2 INTERGENIC REGION.//5.80E-17//204aa//30%//Q03151  
 C-NT2RP3003849//PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)). PKC1.//1.20E-13//126aa//34%//P05130  
 15 C-NT2RP3003874//Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c.//0//2160bp//98%//AJ001381  
 C-NT2RP3003963  
 C-NT2RP3004000  
 C-NT2RP3004025  
 20 C-NT2RP3004067//Homo sapiens mRNA for NESCA, complete cds.//0//1962bp//99%//AB026894  
 C-NT2RP3004075  
 C-NT2RP3004083  
 C-NT2RP3004090//GOLIATH PROTEIN (G1 PROTEIN).//9.00E-33//179aa//47%//Q06003  
 C-NT2RP3004119//PEREGRIN (BR140 PROTEIN).//7.30E-39//227aa//43%//P55201  
 25 C-NT2RP3004130//CELL SURFACE ANTIGEN 114/A10 PRECURSOR.//8.10E-06//71aa//42%//P19467  
 C-NT2RP3004133//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.50E-48//198aa//37%//P43636  
 C-NT2RP3004202  
 C-NT2RP3004294//Xenopus laevis ER1 mRNA, complete cds.//1.20E-71//335bp//79%//AF015454  
 C-NT2RP3004309//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2584bp//99%//AL050118  
 30 C-NT2RP3004321  
 C-NT2RP3004345//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32).//3.90E-18//279aa//27%//P15565  
 C-NT2RP3004355  
 35 C-NT2RP3004374  
 C-NT2RP3004406//HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.//3.20E-15//165aa//33%//P40544  
 C-NT2RP3004481//BUTYROPHILIN PRECURSOR (BT).//8.50E-22//276aa//32%//Q62556  
 C-NT2RP3004552//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTI-GEN).//8.50E-24//263aa//33%//P17927  
 40 C-NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds.//0//2181bp//96%//U11292  
 C-NT2RP3004625//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1339bp//99%//AF082516  
 C-NT2RP3004640//Bos taurus tuftelin mRNA, complete cds.//0//1204bp//88%//AF105228  
 45 C-NT2RP3004647//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.00E-15//220aa//27%//Q03829  
 C-NT2RP4000108//Human gene for neurofilament subunit NF-L.//0//1998bp//99%//X05608  
 C-NT2RP4000634//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//0//1501bp//98%//AF111105  
 C-NT2RP4000962//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//2.60E-18//225aa//32%//P08458  
 50 C-NT2RP4001001//Homo sapiens clone 24856 mRNA sequence, complete cds.//3.90E-301//1374bp//99%//AF131856  
 C-NT2RP4001009//Homo sapiens mRNA for farnesylated-proteins converting enzyme 1.//0//2965bp//99%//Y13834  
 C-NT2RP4001467//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2140bp//99%//X55740  
 55 C-NT2RP4001877//Homo sapiens ribonucleoprotein RBM8 (RBM8) mRNA, complete cds.//0//2770bp//99%//AF127761  
 C-NT2RP4001879  
 C-NT2RP4002187//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2373bp//99%//

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AF078850  
 C-NT2RP4002451  
 C-NT2RP4002715  
 C-NT2RP4002750//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds//1.00E-310//  
 5 2084bp//81%//U70859  
 C-OVARC1000003//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete  
 cds//4.30E-220//1158bp//94%//AF111856  
 C-OVARC1000090  
 C-OVARC1000105//UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 10 LIGASE) (UBIQUITIN CARRIER PROTEIN)//4.20E-47//171aa//56%//P33296  
 C-OVARC1000137  
 C-OVARC1000208//Human calcium-dependent group X phospholipase A2 mRNA, complete cds//1.50E-61//  
 365bp//90%//U95301  
 C-OVARC1000255//H.sapiens syk mRNA for protein-tyrosine kinase//0//1525bp//97%//Z29630  
 15 C-OVARC1000275//DESMOPLAKIN I AND II (DPI AND DPII) (FRAGMENT)//9.90E-16//352aa//23%//P15924  
 C-OVARC1000298  
 C-OVARC1000307//HYPOTHETICAL 29.7 KD PROTEIN CY339.02//3.00E-19//194aa//35%//Q50658  
 C-OVARC1000313//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1)//3.00E-24//353aa//  
 20 27%//Q12730  
 C-OVARC1000331//GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCT-  
 ASE)//9.40E-44//106aa//59%//P36959  
 C-OVARC1000410//Homo sapiens angiopoietin Y1 mRNA, complete cds//2.10E-63//744bp//69%//AF107253  
 C-OVARC1000439//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III//1.40E-  
 33//143aa//53%//P34280  
 25 C-OVARC1000467  
 C-OVARC1000529//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-)//1.40E-23//  
 165aa//39%//P34244  
 C-OVARC1000553//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLE-  
 CULE) (THAM)//1.30E-23//169aa//40%//P28843  
 30 C-OVARC1000775  
 C-OVARC1000811//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT)//6.40E-13//115aa//34%//Q01177  
 C-OVARC1000853  
 C-OVARC1000873//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLU-  
 COSAMINE-6-SULFATASE)//1.00E-09//83aa//40%//P50426  
 35 C-OVARC1000916//H.sapiens PISSLRE mRNA//7.30E-280//1117bp//95%//X78342  
 C-OVARC1000956//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG  
 PROTEIN)//2.20E-09//250aa//28%//P17437  
 C-OVARC1000995  
 C-OVARC1001030//Homo sapiens mRNA for KIAA0886 protein, complete cds//0//907bp//99%//AB020693  
 40 C-OVARC1001049//TRANSCRIPTION FACTOR HES-1 (C-HAIRY1)//7.50E-14//96aa//36%//O57337  
 C-OVARC1001086//Homo sapiens cyclin T2a mRNA, complete cds//0//1593bp//98%//AF048731  
 C-OVARC1001132//GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9)(TCF-  
 9)//2.30E-44//268aa//36%//P16383  
 45 C-OVARC1001163//HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I//2.30E-20//152aa//  
 30%//Q09906  
 C-OVARC1001222  
 C-OVARC1001260  
 C-OVARC1001336//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete  
 cds//0//1435bp//99%//AF111856  
 50 C-OVARC1001338//AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 (EC 2.7.1.-)//8.80E-30//  
 125aa//40%//P53104  
 C-OVARC1001569//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-)//1.50E-22//  
 164aa//39%//P34244  
 55 C-OVARC1001570//Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete cds//0//1792bp//  
 100%//AF190725  
 C-OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds//0//1766bp//99%//  
 AF126062  
 C-OVARC1001607//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds//0//



- 1836bp//96%//U15128  
 C-OVARC1001725//Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.//0//  
 1624bp//99%//AF064800  
 C-OVARC1001727
- 5 C-OVARC1001807//Human TR3 orphan receptor mRNA, complete cds.//1.10E-243//1145bp//98%//L13740  
 C-OVARC1001833//CIS-GOLGI MATRIX PROTEIN GM130.//6.60E-136//363aa//76%//Q62839  
 C-OVARC1001952//TRICHOHYALIN.//3.30E-16//487aa//27%//Q07283  
 C-OVARC1001991//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID).//8.30E-06//114aa//  
 35%//Q01956
- 10 C-OVARC1002058//Human 18S rRNA gene, complete.//1.50E-164//921bp//91%//M10098  
 C-OVARC1002178  
 C-PLACE1000033//VON WILLEBRAND FACTOR PRECURSOR.//3.80E-17//190aa//28%//Q28295  
 C-PLACE1000231//Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds.//  
 2.70E-101//947bp//74%//AF037272
- 15 C-PLACE1000258//ZINC FINGER. PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.70E-55//431aa//  
 35%//Q05481  
 C-PLACE1000442//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//1.00E-88//213aa//67%//P16415  
 C-PLACE1000560  
 C-PLACE1000740//Mus musculus (Notch2) mRNA, complete cds.//5.60E-122//893bp//81%//M93661
- 20 C-PLACE1000907//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.30E-204//396aa//85%//  
 P51522  
 C-PLACE1000912  
 C-PLACE1000914//Homo sapiens PB39 mRNA, complete cds.//7.50E-88//500bp//69%//AF045584  
 C-PLACE1000927//HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X.//6.30E-21//123aa//  
 37%//Q11079
- 25 C-PLACE1000986//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//2055bp//  
 99%//AL117450  
 C-PLACE1001016//SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN).//6.80E-12//133aa//28%//  
 P35500
- 30 C-PLACE1001100//Homo sapiens nephrin (NPHS1) mRNA, complete cds.//3.10E-46//323bp//84%//AF035835  
 C-PLACE1001114//HYPOTHETICAL BHLF1 PROTEIN.//9.20E-06//389aa//31%//P03181  
 C-PLACE1001123//INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).//  
 5.00E-08//95aa//31%//Q04941
- 35 C-PLACE1001183  
 C-PLACE1001229  
 C-PLACE1001231//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete  
 cds.//2.20E-137//918bp//80%//AF026554  
 C-PLACE1001340//MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRI-  
 AL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER)
- 40 (TRANSLOCASE OF OUTER MEMBRANE TOM70).//1.20E-23//231aa//31%//P23231  
 C-PLACE1001401//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE  
 FC RECEPTOR, BETA-SUBUNIT).//3.70E-18//148aa//39%//P13386  
 C-PLACE1001407
- 45 C-PLACE1001464//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2756bp//99%//X55740  
 C-PLACE1001500//Homo sapiens RecQ5 mRNA for DNA helicase, complete cds.//2.30E-271//1230bp//99%//  
 AB006533  
 C-PLACE1001516//240 KD PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL [CONTAINS: GLUTAMIC  
 ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-  
 4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)].//2.30E-08//274aa//28%//  
 Q28181
- 50 C-PLACE1001536  
 C-PLACE1001564//H.sapiens mRNA for HE6 Tm7 receptor.//5.10E-36//499bp//70%//X81892  
 C-PLACE1001655//Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, com-  
 plete cds.//0//1708bp//99%//AF043472
- 55 C-PLACE1001788  
 C-PLACE1001795//HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECUR-  
 SOR.//3.40E-20//159aa//40%//P47032  
 C-PLACE1001836//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEM-

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BRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E]//5.00E-27//134aa//47%/P10269  
 C-PLACE1001918//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-  
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-  
 NENT)//2.30E-53//339aa//33%/P32802  
 5 C-PLACE1001949//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38)//3.00E-75//315aa//44%/Q12697  
 C-PLACE1002080//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//0//1588bp//99%/AF039691  
 C-PLACE1002095  
 C-PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.//0//1202bp//99%/AF095791  
 10 C-PLACE1002329//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8//6.50E-105//213aa//45%/Q08509  
 C-PLACE1002355//COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN]//4.20E-12//131aa//40%/P01029  
 C-PLACE1002374//Human mRNA for pro-cathepsin L (major excreted protein MEP)//1.30E-313//1363bp//97%/X12451  
 15 C-PLACE1002518//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//2.50E-14//396bp//64%/AF064801  
 C-PLACE1002547//MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70)//2.30E-28//277aa//31%/P23231  
 20 C-PLACE1002726//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC)//2.80E-202//926bp//82%/AJ133128  
 C-PLACE1002905//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI)//2.40E-37//188aa//40%/P07106  
 25 C-PLACE1002911//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR//4.50E-39//345aa//32%/P32507  
 C-PLACE1002967//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGEC RECEPTOR, BETA-SUBUNIT)//4.60E-08//156aa//30%/Q01362  
 C-PLACE1003135//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-)//1.30E-47//210aa//49%/P08458  
 30 C-PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.//1.00E-294//1344bp//99%/AF069301  
 C-PLACE1003407//Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.//0//1965bp//99%/AF068227  
 C-PLACE1003428//Homo sapiens mRNA for VNN1 protein.//1.80E-142//676bp//72%/AJ132099  
 35 C-PLACE1003438  
 C-PLACE1003460  
 C-PLACE1003529//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT)//1.30E-09//281aa//22%/P11414  
 C-PLACE1003573//T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN)//3.70E-16//226aa//26%/P20937  
 40 C-PLACE1003598//TRP-ASP REPEATS CONTAINING PROTEIN RBA-1//1.80E-07//161aa//27%/P90917  
 C-PLACE1003644  
 C-PLACE1003737//TOLL PROTEIN PRECURSOR//5.40E-07//203aa//27%/P08953  
 C-PLACE1003772//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//2.40E-12//124aa//38%/P13983  
 45 C-PLACE1003839//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//8.10E-18//771bp//58%/AF095448  
 C-PLACE1003845//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)//3.40E-37//302aa//30%/Q57664  
 C-PLACE1003852//Homo sapiens mRNA for KIAA0758 protein, partial cds.//0//1667bp//99%/AB018301  
 50 C-PLACE1004028  
 C-PLACE1004078//Bovine mRNA for adseverin, complete cds.//0//2218bp//89%/D26549  
 C-PLACE1004166//CREB-BINDING PROTEIN//1.80E-12//147aa//35%/P45481  
 C-PLACE1004168//GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1//9.10E-62//485aa//32%/P25655  
 55 C-PLACE1004199  
 C-PLACE1004279//HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III//1.40E-08//166aa//30%/P30638  
 C-PLACE1004282//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL)//2.10E-11//

189aa//30%/P25234

C-PLACE1004305//RAS-RELATED PROTEIN RAC1.//9.60E-29//197aa//41%/P40792

C-PLACE1004441//Human G protein-coupled receptor (GPR1) gene, complete cds.//0//1880bp//98%/U13666

C-PLACE1004450//AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (LEUKEMIA AN-  
TIGEN CD13).//1.30E-91//562aa//35%/P15541C-PLACE1004482//Rattus norvegicus hematopoietic lineage switch 2 related protein (Hls2-rp) mRNA, complete  
cds.//1.90E-246//1643bp//83%/AF097723

C-PLACE1004492//VERPROLIN//3.30E-07//149aa//29%/P37370

C-PLACE1004519

C-PLACE1004520//Human pregnancy-specific beta-glycoprotein d mRNA, complete cds.//9.10E-279//882bp//  
88%/M20881C-PLACE1004630//Homo sapiens ten integrin EGF-like repeat domains protein precursor (ITGBL1) mRNA, com-  
plete cds.//1.00E-138//643bp//99%/AF072752

C-PLACE1004637

C-PLACE1004648//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-  
DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.40E-18//395aa//25%/P08640

C-PLACE1004816//Homo sapiens mRNA for Hakata antigen, complete cds.//1.00E-166//856bp//94%/D88587

C-PLACE1004887//GOLIATH PROTEIN (G1 PROTENN).//4.80E-33//179aa//47%/Q06003

C-PLACE1005003//PROSTASIN PRECURSOR (EC 3.4.21.-).//2.20E-52//269aa//41%/Q16651

C-PLACE1005005//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.//4.10E-261//  
1209bp//98%/AF032456

C-PLACE1005031//CHLORINE CHANNEL PROTEIN P64.//8.00E-92//205aa//87%/P35526

C-PLACE1005239//Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, PH4-17).//1.80E-235//1010bp//84%/  
AJ2233511C-PLACE1005250//Homo sapiens D-type cyclin-interacting protein 1 (DIP1) mRNA, complete cds.//0//1046bp//  
96%/AF082569

C-PLACE1005383//Homo sapiens UP50 mRNA, complete cds.//0//2019bp//99%/AF093118

C-PLACE1005410//Canis familiaris sec61 homologue mRNA, complete cds.//2.40E-204//673bp//89%/M96629

C-PLACE1005426//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds.//  
0//1629bp//95%/U18469C-PLACE1005519//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//4.60E-108//1070bp//73%/  
AF024636C-PLACE1005539//ACTIN POLYMERIZATION INHIBITOR (HEAT SHOCK 25 KD PROTEIN) (25-KD IAP).//  
3.10E-08//84aa//34%/Q00649C-PLACE1005544//Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.//2.00E-159//  
1237bp//76%/U89915

C-PLACE1005569//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%/AJ132502

C-PLACE1005601

C-PLACE1005660//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.90E-  
33//143aa//53%/P34280

C-PLACE1005669

C-PLACE1005682//B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).//4.90E-09//183aa//33%/P  
20749C-PLACE1005725//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//7.60E-17//295aa//  
27%/Q11073C-PLACE1005736//Human mRNA for BAS-GRIP protein.//0//2378bp//99%/E16311 C-PLACE1005745//ORM1  
PROTEIN.//2.40E-17//137aa//35%/P53224

C-PLACE1005768

C-PLACE1005815//COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).//1.50E-26//274aa//26%/P  
23508

C-PLACE1005878//Bovine chlorine channel protein (p64) mRNA, complete cds.//5.90E-137//889bp//85%/L16547

C-PLACE1005927//HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.//1.60E-38//333aa//  
33%/Q09875C-PLACE1006071//LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).//6.00E-08//215aa//26%/P  
02469C-PLACE1006073//Homo sapiens mRNA for glucuronyltransferase I, complete cds.//4.10E-316//1020bp//96%/  
AB009598

C-PLACE1006079//Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.//0//1379bp//97%/

AF028233

C-PLACE1006093

C-PLACE1006208//Homo sapiens nGAP mRNA, complete cds.//3.30E-151//694bp//100%//AF047711

C-PLACE1006219//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE).//3.50E-37//302aa//30%//Q57664

C-PLACE1006277//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502

C-PLACE1006290//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636

C-PLACE1006443//Homo sapiens PB39 mRNA, complete cds.//4.30E-98//553bp//70%//AF045584

C-PLACE1006515//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2846bp//99%//AB011148

C-PLACE1006716//30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ).//4.60E-25//181aa//35%//Q60994

C-PLACE1006786

C-PLACE1006809//SLS1 PROTEIN PRECURSOR.//9.10E-10//273aa//27%//P08124

C-PLACE1006959

C-PLACE1007028//Homo sapiens TDAG51/lp1 homologue 1 (TIH1) mRNA, complete cds.//1.40E-307//1423bp//99%//AF151100

C-PLACE1007040

C-PLACE1007077//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//2578bp//99%//AB023194

C-PLACE1007081//COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).//5.00E-20//247aa//34%//Q28107

C-PLACE1007096//PUTATIVE SUGAR TRANSPORT PROTEIN GUTA.//2.70E-17//174aa//27%//O34368

C-PLACE1007296//Human mRNA for a presumptive KDEL receptor.//1.10E-185//1038bp//91%//X55885

C-PLACE1007591

C-PLACE1007626//Homo sapiens unknown mRNA, complete cds.//3.00E-246//1122bp//99%//AF047439

C-PLACE1007702//Mus musculus TRA1 mRNA, complete cds.//7.50E-41//662bp//64%//D78335

C-PLACE1007845//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//4.80E-14//158aa//40%//P43636

C-PLACE1007881//HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.//3.10E-99//504aa//42%//Q19425

C-PLACE1007971

C-PLACE1008282//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).//7.10E-274//627aa//82%//P33279

C-PLACE1008297//MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).//1.30E-14//187aa//33%//P90648

C-PLACE1008359//BEM46 PROTEIN (FRAGMENT).//1.70E-50//289aa//42%//P54069

C-PLACE1008469

C-PLACE1008549//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//0//2274bp//99%//AF115403

C-PLACE1008657//Bovine mRNA for adseverin, complete cds.//7.80E-227//1246bp//90%//D26549

C-PLACE1008716//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//1888bp//99%//U15128

C-PLACE1008744//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM) (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).//4.80E-32//338aa//30%//Q01102

C-PLACE1008984

C-PLACE1008985//Mus musculus synaptotagmin VIII mRNA, partial cds.//3.80E-140//650bp//81%//U20107

C-PLACE1009067

C-PLACE1009196

C-PLACE1009279//cDNA encoding novel physiologically active protein which have serine protease activity.//6.60E-86//1414bp//64%//E12965

C-PLACE1009527//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//1.20E-87//585bp//83%//AJ133128

C-PLACE1009546

C-PLACE1009600//Mouse mRNA for tetracycline transporter-like protein, complete cds.//1.10E-264//924bp//88%//D88315

C-PLACE1009735

C-PLACE1009982//SALIVARY GILUE PROTEIN SGS-3 PRECURSOR.//5.20E-08//166aa//28%//P02840

C-PLACE1010011//Homo sapiens AAPT1-like protein mRNA, partial cds.//1.70E-237//1092bp//99%//AF047431

C-PLACE1010078//ORM1 PROTEIN.//3.70E-19//137aa//37%//P53224

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C-PLACE1010081//Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.//0//2033bp//99%//AF027706

C-PLACE1010251//FIBRILLIN 2 PRECURSOR.//1.70E-31//201aa//35%//Q61555

C-PLACE1010445

5 C-PLACE1010713//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//AF078850

C-PLACE1010784//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds.//2.30E-252//1146bp//99%//AF039686

10 C-PLACE1010827//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.90E-19//163aa//34%//P49020

C-PLACE1010968//PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE PHOSPHOHYDROLASE).//3.40E-30//690aa//26%//P16621

C-PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds.//0//2376bp//99%//AF094516

15 C-PLACE1011116//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.30E-09//234aa//27%//P08640

C-PLACE1011181//MSP1 PROTEIN HOMOLOG.//9.40E-82//353aa//47%//P54815

C-PLACE1011236//Mus musculus mRNA for RST, complete cds.//1.70E-90//1398bp//65%//AB005451

C-PLACE1011364//MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DYSTROPHY PROTEIN KINASE) (MDPK) (DM-KINASE) (DMK) (DMPK) (MT-PK).//2.20E-09//153aa//32%//Q09013

20 C-PLACE1011407//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.80E-133//342aa//59%//Q99676

C-PLACE1011516//HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//1.30E-13//139aa//34%//P53073

C-PLACE1011708//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1840bp//98%//AF034611

25 C-PLACE1011824//Human Ste20-like kinase (MST2) mRNA, complete cds.//6.40E-202//561bp//92%//U26424

C-PLACE1011978//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-194//547aa//57%//Q05481

C-PLACE2000118//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//3.20E-27//205aa//43%//P70315

30 C-PLACE2000219

C-PLACE3000181//Human protocadherin 42 mRNA, complete cds for abbreviated PC42.//0//2719bp//95%//L11370

C-PLACE3000213//COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR).//4.60E-68//317aa//34%//P19070

35 C-PLACE4000354//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).//1.00E-129//482aa//29%//P17927

C-PLACE4000455

C-SKNMC1000004

C-SKNMC1000014

40 C-SKNMC1000082//BRITTLE-1 PROTEIN PRECURSOR.//3.70E-31//307aa//130%//P29518

C-THYRO1000036//Homo sapiens collagen alpha 3 type IX (COL9A3) mRNA, complete cds.//1.20E-258//1376bp//93%//L41162

C-THYRO1000061//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.//1.40E-117//1126bp//74%//AB030505

45 C-THYRO1000099

C-THYRO1000196//Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.//0//1632bp//91%//AF016272

C-THYRO1000400//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 25795.//0//1893bp//99%//AL109665

C-THYRO1000580//ZINC FINGER PROTEIN 184 (FRAGMENT).//9.90E-114//279aa//59%//Q99676

50 C-THYRO1000584//EPIDIDYMI-SPECIFIC ALPHA-MANNOSIDASE (EC 3.2.1.24) (ALPHA-D-MANNOSIDE MANNOHYDROLASE) (135 KD PROTEIN).//5.40E-127//335aa//71%//Q28949

C-THYRO1000678//Homo sapiens Cx30 gene.//0//1741bp//97%//AJ005585

C-THYRO1000776//PROBABLE SULFATE PERMEASE SPBC3H7.02.//1.30E-68//442aa//36%//O74377

C-THYRO1000795//C.elegans mRNA for Oxoglutarate/malate carrier protein.//8.80E-42//821bp//63%//X76114

55 C-THYRO1000846

C-THYRO1000866//SHK1 KINASE-BINDING PROTEIN 1.//4.40E-91//449aa//44%//P78963

C-THYRO1000956//Human G protein-coupled receptor APJ gene, complete cds.//0//1583bp//99%//U03642

C-THYRO1000964//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.//1.10E-

- 34//759bp//63%//AF091624  
 C-THYRO1000999  
 C-THYRO1001063  
 5 C-THYRO1001071//GAMMA-ADAPTIN (GOLGI ADAPTOR HA1/AP1 ADAPTIN GAMMA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 GAMMA LARGE CHAIN).//8.20E-14//157aa//33%//P22892  
 C-THYRO1001102  
 C-THYRO1001113//Homo sapiens mRNA; cDNA DKFZp564E1616 (from clone DKFZp564E1616).//0//1361bp//99%//AL096713  
 10 C-THYRO1001128//Homo sapiens mRNA for hypothetical protein (C9orf9 gene).//6.40E-155//648bp//99%//AJ011375  
 C-THYRO1001205  
 C-THYRO1001237//PHYTOENE DEHYDROGENASE (EC 1.3.-.-) (PHYTOENE DESATURASE) (ALBINO-1 PROTEIN).//3.10E-13//346aa//22%//P21334  
 15 C-THYRO1001242//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//0//2468bp//99%//AF037339  
 C-THYRO1001266//Human sodium iodide symporter mRNA, complete cds.//7.20E-81//1466bp//62%//U66088  
 C-THYRO1001327  
 C-THYRO1001456//HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.//9.40E-32//355aa//31%//Q10555  
 20 C-THYRO1001457//H.sapiens mRNA for protein kinase C mu.//2.30E-218//1183bp//73%//X75756  
 C-THYRO1001471  
 C-THYRO1001478//CYTOCHROME B-245 HEAVY CHAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEUTROPHIL CYTOCHROME B, 91 KD POLYPEPTIDE) (CGD91-PHOX) (GP91-PHOX) (CYTOCHROME B(558) BETA CHAIN) (SUPEROXIDE-GENERATING NADPH OXIDASE HEAVY CHAIN SUBUNIT).//8.90E-50//296aa//35%//P04839  
 25 C-THYRO1001495  
 C-THYRO1001523//Homo sapiens mRNA for TM7XN1 protein.//0//3663bp//99%//AJ011001  
 C-THYRO1001529//SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2).//5.50E-25//115aa//53%//Q09925  
 30 C-THYRO1001593//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//3.10E-203//550aa//62%//P27448  
 C-THYRO1001608  
 C-THYRO1001641//Homo sapiens CGI-57 protein mRNA, complete cds.//0//1668bp//99%//AF151815  
 C-THYRO1001700//SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RECEPTOR INTERACTING PROTEIN).//9.70E-33//268aa//37%//Q60855  
 35 C-THYRO1001702//Mus musculus mRNA for myeloid associated differentiation protein.//1.50E-128//1204bp//73%//AJ001616  
 C-THYRO1001725  
 C-THYRO1001770//PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).//6.30E-20//169aa//35%//P53974  
 40 C-THYRO1001803  
 C-Y79AA1000030//Homo sapiens mRNA for Fe65L2, complete cds.//0//1828bp//100%//AB018247  
 C-Y79AA1000127  
 C-Y79AA1000207  
 C-Y79AA1000226  
 45 C-Y79AA1000270//Bos taurus vacuolar H+ ATPase subunit Ac45 mRNA, complete cds.//1.00E-271//1490bp//83%//U10039  
 C-Y79AA1000426//Mus musculus activin beta E subunit mRNA, complete cds.//7.70E-200//1533bp//78%//U96386  
 C-Y79AA1000521  
 C-Y79AA1000750  
 50 C-Y79AA1000776//Mus musculus mRNA for GSG1, complete cds.//2.40E-161//820bp//85%//D87325  
 C-Y79AA1000777//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.10E-48//283aa//38%//Q00808  
 C-Y79AA1000876//PROTEIN DISULHDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72).//1.60E-44//210aa//38%//P13667  
 55 C-Y79AA1000888//TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE).//1.50E-21//267aa//32%//P70973  
 C-Y79AA1000959//Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.//4.80E-283//1405bp//95%//AF093420  
 C-Y79AA1000967//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KI-

NASE I).//1.00E-77//359aa//44%//Q14012

C-Y79AA1001013

C-Y79AA1001056//Homo sapiens MAID protein mRNA, complete cds.//0//1475bp//99%//AF113535

C-Y79AA1001062//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//8.90E-12//132aa//38%//Q13829

C-Y79AA1001090//NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) (NF-KAPPA-B1 P84/NF-KAPPA-B1 P98)[CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT] (FRAGMENT).//4.50E-09//144aa//31%//Q63369

C-Y79AA1001212//Homo sapiens SL15 protein mRNA, complete cds.//6.30E-306//1388bp//99%//AF038961

C-Y79AA1001264//HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.//5.10E-106//351aa//58%//Q10005

C-Y79AA1001272//Homo sapiens retinoic acid repressible protein (RARG-1) mRNA, complete cds.//1.50E-183//867bp//98%//AF172066

C-Y79AA1001328//Mus musculus mRNA for DII3 protein, complete cds.//1.90E-263//1988bp//79%//AB013440

C-Y79AA1001426//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//6.20E-66//609aa//31%//P48751

C-Y79AA1001427//Homo sapiens cytochrome b5 reductase 1 (B5R.1) mRNA, complete cds.//0//1588bp//99%//AF169481

C-Y79AA1001430//Homo sapiens mRNA for KIAA0469 protein, complete cds.//0//2943bp//99%//AB007938

C-Y79AA1001523//Homo sapiens transcriptional intermediary factor 1 alpha mRNA, complete cds.//0//2263bp//99%//AF119042

C-Y79AA1001530//Human beta-tubulin gene (5-beta) with ten Alu family members.//0//1920bp//98%//X00734

C-Y79AA1001592

C-Y79AA1001727//CELL SURFACE A33 ANTIGEN PRECURSOR.//1.10E-13//286aa//27%//Q99795

C-Y79AA1001787//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//1.70E-133//544aa//37%//Q12697

C-Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.//3.70E-126//532bp//78%//D87325

C-Y79AA1001795//Homo sapiens mRNA for GalT4 protein.//2.30E-250//1137bp//99%//Y15061

C-Y79AA1001799//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//3.40E-54//182aa//39%//P23500

C-Y79AA1001803//Homo sapiens secretogranin III mRNA, complete cds.//0//1871bp//99%//AF078851

C-Y79AA1001863

C-Y79AA1002022//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//2.20E-06//140aa//26%//P32507

C-Y79AA1002058//Mus musculus Gng3lg mRNA, complete cds.//4.10E-167//1145bp//83%//AF069954

C-Y79AA1002121//HISTONE H1.//4.90E-12//114aa//35%//P35060

C-Y79AA1002129

C-Y79AA1002213//HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.//1.20E-98//262aa//41%//Q03567

C-Y79AA1002334//GLUCOSE REPRESSION MEDIATOR PROTEIN.//1.70E-10//333aa//23%//P14922

C-Y79AA1002373//Mus musculus mRNA for GSG1, complete cds.//7.20E-147//680bp//79%//D87325

C-Y79AA1002376//Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.//1.50E-304//1667bp//90%//U39045

C-Y79AA1002378//Homo sapiens zinc finger protein NY-REN-21 antigen mRNA, partial cds.//0//963bp//99%//AF155100

C-Y79AA1002381//Homo sapiens cell cycle related kinase mRNA, complete cds.//0//1791bp//98%//AF035013

## Claims

1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-829 and 2545, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides.
2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-829 and 2545, wherein said oligonucleotide comprises at least 15 nucleotides.
3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide com-

prising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence.3'-end nucleotide sequence is selected from the group consisting of:

SEQ ID NO:4 and SEQ ID NO:830  
 SEQ ID NO:5 and SEQ ID NO:831  
 SEQ ID NO:6 and SEQ ID NO:832  
 SEQ ID NO:7 and SEQ ID NO:833  
 SEQ ID NO:8 and SEQ ID NO:834  
 SEQ ID NO:9 and SEQ ID NO:835  
 SEQ ID NO:11 and SEQ ID NO:836  
 SEQ ID NO:12 and SEQ ID NO:837  
 SEQ ID NO:13 and SEQ ID NO:838  
 SEQ ID NO:14 and SEQ ID NO:839  
 SEQ ID NO:15 and SEQ ID NO:840  
 SEQ ID NO:16 and SEQ ID NO:841  
 SEQ ID NO:17 and SEQ ID NO:842  
 SEQ ID NO:18 and SEQ ID NO:843  
 SEQ ID NO:20 and SEQ ID NO:844  
 SEQ ID NO:22 and SEQ ID NO:845  
 SEQ ID NO:23 and SEQ ID NO:846  
 SEQ ID NO:24 and SEQ ID NO:847  
 SEQ ID NO:25 and SEQ ID NO:848  
 SEQ ID NO:26 and SEQ ID NO:849  
 SEQ ID NO:27 and SEQ ID NO:850  
 SEQ ID NO:28 and SEQ ID NO:851  
 SEQ ID NO:29 and SEQ ID NO:852  
 SEQ ID NO:30 and SEQ ID NO:853  
 SEQ ID NO:31 and SEQ ID NO:854  
 SEQ ID NO:32 and SEQ ID NO:855  
 SEQ ID NO:33 and SEQ ID NO:856  
 SEQ ID NO:34 and SEQ ID NO:857  
 SEQ ID NO:35 and SEQ ID NO:858  
 SEQ ID NO:36 and SEQ ID NO:859  
 SEQ ID NO:37 and SEQ ID NO:860  
 SEQ ID NO:39 and SEQ ID NO:861  
 SEQ ID NO:40 and SEQ ID NO:862  
 SEQ ID NO:41 and SEQ ID NO:863  
 SEQ ID NO:42 and SEQ ID NO:864  
 SEQ ID NO:44 and SEQ ID NO:865  
 SEQ ID NO:45 and SEQ ID NO:866  
 SEQ ID NO:46 and SEQ ID NO:867  
 SEQ ID NO:47 and SEQ ID NO:868



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SEQ ID NO:48 and SEQ ID NO:869  
SEQ ID NO:49 and SEQ ID NO:870  
SEQ ID NO:50 and SEQ ID NO:871  
SEQ ID NO:52 and SEQ ID NO:872  
SEQ ID NO:53 and SEQ ID NO:873  
SEQ ID NO:54 and SEQ ID NO:874  
SEQ ID NO:55 and SEQ ID NO:875  
SEQ ID NO:56 and SEQ ID NO:876  
SEQ ID NO:57 and SEQ ID NO:877  
SEQ ID NO:58 and SEQ ID NO:878  
SEQ ID NO:59 and SEQ ID NO:879  
SEQ ID NO:60 and SEQ ID NO:880  
SEQ ID NO:61 and SEQ ID NO:881  
SEQ ID NO:62 and SEQ ID NO:882  
SEQ ID NO:63 and SEQ ID NO:883  
SEQ ID NO:64 and SEQ ID NO:884  
SEQ ID NO:65 and SEQ ID NO:885  
SEQ ID NO:66 and SEQ ID NO:886  
SEQ ID NO:67 and SEQ ID NO:887  
SEQ ID NO:69 and SEQ ID NO:888  
SEQ ID NO:70 and SEQ ID NO:889  
SEQ ID NO:71 and SEQ ID NO:890  
SEQ ID NO:72 and SEQ ID NO:891  
SEQ ID NO:73 and SEQ ID NO:892  
SEQ ID NO:74 and SEQ ID NO:893  
SEQ ID NO:75 and SEQ ID NO:894  
SEQ ID NO:76 and SEQ ID NO:895  
SEQ ID NO:77 and SEQ ID NO:896  
SEQ ID NO:78 and SEQ ID NO:897  
SEQ ID NO:79 and SEQ ID NO:898  
SEQ ID NO:80 and SEQ ID NO:899  
SEQ ID NO:81 and SEQ ID NO:900  
SEQ ID NO:82 and SEQ ID NO:901  
SEQ ID NO:83 and SEQ ID NO:902  
SEQ ID NO:84 and SEQ ID NO:903  
SEQ ID NO:85 and SEQ ID NO:904  
SEQ ID NO:86 and SEQ ID NO:905  
SEQ ID NO:87 and SEQ ID NO:906  
SEQ ID NO:88 and SEQ ID NO:907  
SEQ ID NO:89 and SEQ ID NO:908  
SEQ ID NO:90 and SEQ ID NO:909  
SEQ ID NO:91 and SEQ ID NO:910  
SEQ ID NO:92 and SEQ ID NO:911  
SEQ ID NO:93 and SEQ ID NO:912  
SEQ ID NO:94 and SEQ ID NO:913  
SEQ ID NO:95 and SEQ ID NO:914  
SEQ ID NO:96 and SEQ ID NO:915  
SEQ ID NO:97 and SEQ ID NO:916  
SEQ ID NO:98 and SEQ ID NO:917  
SEQ ID NO:99 and SEQ ID NO:918  
SEQ ID NO:100 and SEQ ID NO:919  
SEQ ID NO:101 and SEQ ID NO:920

5 SEQ ID NO:102 and SEQ ID NO:921  
 SEQ ID NO:103 and SEQ ID NO:922  
 SEQ ID NO:104 and SEQ ID NO:923  
 SEQ ID NO:105 and SEQ ID NO:924  
 SEQ ID NO:106 and SEQ ID NO:925  
 SEQ ID NO:107 and SEQ ID NO:926  
 10 SEQ ID NO:108 and SEQ ID NO:927  
 SEQ ID NO:109 and SEQ ID NO:928  
 SEQ ID NO:110 and SEQ ID NO:929  
 SEQ ID NO:111 and SEQ ID NO:930  
 SEQ ID NO:112 and SEQ ID NO:931  
 SEQ ID NO:113 and SEQ ID NO:932  
 15 SEQ ID NO:114 and SEQ ID NO:933  
 SEQ ID NO:115 and SEQ ID NO:934  
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 SEQ ID NO:2545 and SEQ ID NO:2546

4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.

5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.

6. A substantially pure protein encoded by polynucleotide of claim 4.

7. A partial peptide of the protein of claim 6.

8. An isolated polynucleotide selected from the group consisting of

(a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following SEQ ID NOs:

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(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence

**EP 1 130 094 A2**

set forth in any one of the following SEQ ID NOs:

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SEQ ID NO:4073, SEQ ID NO:4075, SEQ ID NO:4077  
SEQ ID NO:4079, SEQ ID NO:4081, SEQ ID NO:4083, SEQ ID NO:4085, SEQ ID NO:4087,  
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50 SEQ ID NO:4100, SEQ ID NO:4102, SEQ ID NO:4104, SEQ ID NO:4106, SEQ ID NO:4108,  
SEQ ID NO:4110, SEQ ID NO:4112, SEQ ID NO:4114, SEQ ID NO:4116, SEQ ID NO:4118,  
SEQ ID NO:4120, SEQ ID NO:4122, SEQ ID NO:4124, SEQ ID NO:4126, SEQ ID NO:4128,  
SEQ ID NO:4130, SEQ ID NO:4133, SEQ ID NO:4135, SEQ ID NO:4138, SEQ ID NO:4141,  
SEQ ID NO:4143, SEQ ID NO:4145, SEQ ID NO:4147, SEQ ID NO:4149, SEQ ID NO:4151,  
55 SEQ ID NO:4153, SEQ ID NO:4156, SEQ ID NO:4158, SEQ ID NO:4160, SEQ ID NO:4162,

SEQ ID NO:4164, SEQ ID NO:4166

SEQ ID NO:4169, SEQ ID NO:4171, SEQ ID NO:4173, SEQ ID NO:4175, SEQ ID NO:4177,  
and SEQ ID NO:4179

- (c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences of (b);
  - (d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);
  - (e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);
  - (f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence of (a).
9. A substantially pure protein encoded by the polynucleotide of claim 8.
  10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.
  11. A vector comprising the polynucleotide of claim 5 or 8.
  12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
  13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
  14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.
  15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.
  16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.
  17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.
  18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.
  19. A method for synthesizing a polynucleotide, the method comprising:
    - a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
    - b) recovering the synthesized product.
  20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.
  21. The method of claim 19, wherein the complementary strand is obtainable by PCR.
  22. A method for detecting the polynucleotide of claim 8, the method comprising:
    - a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
    - b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.
  23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium

on which the database is stored.

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Figure 1

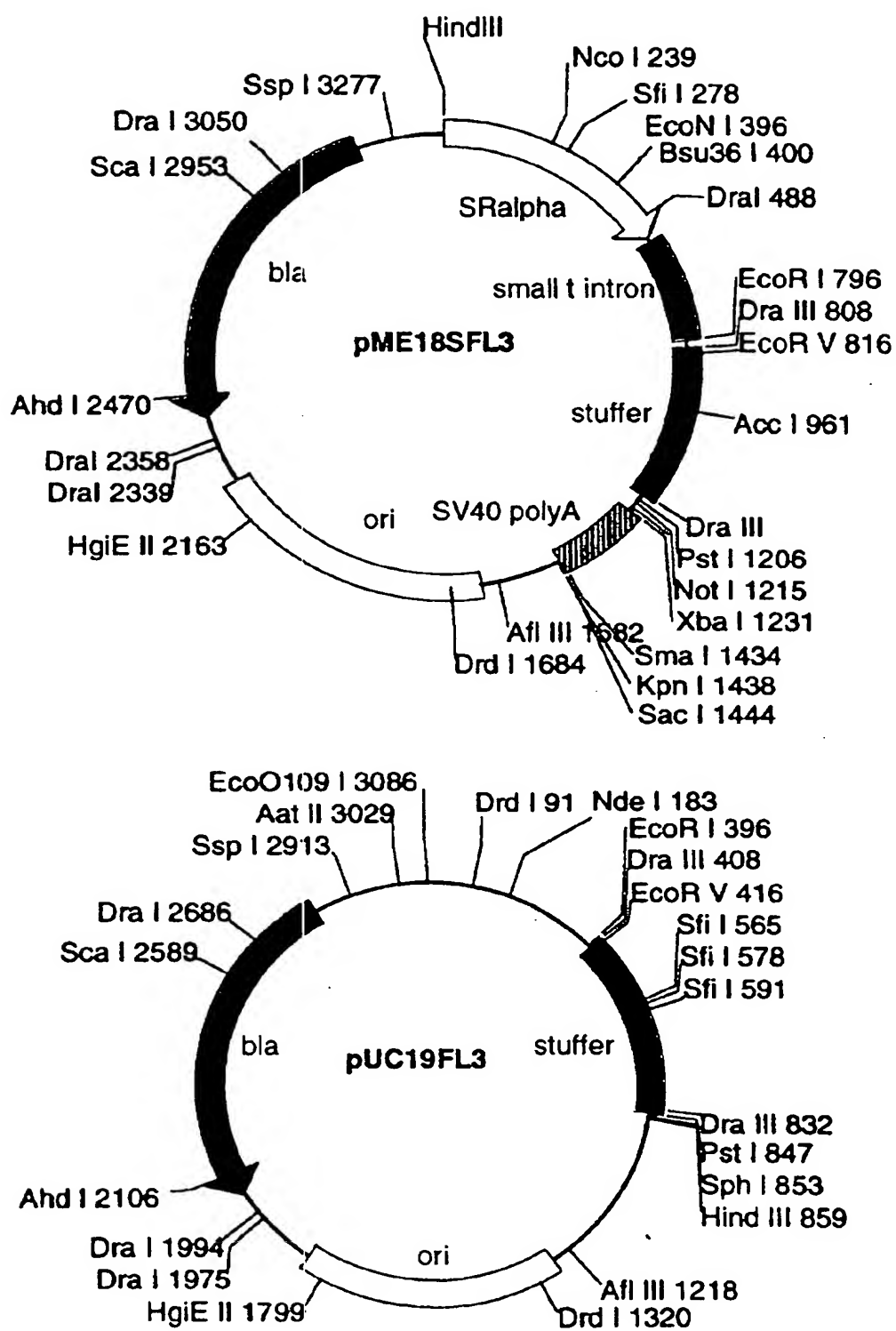


Figure 2

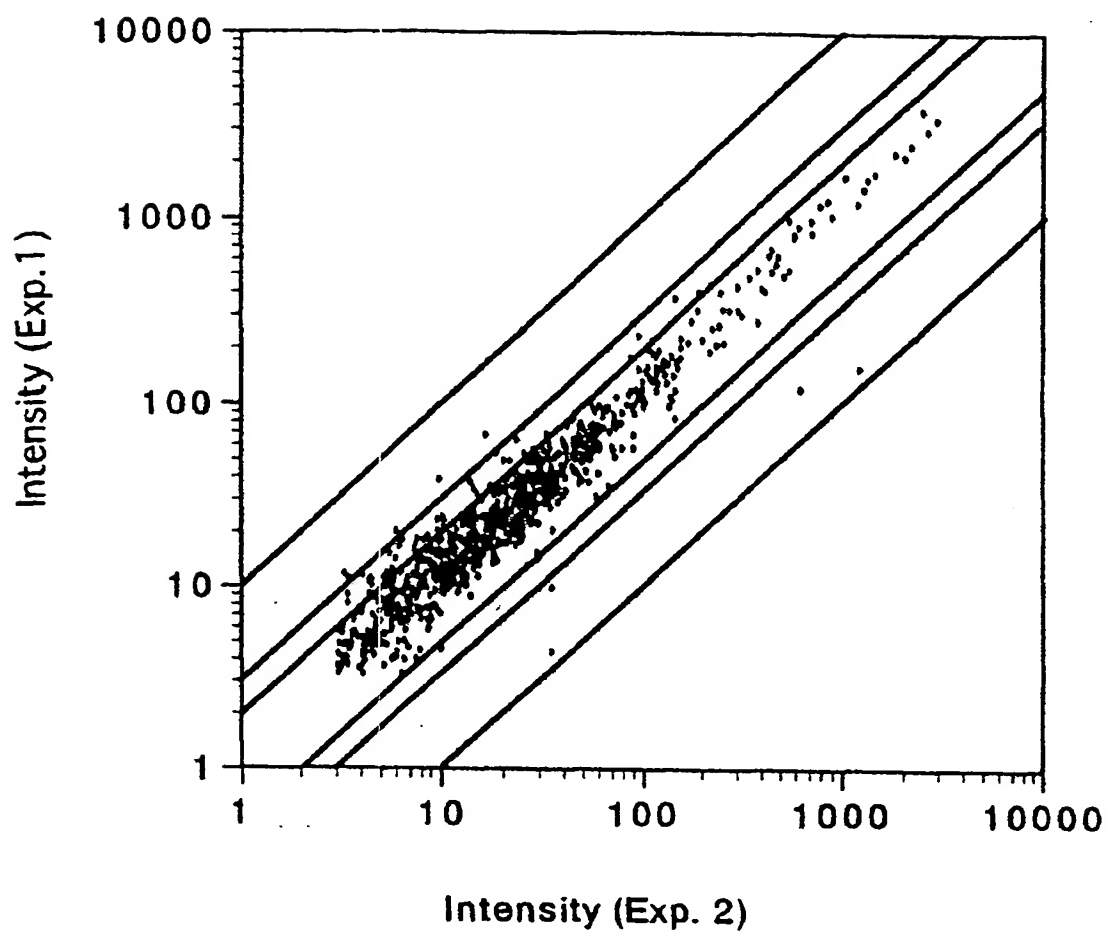
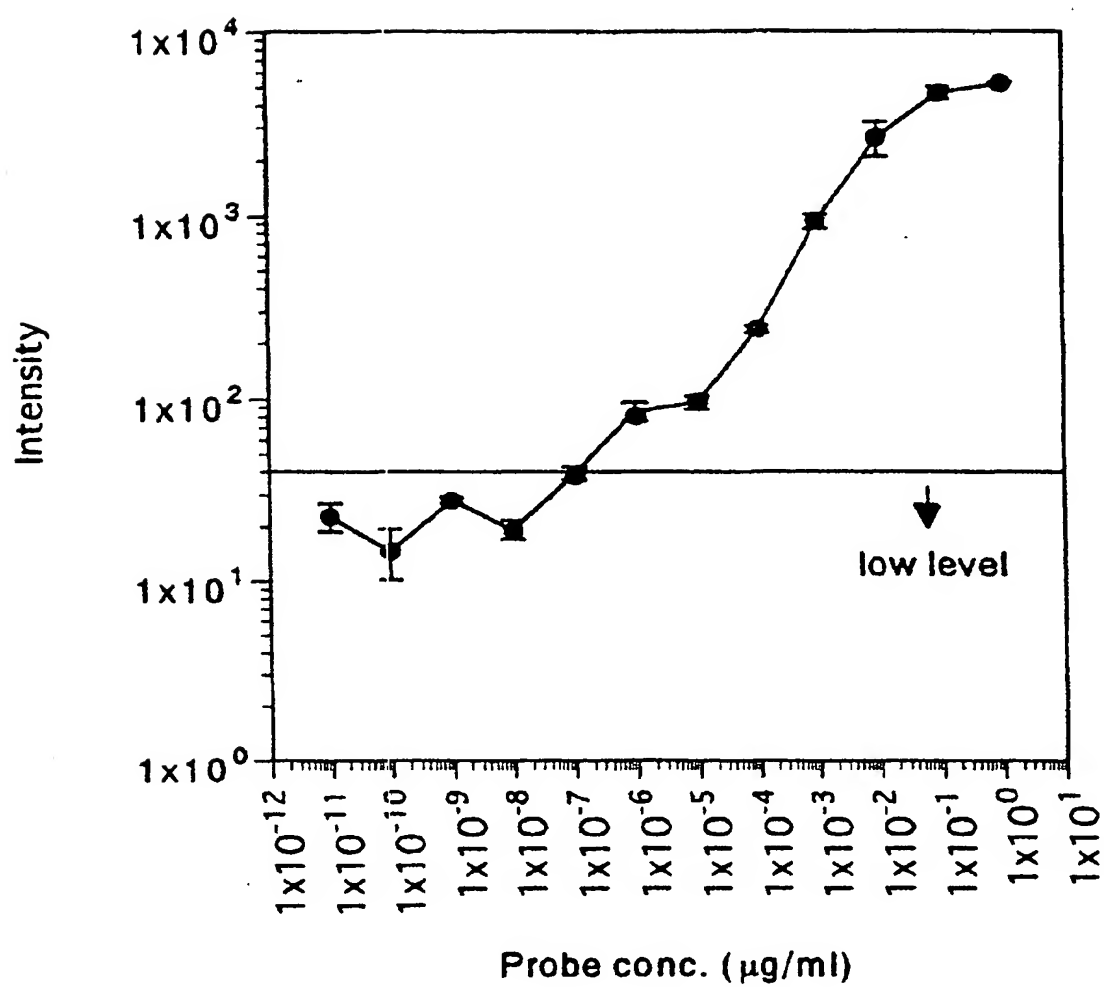
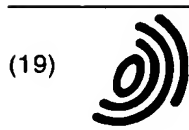


Figure 3



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Office européen des brevets



(11) **EP 1 130 094 A3**

(12) **EUROPEAN PATENT APPLICATION**

(88) Date of publication A3:  
21.11.2001 Bulletin 2001/47

(43) Date of publication A2:  
05.09.2001 Bulletin 2001/36

(21) Application number: 00114089.6

(22) Date of filing: 07.07.2000

(51) Int Cl.7: **C12N 15/12, C12N 15/11,  
C12N 15/10, C12N 15/70,  
C12N 15/85, C12N 5/10,  
C12N 1/21, C07K 14/47,  
C07K 16/18, C12Q 1/68**

(84) Designated Contracting States:  
**AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU  
MC NL PT SE**  
Designated Extension States:  
**AL LT LV MK RO SI**

(30) Priority: 08.07.1999 JP 19448699  
11.01.2000 JP 2000118774  
02.05.2000 JP 2000183765

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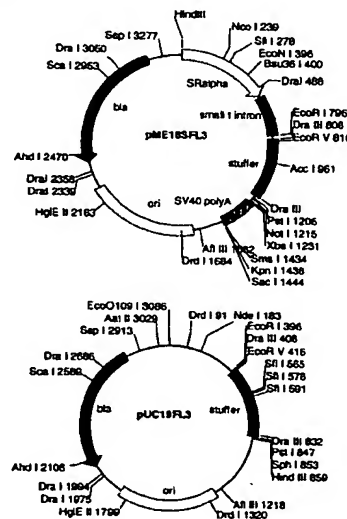
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(54) **Primers for synthesizing full length cDNA clones and their use**

(57) Primers for synthesizing full length cDNAs and their use are provided.

830 cDNA encoding a human protein has been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA have been determined. Furthermore, primers for synthesizing the full length cDNA have been provided to clarify the function of the protein encoded by the cDNA. The full length cDNA of the present invention containing the translation start site provides information useful for analyzing the functions of the protein.

Figure 1



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## EUROPEAN SEARCH REPORT

Application Number  
EP 00 11 4089

DOCUMENTS CONSIDERED TO BE RELEVANT			
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<del>The present search report has been drawn up for all claims</del>			
Place of search		Date of completion of the search	Examiner
THE HAGUE		19 June 2001	HORNIG H.
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document			

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### CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

☐ Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):

☐ No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

### LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet B

☐ All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.

☐ As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.

☐ Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:

☒ None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:

1,2,4-22 - partially



European Patent  
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# EUROPEAN SEARCH REPORT

Application Number  
EP 00 11 4089

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<p>--- -/-</p>			
<p>The present search report has been drawn up for all claims</p>			
Place of search <b>THE HAGUE</b>		Date of completion of the search <b>19 June 2001</b>	Examiner <b>HORNIG H.</b>
<p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons</p> <p>&amp; : member of the same patent family, corresponding document</p>			

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LACK OF UNITY OF INVENTION  
SHEET B

Application Number  
EP 00 11 4089

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

1. Claims: (1,2,4-22)-partially

Use of an oligonucleotide as a primer for synthesizing the polynucleotide sequence of clone BNGH41000020 comprising the nucleotide sequence of SEQ ID No. 1, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides; a primer set for synthesizing polynucleotides, the primer set comprises an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide sequence SEQ ID No. 1; a polynucleotide which can be synthesized with said primer set; a protein coding for said polynucleotide; a partial peptide of said protein; an isolated polynucleotide comprises (a) a coding region of SEQ ID No. 3595 or (b) a polynucleotide comprises a nucleotide sequence encoding a protein comprising the amino acid SEQ ID No. 3596; an antibody against said protein; a vector comprises said polynucleotide; a transformant expressing said vector; an antisense polynucleotide against said polynucleotide; a method of synthesizing said polynucleotide; a method for detecting said polynucleotide;

2. Claims: (1,2,4-22)-partially

Idem as subject 1 but limited to BNGH41000087; SEQ ID No. 2, SEQ ID Nos. 4078 and 4079;

3. Claims: (1,2,4-22)-partially

Idem as subject 1 but limited to BNGH41000091; SEQ ID No. 3, SEQ ID Nos. 3597 and 3598;

4. Claims: (1-22)-partially and as far as applicable

Idem as subject 1 but limited to HEMBA1000006, respectively SEQ ID nos. 2547 and 2548; a primer set for synthesizing polynucleotides, the primer set comprises a combination of an oligonucleotide comprises a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotide comprises at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence 3'-end nucleotide sequence is selected from SEQ ID Nos. 4 and 830;

5.-830. Claims: (1-23)-partially

Idem as subject 4 but limited to HEMBA1000121 to



European Patent  
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LACK OF UNITY OF INVENTION  
SHEET B

Application Number  
EP 00 11 4089

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

NT2RP2006580; (Invention 5 is limited to HEMBA1000121 respectively SEQ ID Nos. 5,831,2551 and 2552; Invention 6 is limited to HEMBA100128 respectively SEQ ID Nos. 6,832,2553 and 2554; ..... Invention 830 is limited to NT2RP2006580 respectively SEQ ID Nos. 2545, 2546, 4178 and 4179).

831. Claim: 23-complete

A database of nucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotides of clone BNGH41000020 (SEQ ID Nos. 1, 3595 and 3596) to NT2RP2006580 (SEQ ID Nos. 2545,2546,4178 and 4179).



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Office

# EUROPEAN SEARCH REPORT

Application Number  
EP 00 11 4089

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
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The present search report has been drawn up for all claims			
Place of search <b>THE HAGUE</b>		Date of completion of the search <b>19 June 2001</b>	Examiner <b>HORNIG H.</b>
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	

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ANNEX TO THE EUROPEAN SEARCH REPORT  
ON EUROPEAN PATENT APPLICATION NO.

EP 00 11 4089

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report.  
The members are as contained in the European Patent Office EDP file on  
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19-06-2001

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